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(54) Title: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS

(57) Abstract: The present invention provides purified human polynucleotides for diagnostics and therapeutics (dithp). Also encompassed are the polypeptides (DITHP) encoded by dithp. The invention also provides for the use of dithp, or complements, oligonucleotides, or fragments thereof in diagnostic assays. The invention further provides for vectors and host cells containing dithp for the expression of DITHP. The invention additionally provides for the use of isolated and purified DITHP to induce antibodies and to screen libraries of compounds and the use of anti-DITHP antibodies in diagnostic assays. Also provided are microarrays containing dithp and methods of use.

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## MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS

### TECHNICAL FIELD

5       The present invention relates to human molecules and to the use of these sequences in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, the expression of human molecules.

### BACKGROUND OF THE INVENTION

10       The human genome is comprised of thousands of genes, many encoding gene products that function in the maintenance and growth of the various cells and tissues in the body. Aberrant expression or mutations in these genes and their products is the cause of, or is associated with, a variety of human diseases such as cancer and other cell proliferative disorders, autoimmune/inflammatory disorders, infections, developmental disorders, endocrine disorders,  
15       metabolic disorders, neurological disorders, gastrointestinal disorders, transport disorders, and connective tissue disorders. The identification of these genes and their products is the basis of an ever-expanding effort to find markers for early detection of diseases, and targets for their prevention and treatment. Therefore, these genes and their products are useful as diagnostics and therapeutics. These genes may encode, for example, enzyme molecules, molecules associated with growth and  
20       development, biochemical pathway molecules, extracellular information transmission molecules, receptor molecules, intracellular signaling molecules, membrane transport molecules, protein modification and maintenance molecules, nucleic acid synthesis and modification molecules, adhesion molecules, antigen recognition molecules, secreted and extracellular matrix molecules, cytoskeletal molecules, ribosomal molecules, electron transfer associated molecules, transcription  
25       factor molecules, chromatin molecules, cell membrane molecules, and organelle associated molecules.

For example, cancer represents a type of cell proliferative disorder that affects nearly every tissue in the body. A wide variety of molecules, either aberrantly expressed or mutated, can be the cause of, or involved with, various cancers because tissue growth involves complex and ordered  
30       patterns of cell proliferation, cell differentiation, and apoptosis. Cell proliferation must be regulated to maintain both the number of cells and their spatial organization. This regulation depends upon the appropriate expression of proteins which control cell cycle progression in response to extracellular signals such as growth factors and other mitogens, and intracellular cues such as DNA damage or nutrient starvation. Molecules which directly or indirectly modulate cell cycle progression fall into  
35       several categories, including growth factors and their receptors, second messenger and signal transduction proteins, oncogene products, tumor-suppressor proteins, and mitosis-promoting factors. Aberrant expression or mutations in any of these gene products can result in cell proliferative

disorders such as cancer. Oncogenes are genes generally derived from normal genes that, through abnormal expression or mutation, can effect the transformation of a normal cell to a malignant one (oncogenesis). Oncoproteins, encoded by oncogenes, can affect cell proliferation in a variety of ways and include growth factors, growth factor receptors, intracellular signal transducers, nuclear transcription factors, and cell-cycle control proteins. In contrast, tumor-suppressor genes are involved in inhibiting cell proliferation. Mutations which cause reduced function or loss of function in tumor-suppressor genes result in aberrant cell proliferation and cancer. Although many different genes and their products have been found to be associated with cell proliferative disorders such as cancer, many more may exist that are yet to be discovered.

DNA-based arrays can provide a simple way to explore the expression of a single polymorphic gene or a large number of genes. When the expression of a single gene is explored, DNA-based arrays are employed to detect the expression of specific gene variants. For example, a p53 tumor suppressor gene array is used to determine whether individuals are carrying mutations that predispose them to cancer. A cytochrome p450 gene array is useful to determine whether individuals have one of a number of specific mutations that could result in increased drug metabolism, drug resistance or drug toxicity.

DNA-based array technology is especially relevant for the rapid screening of expression of a large number of genes. There is a growing awareness that gene expression is affected in a global fashion. A genetic predisposition, disease or therapeutic treatment may affect, directly or indirectly, the expression of a large number of genes. In some cases the interactions may be expected, such as when the genes are part of the same signaling pathway. In other cases, such as when the genes participate in separate signaling pathways, the interactions may be totally unexpected. Therefore, DNA-based arrays can be used to investigate how genetic predisposition, disease, or therapeutic treatment affects the expression of a large number of genes.

### Enzyme Molecules

The cellular processes of biogenesis and biodegradation involve a number of key enzyme classes including oxidoreductases, transferases, hydrolases, lyases, isomerases, and ligases. These enzyme classes are each comprised of numerous substrate-specific enzymes having precise and well regulated functions. These enzymes function by facilitating metabolic processes such as glycolysis, the tricarboxylic cycle, and fatty acid metabolism; synthesis or degradation of amino acids, steroids, phospholipids, alcohols, etc.; regulation of cell signalling, proliferation, inflammation, apoptosis, etc., and through catalyzing critical steps in DNA replication and repair, and the process of translation.

#### Oxidoreductases

Many pathways of biogenesis and biodegradation require oxidoreductase (dehydrogenase or reductase) activity, coupled to the reduction or oxidation of a donor or acceptor cofactor. Potential



cofactors include cytochromes, oxygen, disulfide, iron-sulfur proteins, flavin adenine dinucleotide (FAD), and the nicotinamide adenine dinucleotides NAD and NADP (Newsholme, E.A. and A.R. Leech (1983) Biochemistry for the Medical Sciences, John Wiley and Sons, Chichester, U.K., pp. 779-793). Reductase activity catalyzes the transfer of electrons between substrate(s) and cofactor(s) with concurrent oxidation of the cofactor. The reverse dehydrogenase reaction catalyzes the reduction of a cofactor and consequent oxidation of the substrate. Oxidoreductase enzymes are a broad superfamily of proteins that catalyze numerous reactions in all cells of organisms ranging from bacteria to plants to humans. These reactions include metabolism of sugar, certain detoxification reactions in the liver, and the synthesis or degradation of fatty acids, amino acids, glucocorticoids, estrogens, androgens, and prostaglandins. Different family members are named according to the direction in which their reactions are typically catalyzed; thus they may be referred to as oxidoreductases, oxidases, reductases, or dehydrogenases. In addition, family members often have distinct cellular localizations, including the cytosol, the plasma membrane, mitochondrial inner or outer membrane, and peroxisomes.

Short-chain alcohol dehydrogenases (SCADs) are a family of dehydrogenases that only share 15% to 30% sequence identity, with similarity predominantly in the coenzyme binding domain and the substrate binding domain. In addition to the well-known role in detoxification of ethanol, SCADs are also involved in synthesis and degradation of fatty acids, steroids, and some prostaglandins, and are therefore implicated in a variety of disorders such as lipid storage disease, myopathy, SCAD deficiency, and certain genetic disorders. For example, retinol dehydrogenase is a SCAD-family member (Simon, A. et al. (1995) *J. Biol. Chem.* 270:1107-1112) that converts retinol to retinal, the precursor of retinoic acid. Retinoic acid, a regulator of differentiation and apoptosis, has been shown to down-regulate genes involved in cell proliferation and inflammation (Chai, X. et al. (1995) *J. Biol. Chem.* 270:3900-3904). In addition, retinol dehydrogenase has been linked to hereditary eye diseases such as autosomal recessive childhood-onset severe retinal dystrophy (Simon, A. et al. (1996) *Genomics* 36:424-430).

Propagation of nerve impulses, modulation of cell proliferation and differentiation, induction of the immune response, and tissue homeostasis involve neurotransmitter metabolism (Weiss, B. (1991) *Neurotoxicology* 12:379-386; Collins, S.M. et al. (1992) *Ann. N.Y. Acad. Sci.* 664:415-424; Brown, J.K. and H. Imam (1991) *J. Inherit. Metab. Dis.* 14:436-458). Many pathways of neurotransmitter metabolism require oxidoreductase activity, coupled to reduction or oxidation of a cofactor, such as NAD<sup>+</sup>/NADH (Newsholme, E.A. and A.R. Leech (1983) Biochemistry for the Medical Sciences, John Wiley and Sons, Chichester, U.K. pp. 779-793). Degradation of catecholamines (epinephrine or norepinephrine) requires alcohol dehydrogenase (in the brain) or aldehyde dehydrogenase (in peripheral tissue). NAD<sup>+</sup>-dependent aldehyde dehydrogenase oxidizes 5-hydroxyindole-3-acetate (the product of 5-hydroxytryptamine (serotonin) metabolism) in the brain,

blood platelets, liver and pulmonary endothelium (Newsholme, supra, p. 786). Other neurotransmitter degradation pathways that utilize NAD<sup>+</sup>/NADH-dependent oxidoreductase activity include those of L-DOPA (precursor of dopamine, a neuronal excitatory compound), glycine (an inhibitory neurotransmitter in the brain and spinal cord), histamine (liberated from mast cells during the inflammatory response), and taurine (an inhibitory neurotransmitter of the brain stem, spinal cord and retina) (Newsholme, supra, pp. 790, 792). Epigenetic or genetic defects in neurotransmitter metabolic pathways can result in a spectrum of disease states in different tissues including Parkinson disease and inherited myoclonus (McCance, K.L. and S.E. Huether (1994) Pathophysiology, Mosby-Year Book, Inc., St. Louis MO, pp. 402-404; Gundlach, A.L. (1990) FASEB J. 4:2761-2766).

Tetrahydrofolate is a derivatized glutamate molecule that acts as a carrier, providing activated one-carbon units to a wide variety of biosynthetic reactions, including synthesis of purines, pyrimidines, and the amino acid methionine. Tetrahydrofolate is generated by the activity of a holoenzyme complex called tetrahydrofolate synthase, which includes three enzyme activities: tetrahydrofolate dehydrogenase, tetrahydrofolate cyclohydrolase, and tetrahydrofolate synthetase. Thus, tetrahydrofolate dehydrogenase plays an important role in generating building blocks for nucleic and amino acids, crucial to proliferating cells.

3-Hydroxyacyl-CoA dehydrogenase (3HACD) is involved in fatty acid metabolism. It catalyzes the reduction of 3-hydroxyacyl-CoA to 3-oxoacyl-CoA, with concomitant oxidation of NAD to NADH, in the mitochondria and peroxisomes of eukaryotic cells. In peroxisomes, 3HACD and enoyl-CoA hydratase form an enzyme complex called bifunctional enzyme, defects in which are associated with peroxisomal bifunctional enzyme deficiency. This interruption in fatty acid metabolism produces accumulation of very-long chain fatty acids, disrupting development of the brain, bone, and adrenal glands. Infants born with this deficiency typically die within 6 months (Watkins, P. et al. (1989) J. Clin. Invest. 83:771-777; Online Mendelian Inheritance in Man (OMIM), #261515). The neurodegeneration that is characteristic of Alzheimer's disease involves development of extracellular plaques in certain brain regions. A major protein component of these plaques is the peptide amyloid- $\beta$  (A $\beta$ ), which is one of several cleavage products of amyloid precursor protein (APP). 3HACD has been shown to bind the A $\beta$  peptide, and is overexpressed in neurons affected in Alzheimer's disease. In addition, an antibody against 3HACD can block the toxic effects of A $\beta$  in a cell culture model of Alzheimer's disease (Yan, S. et al. (1997) Nature 389:689-695; OMIM, #602057).

Steroids, such as estrogen, testosterone, corticosterone, and others, are generated from a common precursor, cholesterol, and are interconverted into one another. A wide variety of enzymes act upon cholesterol, including a number of dehydrogenases. Steroid dehydrogenases, such as the hydroxysteroid dehydrogenases, are involved in hypertension, fertility, and cancer (Duax, W.L. and D. Ghosh (1997) Steroids 62:95-100). One such dehydrogenase is 3-oxo-5- $\alpha$ -steroid dehydrogenase

(OASD), a microsomal membrane protein highly expressed in prostate and other androgen-responsive tissues. OASD catalyzes the conversion of testosterone into dihydrotestosterone, which is the most potent androgen. Dihydrotestosterone is essential for the formation of the male phenotype during embryogenesis, as well as for proper androgen-mediated growth of tissues such as the prostate and male genitalia. A defect in OASD that prevents the conversion of testosterone into dihydrotestosterone leads to a rare form of male pseudohermaphroditis, characterized by defective formation of the external genitalia (Andersson, S. et al. (1991) *Nature* 354:159-161; Labrie, F. et al. (1992) *Endocrinology* 131:1571-1573; OMIM #264600). Thus, OASD plays a central role in sexual differentiation and androgen physiology.

17 $\beta$ -hydroxysteroid dehydrogenase (17 $\beta$ HSD6) plays an important role in the regulation of the male reproductive hormone, dihydrotestosterone (DHTT). 17 $\beta$ HSD6 acts to reduce levels of DHTT by oxidizing a precursor of DHTT, 3 $\alpha$ -diol, to androsterone which is readily glucuronidated and removed from tissues. 17 $\beta$ HSD6 is active with both androgen and estrogen substrates when expressed in embryonic kidney 293 cells. At least five other isozymes of 17 $\beta$ HSD have been identified that catalyze oxidation and/or reduction reactions in various tissues with preferences for different steroid substrates (Biswas, M.G. and D.W. Russell (1997) *J. Biol. Chem.* 272:15959-15966). For example, 17 $\beta$ HSD1 preferentially reduces estradiol and is abundant in the ovary and placenta. 17 $\beta$ HSD2 catalyzes oxidation of androgens and is present in the endometrium and placenta. 17 $\beta$ HSD3 is exclusively a reductive enzyme in the testis (Geissler, W.M. et al. (1994) *Nat. Genet.* 7:34-39). An excess of androgens such as DHTT can contribute to certain disease states such as benign prostatic hyperplasia and prostate cancer.

Oxidoreductases are components of the fatty acid metabolism pathways in mitochondria and peroxisomes. The main beta-oxidation pathway degrades both saturated and unsaturated fatty acids, while the auxiliary pathway performs additional steps required for the degradation of unsaturated fatty acids. The auxiliary beta-oxidation enzyme 2,4-dienoyl-CoA reductase catalyzes the removal of even-numbered double bonds from unsaturated fatty acids prior to their entry into the main beta-oxidation pathway. The enzyme may also remove odd-numbered double bonds from unsaturated fatty acids (Koivuranta, K.T. et al. (1994) *Biochem. J.* 304:787-792; Smeland, T.E. et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:6673-6677). 2,4-dienoyl-CoA reductase is located in both mitochondria and peroxisomes. Inherited deficiencies in mitochondrial and peroxisomal beta-oxidation enzymes are associated with severe diseases, some of which manifest themselves soon after birth and lead to death within a few years. Defects in beta-oxidation are associated with Reye's syndrome, Zellweger syndrome, neonatal adrenoleukodystrophy, infantile Refsum's disease, acyl-CoA oxidase deficiency, and bifunctional protein deficiency (Suzuki, Y. et al. (1994) *Am. J. Hum. Genet.* 54:36-43; Hoefler, *supra*; Cotran, R.S. et al. (1994) *Robbins Pathologic Basis of Disease*, W.B. Saunders Co., Philadelphia PA, p.866). Peroxisomal beta-oxidation is impaired in cancerous tissue. Although

neoplastic human breast epithelial cells have the same number of peroxisomes as do normal cells, fatty acyl-CoA oxidase activity is lower than in control tissue (el Bouhtoury, F. et al. (1992) J. Pathol. 166:27-35). Human colon carcinomas have fewer peroxisomes than normal colon tissue and have lower fatty-acyl-CoA oxidase and bifunctional enzyme (including enoyl-CoA hydratase) activities than normal tissue (Cable, S. et al. (1992) Virchows Arch. B Cell Pathol. Incl. Mol. Pathol. 62:221-226). Another important oxidoreductase is isocitrate dehydrogenase, which catalyzes the conversion of isocitrate to  $\alpha$ -ketoglutarate, a substrate of the citric acid cycle. Isocitrate dehydrogenase can be either NAD or NADP dependent, and is found in the cytosol, mitochondria, and peroxisomes. Activity of isocitrate dehydrogenase is regulated developmentally, and by hormones,

10 neurotransmitters, and growth factors.

Hydroxypyruvate reductase (HPR), a peroxisomal 2-hydroxyacid dehydrogenase in the glycolate pathway, catalyzes the conversion of hydroxypyruvate to glycerate with the oxidation of both NADH and NADPH. The reverse dehydrogenase reaction reduces  $\text{NAD}^+$  and  $\text{NADP}^+$ . HPR recycles nucleotides and bases back into pathways leading to the synthesis of ATP and GTP. ATP and GTP are used to produce DNA and RNA and to control various aspects of signal transduction and energy metabolism. Inhibitors of purine nucleotide biosynthesis have long been employed as antiproliferative agents to treat cancer and viral diseases. HPR also regulates biochemical synthesis of serine and cellular serine levels available for protein synthesis.

The mitochondrial electron transport (or respiratory) chain is a series of oxidoreductase-type enzyme complexes in the mitochondrial membrane that is responsible for the transport of electrons from NADH through a series of redox centers within these complexes to oxygen, and the coupling of this oxidation to the synthesis of ATP (oxidative phosphorylation). ATP then provides the primary source of energy for driving a cell's many energy-requiring reactions. The key complexes in the respiratory chain are NADH:ubiquinone oxidoreductase (complex I), succinate:ubiquinone oxidoreductase (complex II), cytochrome  $c_1$ -b oxidoreductase (complex III), cytochrome c oxidase (complex IV), and ATP synthase (complex V) (Alberts, B. et al. (1994) Molecular Biology of the Cell, Garland Publishing, Inc., New York NY, pp. 677-678). All of these complexes are located on the inner matrix side of the mitochondrial membrane except complex II, which is on the cytosolic side. Complex II transports electrons generated in the citric acid cycle to the respiratory chain. The electrons generated by oxidation of succinate to fumarate in the citric acid cycle are transferred through electron carriers in complex II to membrane bound ubiquinone (Q). Transcriptional regulation of these nuclear-encoded genes appears to be the predominant means for controlling the biogenesis of respiratory enzymes. Defects and altered expression of enzymes in the respiratory chain are associated with a variety of disease conditions.

35 Other dehydrogenase activities using NAD as a cofactor are also important in mitochondrial function. 3-hydroxyisobutyrate dehydrogenase (3HBD), important in valine catabolism, catalyzes the

NAD-dependent oxidation of 3-hydroxyisobutyrate to methylmalonate semialdehyde within mitochondria. Elevated levels of 3-hydroxyisobutyrate have been reported in a number of disease states, including ketoacidosis, methylmalonic acidemia, and other disorders associated with deficiencies in methylmalonate semialdehyde dehydrogenase (Rougraff, P.M. et al. (1989) J. Biol.

5 Chem. 264:5899-5903).

Another mitochondrial dehydrogenase important in amino acid metabolism is the enzyme isovaleryl-CoA-dehydrogenase (IVD). IVD is involved in leucine metabolism and catalyzes the oxidation of isovaleryl-CoA to 3-methylcrotonyl-CoA. Human IVD is a tetrameric flavoprotein that is encoded in the nucleus and synthesized in the cytosol as a 45 kDa precursor with a mitochondrial

10 import signal sequence. A genetic deficiency, caused by a mutation in the gene encoding IVD, results in the condition known as isovaleric acidemia. This mutation results in inefficient mitochondrial import and processing of the IVD precursor (Vockley, J. et al. (1992) J. Biol. Chem. 267:2494-2501).

#### Transferases

15 Transferases are enzymes that catalyze the transfer of molecular groups. The reaction may involve an oxidation, reduction, or cleavage of covalent bonds, and is often specific to a substrate or to particular sites on a type of substrate. Transferases participate in reactions essential to such functions as synthesis and degradation of cell components, regulation of cell functions including cell signaling, cell proliferation, inflammation, apoptosis, secretion and excretion. Transferases are

20 involved in key steps in disease processes involving these functions. Transferases are frequently classified according to the type of group transferred. For example, methyl transferases transfer one-carbon methyl groups, amino transferases transfer nitrogenous amino groups, and similarly denominated enzymes transfer aldehyde or ketone, acyl, glycosyl, alkyl or aryl, isoprenyl, saccharyl, phosphorous-containing, sulfur-containing, or selenium-containing groups, as well as small

25 enzymatic groups such as Coenzyme A.

Acyl transferases include peroxisomal carnitine octanoyl transferase, which is involved in the fatty acid beta-oxidation pathway, and mitochondrial carnitine palmitoyl transferases, involved in fatty acid metabolism and transport. Choline O-acetyl transferase catalyzes the biosynthesis of the neurotransmitter acetylcholine.

30 Amino transferases play key roles in protein synthesis and degradation, and they contribute to other processes as well. For example, the amino transferase 5-aminolevulinic acid synthase catalyzes the addition of succinyl-CoA to glycine, the first step in heme biosynthesis. Other amino transferases participate in pathways important for neurological function and metabolism. For example, glutamine-phenylpyruvate amino transferase, also known as glutamine transaminase K (GTK),

35 catalyzes several reactions with a pyridoxal phosphate cofactor. GTK catalyzes the reversible conversion of L-glutamine and phenylpyruvate to 2-oxoglutaramate and L-phenylalanine. Other

amino acid substrates for GTK include L-methionine, L-histidine, and L-tyrosine. GTK also catalyzes the conversion of kynurenine to kynurenic acid, a tryptophan metabolite that is an antagonist of the N-methyl-D-aspartate (NMDA) receptor in the brain and may exert a neuromodulatory function. Alteration of the kynurenine metabolic pathway may be associated with several neurological disorders. GTK also plays a role in the metabolism of halogenated xenobiotics conjugated to glutathione, leading to nephrotoxicity in rats and neurotoxicity in humans. GTK is expressed in kidney, liver, and brain. Both human and rat GTKs contain a putative pyridoxal phosphate binding site (ExPASy ENZYME: EC 2.6.1.64; Perry, S.J. et al. (1993) *Mol. Pharmacol.* 43:660-665; Perry, S. et al. (1995) *FEBS Lett.* 360:277-280; and Alberati-Giani, D. et al. (1995) *J. Neurochem.* 64:1448-1455). A second amino transferase associated with this pathway is kynurenine/ $\alpha$ -amino adipate amino transferase (AadAT). AadAT catalyzes the reversible conversion of  $\alpha$ -amino adipate and  $\alpha$ -ketoglutarate to  $\alpha$ -ketoadipate and L-glutamate during lysine metabolism. AadAT also catalyzes the transamination of kynurenine to kynurenic acid. A cytosolic AadAT is expressed in rat kidney, liver, and brain (Nakatani, Y. et al. (1970) *Biochim. Biophys. Acta* 198:219-228; Buchli, R. et al. (1995) *J. Biol. Chem.* 270:29330-29335).

Glycosyl transferases include the mammalian UDP-glucuronosyl transferases, a family of membrane-bound microsomal enzymes catalyzing the transfer of glucuronic acid to lipophilic substrates in reactions that play important roles in detoxification and excretion of drugs, carcinogens, and other foreign substances. Another mammalian glycosyl transferase, mammalian UDP-galactose-ceramide galactosyl transferase, catalyzes the transfer of galactose to ceramide in the synthesis of galactocerebrosides in myelin membranes of the nervous system. The UDP-glycosyl transferases share a conserved signature domain of about 50 amino acid residues (PROSITE: PDOC00359, <http://expasy.hcuge.ch/sprot/prosite.html>).

Methyl transferases are involved in a variety of pharmacologically important processes. Nicotinamide N-methyl transferase catalyzes the N-methylation of nicotinamides and other pyridines, an important step in the cellular handling of drugs and other foreign compounds. Phenylethanolamine N-methyl transferase catalyzes the conversion of noradrenalin to adrenalin. 6-O-methylguanine-DNA methyl transferase reverses DNA methylation, an important step in carcinogenesis. Uroporphyrin-III C-methyl transferase, which catalyzes the transfer of two methyl groups from S-adenosyl-L-methionine to uroporphyrinogen III, is the first specific enzyme in the biosynthesis of cobalamin, a dietary enzyme whose uptake is deficient in pernicious anemia. Protein-arginine methyl transferases catalyze the posttranslational methylation of arginine residues in proteins, resulting in the mono- and dimethylation of arginine on the guanidino group. Substrates include histones, myelin basic protein, and heterogeneous nuclear ribonucleoproteins involved in mRNA processing, splicing, and transport. Protein-arginine methyl transferase interacts with proteins upregulated by mitogens, with proteins involved in chronic lymphocytic leukemia, and with

interferon, suggesting an important role for methylation in cytokine receptor signaling (Lin, W.-J. et al. (1996) *J. Biol. Chem.* 271:15034-15044; Abramovich, C. et al. (1997) *EMBO J.* 16:260-266; and Scott, H.S. et al. (1998) *Genomics* 48:330-340).

Phosphotransferases catalyze the transfer of high-energy phosphate groups and are important in energy-requiring and -releasing reactions. The metabolic enzyme creatine kinase catalyzes the reversible phosphate transfer between creatine/creatine phosphate and ATP/ADP. Glycocyamine kinase catalyzes phosphate transfer from ATP to guanidoacetate, and arginine kinase catalyzes phosphate transfer from ATP to arginine. A cysteine-containing active site is conserved in this family (PROSITE: PDOC00103).

Prenyl transferases are heterodimers, consisting of an alpha and a beta subunit, that catalyze the transfer of an isoprenyl group. An example of a prenyl transferase is the mammalian protein farnesyl transferase. The alpha subunit of farnesyl transferase consists of 5 repeats of 34 amino acids each, with each repeat containing an invariant tryptophan (PROSITE: PDOC00703).

Saccharyl transferases are glycosylating enzymes involved in a variety of metabolic processes.

Oligosaccharyl transferase-48, for example, is a receptor for advanced glycation endproducts. Accumulation of these endproducts is observed in vascular complications of diabetes, macrovascular disease, renal insufficiency, and Alzheimer's disease (Thornalley, P.J. (1998) *Cell Mol. Biol. (Noisy-Le-Grand)* 44:1013-1023).

Coenzyme A (CoA) transferase catalyzes the transfer of CoA between two carboxylic acids. Succinyl CoA:3-oxoacid CoA transferase, for example, transfers CoA from succinyl-CoA to a recipient such as acetoacetate. Acetoacetate is essential to the metabolism of ketone bodies, which accumulate in tissues affected by metabolic disorders such as diabetes (PROSITE: PDOC00980).

#### Hydrolases

Hydrolysis is the breaking of a covalent bond in a substrate by introduction of a molecule of water. The reaction involves a nucleophilic attack by the water molecule's oxygen atom on a target bond in the substrate. The water molecule is split across the target bond, breaking the bond and generating two product molecules. Hydrolases participate in reactions essential to such functions as synthesis and degradation of cell components, and for regulation of cell functions including cell signaling, cell proliferation, inflammation, apoptosis, secretion and excretion. Hydrolases are involved in key steps in disease processes involving these functions. Hydrolytic enzymes, or hydrolases, may be grouped by substrate specificity into classes including phosphatases, peptidases, lysophospholipases, phosphodiesterases, glycosidases, and glyoxalases.

Phosphatases hydrolytically remove phosphate groups from proteins, an energy-providing step that regulates many cellular processes, including intracellular signaling pathways that in turn control cell growth and differentiation, cell-cell contact, the cell cycle, and oncogenesis.

Lysophospholipases (LPLs) regulate intracellular lipids by catalyzing the hydrolysis of ester

bonds to remove an acyl group, a key step in lipid degradation. Small LPL isoforms, approximately 15-30 kD, function as hydrolases; larger isoforms function both as hydrolases and transacylases. A particular substrate for LPLs, lysophosphatidylcholine, causes lysis of cell membranes. LPL activity is regulated by signaling molecules important in numerous pathways, including the inflammatory response.

Peptidases, also called proteases, cleave peptide bonds that form the backbone of peptide or protein chains. Proteolytic processing is essential to cell growth, differentiation, remodeling, and homeostasis as well as inflammation and immune response. Since typical protein half-lives range from hours to a few days, peptidases are continually cleaving precursor proteins to their active form, removing signal sequences from targeted proteins, and degrading aged or defective proteins. Peptidases function in bacterial, parasitic, and viral invasion and replication within a host. Examples of peptidases include trypsin and chymotrypsin (components of the complement cascade and the blood-clotting cascade) lysosomal cathepsins, calpains, pepsin, renin, and chymosin (Beynon, R.J. and J.S. Bond (1994) Proteolytic Enzymes: A Practical Approach, Oxford University Press, New York NY, pp. 1-5).

The phosphodiesterases catalyze the hydrolysis of one of the two ester bonds in a phosphodiester compound. Phosphodiesterases are therefore crucial to a variety of cellular processes. Phosphodiesterases include DNA and RNA endo- and exo-nucleases, which are essential to cell growth and replication as well as protein synthesis. Another phosphodiesterase is acid sphingomyelinase, which hydrolyzes the membrane phospholipid sphingomyelin to ceramide and phosphorylcholine. Phosphorylcholine is used in the synthesis of phosphatidylcholine, which is involved in numerous intracellular signaling pathways. Ceramide is an essential precursor for the generation of gangliosides, membrane lipids found in high concentration in neural tissue. Defective acid sphingomyelinase phosphodiesterase leads to a build-up of sphingomyelin molecules in lysosomes, resulting in Niemann-Pick disease.

Glycosidases catalyze the cleavage of hemiacetyl bonds of glycosides, which are compounds that contain one or more sugar. Mammalian lactase-phlorizin hydrolase, for example, is an intestinal enzyme that splits lactose. Mammalian beta-galactosidase removes the terminal galactose from gangliosides, glycoproteins, and glycosaminoglycans, and deficiency of this enzyme is associated with a gangliosidosis known as Morquio disease type B. Vertebrate lysosomal alpha-glucosidase, which hydrolyzes glycogen, maltose, and isomaltose, and vertebrate intestinal sucrase-isomaltase, which hydrolyzes sucrose, maltose, and isomaltose, are widely distributed members of this family with highly conserved sequences at their active sites.

The glyoxylase system is involved in gluconeogenesis, the production of glucose from storage compounds in the body. It consists of glyoxylase I, which catalyzes the formation of S-D-lactoylglutathione from methyglyoxal, a side product of triose-phosphate energy metabolism, and



glyoxylase II, which hydrolyzes S-D-lactoylglutathione to D-lactic acid and reduced glutathione. Glyoxylases are involved in hyperglycemia, non-insulin-dependent diabetes mellitus, the detoxification of bacterial toxins, and in the control of cell proliferation and microtubule assembly.

### Lyases

5 Lyases are a class of enzymes that catalyze the cleavage of C-C, C-O, C-N, C-S, C-(halide), P-O or other bonds without hydrolysis or oxidation to form two molecules, at least one of which contains a double bond (Stryer, L. (1995) Biochemistry W.H. Freeman and Co. New York, NY p.620). Lyases are critical components of cellular biochemistry with roles in metabolic energy production including fatty acid metabolism, as well as other diverse enzymatic processes. Further  
10 classification of lyases reflects the type of bond cleaved as well as the nature of the cleaved group.

The group of C-C lyases include carboxyl-lyases (decarboxylases), aldehyde-lyases (aldolases), oxo-acid-lyases and others. The C-O lyase group includes hydro-lyases, lyases acting on polysaccharides and other lyases. The C-N lyase group includes ammonia-lyases, amidine-lyases, amine-lyases (deaminases) and other lyases.

15 Proper regulation of lyases is critical to normal physiology. For example, mutation induced deficiencies in the uroporphyrinogen decarboxylase can lead to photosensitive cutaneous lesions in the genetically-linked disorder familial porphyria cutanea tarda (Mendez, M. et al. (1998) Am. J. Genet. 63:1363-1375). It has also been shown that adenosine deaminase (ADA) deficiency stems from genetic mutations in the ADA gene, resulting in the disorder severe combined  
20 immunodeficiency disease (SCID) (Hershfield, M.S. (1998) Semin. Hematol. 35:291-298).

### Isomerases

Isomerases are a class of enzymes that catalyze geometric or structural changes within a molecule to form a single product. This class includes racemases and epimerases, cis-trans-isomerases, intramolecular oxidoreductases, intramolecular transferases (mutases) and intramolecular  
25 lyases. Isomerases are critical components of cellular biochemistry with roles in metabolic energy production including glycolysis, as well as other diverse enzymatic processes (Stryer, L. (1995) Biochemistry, W.H. Freeman and Co., New York NY, pp.483-507).

Racemases are a subset of isomerases that catalyze inversion of a molecules configuration around the asymmetric carbon atom in a substrate having a single center of asymmetry, thereby  
30 interconverting two racemers. Epimerases are another subset of isomerases that catalyze inversion of configuration around an asymmetric carbon atom in a substrate with more than one center of symmetry, thereby interconverting two epimers. Racemases and epimerases can act on amino acids and derivatives, hydroxy acids and derivatives, as well as carbohydrates and derivatives. The interconversion of UDP-galactose and UDP-glucose is catalyzed by UDP-galactose-4'-epimerase.  
35 Proper regulation and function of this epimerase is essential to the synthesis of glycoproteins and glycolipids. Elevated blood galactose levels have been correlated with UDP-galactose-4'-epimerase

deficiency in screening programs of infants (Gitzelmann, R. (1972) *Helv. Paediat. Acta* 27:125-130).

Oxidoreductases can be isomerases as well. Oxidoreductases catalyze the reversible transfer of electrons from a substrate that becomes oxidized to a substrate that becomes reduced. This class of enzymes includes dehydrogenases, hydroxylases, oxidases, oxygenases, peroxidases, and  
5 reductases. Proper maintenance of oxidoreductase levels is physiologically important. For example, genetically-linked deficiencies in lipoamide dehydrogenase can result in lactic acidosis (Robinson, B.H. et al. (1977) *Pediat. Res.* 11:1198-1202).

Another subgroup of isomerases are the transferases (or mutases). Transferases transfer a chemical group from one compound (the donor) to another compound (the acceptor). The types of  
10 groups transferred by these enzymes include acyl groups, amino groups, phosphate groups (phosphotransferases or phosphomutases), and others. The transferase carnitine palmitoyltransferase is an important component of fatty acid metabolism. Genetically-linked deficiencies in this transferase can lead to myopathy (Scriver, C.R. et al. (1995) The Metabolic and Molecular Basis of Inherited Disease, McGraw-Hill, New York NY, pp.1501-1533).

15 Yet another subgroup of isomerases are the topoisomerases. Topoisomerases are enzymes that affect the topological state of DNA. For example, defects in topoisomerases or their regulation can affect normal physiology. Reduced levels of topoisomerase II have been correlated with some of the DNA processing defects associated with the disorder ataxia-telangiectasia (Singh, S.P. et al. (1988) *Nucleic Acids Res.* 16:3919-3929).

## 20 Ligases

Ligases catalyze the formation of a bond between two substrate molecules. The process involves the hydrolysis of a pyrophosphate bond in ATP or a similar energy donor. Ligases are classified based on the nature of the type of bond they form, which can include carbon-oxygen, carbon-sulfur, carbon-nitrogen, carbon-carbon and phosphoric ester bonds.

25 Ligases forming carbon-oxygen bonds include the aminoacyl-transfer RNA (tRNA) synthetases which are important RNA-associated enzymes with roles in translation. Protein biosynthesis depends on each amino acid forming a linkage with the appropriate tRNA. The aminoacyl-tRNA synthetases are responsible for the activation and correct attachment of an amino acid with its cognate tRNA. The 20 aminoacyl-tRNA synthetase enzymes can be divided into two  
30 structural classes, and each class is characterized by a distinctive topology of the catalytic domain. Class I enzymes contain a catalytic domain based on the nucleotide-binding Rossmann fold. Class II enzymes contain a central catalytic domain, which consists of a seven-stranded antiparallel  $\beta$ -sheet motif, as well as N- and C- terminal regulatory domains. Class II enzymes are separated into two groups based on the heterodimeric or homodimeric structure of the enzyme; the latter group is further  
35 subdivided by the structure of the N- and C-terminal regulatory domains (Hartlein, M. and S. Cusack (1995) *J. Mol. Evol.* 40:519-530). Autoantibodies against aminoacyl-tRNAs are generated by

patients with dermatomyositis and polymyositis, and correlate strongly with complicating interstitial lung disease (ILD). These antibodies appear to be generated in response to viral infection, and coxsackie virus has been used to induce experimental viral myositis in animals.

Ligases forming carbon-sulfur bonds (Acid-thiol ligases) mediate a large number of cellular biosynthetic intermediary metabolism processes involve intermolecular transfer of carbon atom-containing substrates (carbon substrates). Examples of such reactions include the tricarboxylic acid cycle, synthesis of fatty acids and long-chain phospholipids, synthesis of alcohols and aldehydes, synthesis of intermediary metabolites, and reactions involved in the amino acid degradation pathways. Some of these reactions require input of energy, usually in the form of conversion of ATP to either ADP or AMP and pyrophosphate.

In many cases, a carbon substrate is derived from a small molecule containing at least two carbon atoms. The carbon substrate is often covalently bound to a larger molecule which acts as a carbon substrate carrier molecule within the cell. In the biosynthetic mechanisms described above, the carrier molecule is coenzyme A. Coenzyme A (CoA) is structurally related to derivatives of the nucleotide ADP and consists of 4'-phosphopantetheine linked via a phosphodiester bond to the alpha phosphate group of adenosine 3',5'-bisphosphate. The terminal thiol group of 4'-phosphopantetheine acts as the site for carbon substrate bond formation. The predominant carbon substrates which utilize CoA as a carrier molecule during biosynthesis and intermediary metabolism in the cell are acetyl, succinyl, and propionyl moieties, collectively referred to as acyl groups. Other carbon substrates include enoyl lipid, which acts as a fatty acid oxidation intermediate, and carnitine, which acts as an acetyl-CoA flux regulator/ mitochondrial acyl group transfer protein. Acyl-CoA and acetyl-CoA are synthesized in the cell by acyl-CoA synthetase and acetyl-CoA synthetase, respectively.

Activation of fatty acids is mediated by at least three forms of acyl-CoA synthetase activity: i) acetyl-CoA synthetase, which activates acetate and several other low molecular weight carboxylic acids and is found in muscle mitochondria and the cytosol of other tissues; ii) medium-chain acyl-CoA synthetase, which activates fatty acids containing between four and eleven carbon atoms (predominantly from dietary sources), and is present only in liver mitochondria; and iii) acyl CoA synthetase, which is specific for long chain fatty acids with between six and twenty carbon atoms, and is found in microsomes and the mitochondria. Proteins associated with acyl-CoA synthetase activity have been identified from many sources including bacteria, yeast, plants, mouse, and man. The activity of acyl-CoA synthetase may be modulated by phosphorylation of the enzyme by cAMP-dependent protein kinase.

Ligases forming carbon-nitrogen bonds include amide synthases such as glutamine synthetase (glutamate-ammonia ligase) that catalyzes the amination of glutamic acid to glutamine by ammonia using the energy of ATP hydrolysis. Glutamine is the primary source for the amino group in various amide transfer reactions involved in de novo pyrimidine nucleotide synthesis and in purine

and pyrimidine ribonucleotide interconversions. Overexpression of glutamine synthetase has been observed in primary liver cancer (Christa, L. et al. (1994) Gastroent. 106:1312-1320).

Acid-amino-acid ligases (peptide synthases) are represented by the ubiquitin proteases which are associated with the ubiquitin conjugation system (UCS), a major pathway for the degradation of cellular proteins in eukaryotic cells and some bacteria. The UCS mediates the elimination of abnormal proteins and regulates the half-lives of important regulatory proteins that control cellular processes such as gene transcription and cell cycle progression. In the UCS pathway, proteins targeted for degradation are conjugated to a ubiquitin (Ub), a small heat stable protein. Ub is first activated by a ubiquitin-activating enzyme (E1), and then transferred to one of several Ub-conjugating enzymes (E2). E2 then links the Ub molecule through its C-terminal glycine to an internal lysine (acceptor lysine) of a target protein. The ubiquitinated protein is then recognized and degraded by proteasome, a large, multisubunit proteolytic enzyme complex, and ubiquitin is released for reutilization by ubiquitin protease. The UCS is implicated in the degradation of mitotic cyclic kinases, oncoproteins, tumor suppressor genes such as p53, viral proteins, cell surface receptors associated with signal transduction, transcriptional regulators, and mutated or damaged proteins (Ciechanover, A. (1994) Cell 79:13-21). A murine proto-oncogene, Unp, encodes a nuclear ubiquitin protease whose overexpression leads to oncogenic transformation of NIH3T3 cells, and the human homolog of this gene is consistently elevated in small cell tumors and adenocarcinomas of the lung (Gray, D.A. (1995) Oncogene 10:2179-2183).

Cyclo-ligases and other carbon-nitrogen ligases comprise various enzymes and enzyme complexes that participate in the de novo pathways to purine and pyrimidine biosynthesis. Because these pathways are critical to the synthesis of nucleotides for replication of both RNA and DNA, many of these enzymes have been the targets of clinical agents for the treatment of cell proliferative disorders such as cancer and infectious diseases.

Purine biosynthesis occurs de novo from the amino acids glycine and glutamine, and other small molecules. Three of the key reactions in this process are catalyzed by a trifunctional enzyme composed of glycinamide-ribonucleotide synthetase (GARS), aminoimidazole ribonucleotide synthetase (AIRS), and glycinamide ribonucleotide transformylase (GART). Together these three enzymes combine ribosylamine phosphate with glycine to yield phosphoribosyl aminoimidazole, a precursor to both adenylylate and guanylate nucleotides. This trifunctional protein has been implicated in the pathology of Downs syndrome (Aimi, J. et al. (1990) Nucleic Acid Res. 18:6665-6672). Adenylosuccinate synthetase catalyzes a later step in purine biosynthesis that converts inosinic acid to adenylosuccinate, a key step on the path to ATP synthesis. This enzyme is also similar to another carbon-nitrogen ligase, argininosuccinate synthetase, that catalyzes a similar reaction in the urea cycle (Powell, S.M. et al. (1992) FEBS Lett. 303:4-10).

Like the de novo biosynthesis of purines, de novo synthesis of the pyrimidine nucleotides

uridylylate and cytidylylate also arises from a common precursor, in this instance the nucleotide orotidylylate derived from orotate and phosphoribosyl pyrophosphate (PPRP). Again a trifunctional enzyme comprising three carbon-nitrogen ligases plays a key role in the process. In this case the enzymes aspartate transcarbamylase (ATCase), carbamyl phosphate synthetase II, and dihydroorotase  
5 (DHOase) are encoded by a single gene called CAD. Together these three enzymes combine the initial reactants in pyrimidine biosynthesis, glutamine, CO<sub>2</sub> and ATP to form dihydroorotate, the precursor to orotate and orotidylylate (Iwahana, H. et al. (1996) *Biochem. Biophys. Res. Commun.* 219:249-255). Further steps then lead to the synthesis of uridine nucleotides from orotidylylate. Cytidine nucleotides are derived from uridine-5'-triphosphate (UTP) by the amidation of UTP using  
10 glutamine as the amino donor and the enzyme CTP synthetase. Regulatory mutations in the human CTP synthetase are believed to confer multi-drug resistance to agents widely used in cancer therapy (Yamauchi, M. et al. (1990) *EMBO J.* 9:2095-2099).

Ligases forming carbon-carbon bonds include the carboxylases acetyl-CoA carboxylase and pyruvate carboxylase. Acetyl-CoA carboxylase catalyzes the carboxylation of acetyl-CoA from CO<sub>2</sub>  
15 and H<sub>2</sub>O using the energy of ATP hydrolysis. Acetyl-CoA carboxylase is the rate-limiting step in the biogenesis of long-chain fatty acids. Two isoforms of acetyl-CoA carboxylase, types I and types II, are expressed in human in a tissue-specific manner (Ha, J. et al. (1994) *Eur. J. Biochem.* 219:297-306). Pyruvate carboxylase is a nuclear-encoded mitochondrial enzyme that catalyzes the conversion of pyruvate to oxaloacetate, a key intermediate in the citric acid cycle.

Ligases forming phosphoric ester bonds include the DNA ligases involved in both DNA replication and repair. DNA ligases seal phosphodiester bonds between two adjacent nucleotides in a DNA chain using the energy from ATP hydrolysis to first activate the free 5'-phosphate of one nucleotide and then react it with the 3'-OH group of the adjacent nucleotide. This resealing reaction is used in both DNA replication to join small DNA fragments called Okazaki fragments that are  
25 transiently formed in the process of replicating new DNA, and in DNA repair. DNA repair is the process by which accidental base changes, such as those produced by oxidative damage, hydrolytic attack, or uncontrolled methylation of DNA, are corrected before replication or transcription of the DNA can occur. Bloom's syndrome is an inherited human disease in which individuals are partially deficient in DNA ligation and consequently have an increased incidence of cancer (Alberts, B. et al.  
30 (1994) The Molecular Biology of the Cell, Garland Publishing Inc., New York NY, p. 247).

### **Molecules Associated with Growth and Development**

Human growth and development requires the spatial and temporal regulation of cell differentiation, cell proliferation, and apoptosis. These processes coordinately control reproduction,  
35 aging, embryogenesis, morphogenesis, organogenesis, and tissue repair and maintenance. At the cellular level, growth and development is governed by the cell's decision to enter into or exit from

the cell division cycle and by the cell's commitment to a terminally differentiated state. These decisions are made by the cell in response to extracellular signals and other environmental cues it receives. The following discussion focuses on the molecular mechanisms of cell division, reproduction, cell differentiation and proliferation, apoptosis, and aging.

## 5 Cell Division

Cell division is the fundamental process by which all living things grow and reproduce. In unicellular organisms such as yeast and bacteria, each cell division doubles the number of organisms, while in multicellular species many rounds of cell division are required to replace cells lost by wear or by programmed cell death, and for cell differentiation to produce a new tissue or organ. Details of  
10 the cell division cycle may vary, but the basic process consists of three principle events. The first event, interphase, involves preparations for cell division, replication of the DNA, and production of essential proteins. In the second event, mitosis, the nuclear material is divided and separates to opposite sides of the cell. The final event, cytokinesis, is division and fission of the cell cytoplasm. The sequence and timing of cell cycle transitions is under the control of the cell cycle regulation  
15 system which controls the process by positive or negative regulatory circuits at various check points.

Regulated progression of the cell cycle depends on the integration of growth control pathways with the basic cell cycle machinery. Cell cycle regulators have been identified by selecting for human and yeast cDNAs that block or activate cell cycle arrest signals in the yeast mating pheromone pathway when they are overexpressed. Known regulators include human CPR (cell cycle  
20 progression restoration) genes, such as CPR8 and CPR2, and yeast CDC (cell division control) genes, including CDC91, that block the arrest signals. The CPR genes express a variety of proteins including cyclins, tumor suppressor binding proteins, chaperones, transcription factors, translation factors, and RNA-binding proteins (Edwards, M.C. et al.(1997) Genetics 147:1063-1076).

Several cell cycle transitions, including the entry and exit of a cell from mitosis, are  
25 dependent upon the activation and inhibition of cyclin-dependent kinases (Cdks). The Cdks are composed of a kinase subunit, Cdk, and an activating subunit, cyclin, in a complex that is subject to many levels of regulation. There appears to be a single Cdk in Saccharomyces cerevisiae and Saccharomyces pombe whereas mammals have a variety of specialized Cdks. Cyclins act by binding to and activating cyclin-dependent protein kinases which then phosphorylate and activate selected  
30 proteins involved in the mitotic process. The Cdk-cyclin complex is both positively and negatively regulated by phosphorylation, and by targeted degradation involving molecules such as CDC4 and CDC53. In addition, Cdks are further regulated by binding to inhibitors and other proteins such as Suc1 that modify their specificity or accessibility to regulators (Patra, D. and W.G. Dunphy (1996) Genes Dev. 10:1503-1515; and Mathias, N. et al. (1996) Mol. Cell Biol. 16:6634-6643).

## 35 Reproduction

The male and female reproductive systems are complex and involve many aspects of growth

and development. The anatomy and physiology of the male and female reproductive systems are reviewed in (Guyton, A.C. (1991) Textbook of Medical Physiology, W.B. Saunders Co., Philadelphia PA, pp. 899-928).

The male reproductive system includes the process of spermatogenesis, in which the sperm  
5 are formed, and male reproductive functions are regulated by various hormones and their effects on accessory sexual organs, cellular metabolism, growth, and other bodily functions.

Spermatogenesis begins at puberty as a result of stimulation by gonadotropic hormones released from the anterior pituitary. Immature sperm (spermatogonia) undergo several mitotic cell divisions before undergoing meiosis and full maturation. The testes secrete several male sex  
10 hormones, the most abundant being testosterone, that is essential for growth and division of the immature sperm, and for the masculine characteristics of the male body. Three other male sex hormones, gonadotropin-releasing hormone (GnRH), luteinizing hormone (LH), and follicle-stimulating hormone (FSH) control sexual function.

The uterus, ovaries, fallopian tubes, vagina, and breasts comprise the female reproductive  
15 system. The ovaries and uterus are the source of ova and the location of fetal development, respectively. The fallopian tubes and vagina are accessory organs attached to the top and bottom of the uterus, respectively. Both the uterus and ovaries have additional roles in the development and loss of reproductive capability during a female's lifetime. The primary role of the breasts is lactation. Multiple endocrine signals from the ovaries, uterus, pituitary, hypothalamus, adrenal glands, and  
20 other tissues coordinate reproduction and lactation. These signals vary during the monthly menstruation cycle and during the female's lifetime. Similarly, the sensitivity of reproductive organs to these endocrine signals varies during the female's lifetime.

A combination of positive and negative feedback to the ovaries, pituitary and hypothalamus glands controls physiologic changes during the monthly ovulation and endometrial cycles. The  
25 anterior pituitary secretes two major gonadotropin hormones, follicle-stimulating hormone (FSH) and luteinizing hormone (LH), regulated by negative feedback of steroids, most notably by ovarian estradiol. If fertilization does not occur, estrogen and progesterone levels decrease. This sudden reduction of the ovarian hormones leads to menstruation, the desquamation of the endometrium.

Hormones further govern all the steps of pregnancy, parturition, lactation, and menopause.  
30 During pregnancy large quantities of human chorionic gonadotropin (hCG), estrogens, progesterone, and human chorionic somatomammotropin (hCS) are formed by the placenta. hCG, a glycoprotein similar to luteinizing hormone, stimulates the corpus luteum to continue producing more progesterone and estrogens, rather than to involute as occurs if the ovum is not fertilized. hCS is similar to growth hormone and is crucial for fetal nutrition.

35 The female breast also matures during pregnancy. Large amounts of estrogen secreted by the placenta trigger growth and branching of the breast milk ductal system while lactation is initiated by

the secretion of prolactin by the pituitary gland.

Parturition involves several hormonal changes that increase uterine contractility toward the end of pregnancy, as follows. The levels of estrogens increase more than those of progesterone.

Oxytocin is secreted by the neurohypophysis. Concomitantly, uterine sensitivity to oxytocin  
5 increases. The fetus itself secretes oxytocin, cortisol (from adrenal glands), and prostaglandins.

Menopause occurs when most of the ovarian follicles have degenerated. The ovary then produces less estradiol, reducing the negative feedback on the pituitary and hypothalamus glands. Mean levels of circulating FSH and LH increase, even as ovulatory cycles continue. Therefore, the ovary is less responsive to gonadotropins, and there is an increase in the time between menstrual  
10 cycles. Consequently, menstrual bleeding ceases and reproductive capability ends.

#### Cell Differentiation and Proliferation

Tissue growth involves complex and ordered patterns of cell proliferation, cell differentiation, and apoptosis. Cell proliferation must be regulated to maintain both the number of cells and their spatial organization. This regulation depends upon the appropriate expression of  
15 proteins which control cell cycle progression in response to extracellular signals, such as growth factors and other mitogens, and intracellular cues, such as DNA damage or nutrient starvation. Molecules which directly or indirectly modulate cell cycle progression fall into several categories, including growth factors and their receptors, second messenger and signal transduction proteins, oncogene products, tumor-suppressor proteins, and mitosis-promoting factors.

20 Growth factors were originally described as serum factors required to promote cell proliferation. Most growth factors are large, secreted polypeptides that act on cells in their local environment. Growth factors bind to and activate specific cell surface receptors and initiate intracellular signal transduction cascades. Many growth factor receptors are classified as receptor tyrosine kinases which undergo autophosphorylation upon ligand binding. Autophosphorylation  
25 enables the receptor to interact with signal transduction proteins characterized by the presence of SH2 or SH3 domains (Src homology regions 2 or 3). These proteins then modulate the activity state of small G-proteins, such as Ras, Rab, and Rho, along with GTPase activating proteins (GAPs), guanine nucleotide releasing proteins (GNRPs), and other guanine nucleotide exchange factors. Small G proteins act as molecular switches that activate other downstream events, such as mitogen-activated  
30 protein kinase (MAP kinase) cascades. MAP kinases ultimately activate transcription of mitosis-promoting genes.

In addition to growth factors, small signaling peptides and hormones also influence cell proliferation. These molecules bind primarily to another class of receptor, the trimeric G-protein coupled receptor (GPCR), found predominantly on the surface of immune, neuronal and  
35 neuroendocrine cells. Upon ligand binding, the GPCR activates a trimeric G protein which in turn triggers increased levels of intracellular second messengers such as phospholipase C, Ca<sup>2+</sup>, and



cyclic AMP. Most GPCR-mediated signaling pathways indirectly promote cell proliferation by causing the secretion or breakdown of other signaling molecules that have direct mitogenic effects. These signaling cascades often involve activation of kinases and phosphatases. Some growth factors, such as some members of the transforming growth factor beta (TGF- $\beta$ ) family, act on some cells to stimulate cell proliferation and on other cells to inhibit it. Growth factors may also stimulate a cell at one concentration and inhibit the same cell at another concentration. Most growth factors also have a multitude of other actions besides the regulation of cell growth and division: they can control the proliferation, survival, differentiation, migration, or function of cells depending on the circumstance. For example, the tumor necrosis factor/nerve growth factor (TNF/NGF) family can activate or inhibit cell death, as well as regulate proliferation and differentiation. The cell response depends on the type of cell, its stage of differentiation and transformation status, which surface receptors are stimulated, and the types of stimuli acting on the cell (Smith, A. et al. (1994) *Cell* 76:959-962; and Nocentini, G. et al. (1997) *Proc. Natl. Acad. Sci. USA* 94:6216-6221).

Neighboring cells in a tissue compete for growth factors, and when provided with "unlimited" quantities in a perfused system will grow to even higher cell densities before reaching density-dependent inhibition of cell division. Cells often demonstrate an anchorage dependence of cell division as well. This anchorage dependence may be associated with the formation of focal contacts linking the cytoskeleton with the extracellular matrix (ECM). The expression of ECM components can be stimulated by growth factors. For example, TGF- $\beta$  stimulates fibroblasts to produce a variety of ECM proteins, including fibronectin, collagen, and tenascin (Pearson, C.A. et al. (1988) *EMBO J.* 7:2677-2981). In fact, for some cell types specific ECM molecules, such as laminin or fibronectin, may act as growth factors. Tenascin-C and -R, expressed in developing and lesioned neural tissue, provide stimulatory/anti-adhesive or inhibitory properties, respectively, for axonal growth (Faissner, A. (1997) *Cell Tissue Res.* 290:331-341).

Cancers are associated with the activation of oncogenes which are derived from normal cellular genes. These oncogenes encode oncoproteins which convert normal cells into malignant cells. Some oncoproteins are mutant isoforms of the normal protein, and other oncoproteins are abnormally expressed with respect to location or amount of expression. The latter category of oncoprotein causes cancer by altering transcriptional control of cell proliferation. Five classes of oncoproteins are known to affect cell cycle controls. These classes include growth factors, growth factor receptors, intracellular signal transducers, nuclear transcription factors, and cell-cycle control proteins. Viral oncogenes are integrated into the human genome after infection of human cells by certain viruses. Examples of viral oncogenes include v-src, v-abl, and v-fps.

Many oncogenes have been identified and characterized. These include sis, erbA, erbB, her-2, mutated G<sub>s</sub>, src, abl, ras, crk, jun, fos, myc, and mutated tumor-suppressor genes such as RB, p53, mdm2, Cip1, p16, and cyclin D. Transformation of normal genes to oncogenes may also occur by

chromosomal translocation. The Philadelphia chromosome, characteristic of chronic myeloid leukemia and a subset of acute lymphoblastic leukemias, results from a reciprocal translocation between chromosomes 9 and 22 that moves a truncated portion of the proto-oncogene c-abl to the breakpoint cluster region (bcr) on chromosome 22.

5 Tumor-suppressor genes are involved in regulating cell proliferation. Mutations which cause reduced or loss of function in tumor-suppressor genes result in uncontrolled cell proliferation. For example, the retinoblastoma gene product (RB), in a non-phosphorylated state, binds several early-response genes and suppresses their transcription, thus blocking cell division. Phosphorylation of RB causes it to dissociate from the genes, releasing the suppression, and allowing cell division to  
10 proceed.

#### Apoptosis

Apoptosis is the genetically controlled process by which unneeded or defective cells undergo programmed cell death. Selective elimination of cells is as important for morphogenesis and tissue remodeling as is cell proliferation and differentiation. Lack of apoptosis may result in hyperplasia  
15 and other disorders associated with increased cell proliferation. Apoptosis is also a critical component of the immune response. Immune cells such as cytotoxic T-cells and natural killer cells prevent the spread of disease by inducing apoptosis in tumor cells and virus-infected cells. In addition, immune cells that fail to distinguish self molecules from foreign molecules must be eliminated by apoptosis to avoid an autoimmune response.

20 Apoptotic cells undergo distinct morphological changes. Hallmarks of apoptosis include cell shrinkage, nuclear and cytoplasmic condensation, and alterations in plasma membrane topology. Biochemically, apoptotic cells are characterized by increased intracellular calcium concentration, fragmentation of chromosomal DNA, and expression of novel cell surface components.

The molecular mechanisms of apoptosis are highly conserved, and many of the key protein  
25 regulators and effectors of apoptosis have been identified. Apoptosis generally proceeds in response to a signal which is transduced intracellularly and results in altered patterns of gene expression and protein activity. Signaling molecules such as hormones and cytokines are known both to stimulate and to inhibit apoptosis through interactions with cell surface receptors. Transcription factors also play an important role in the onset of apoptosis. A number of downstream effector molecules,  
30 particularly proteases such as the cysteine proteases called caspases, have been implicated in the degradation of cellular components and the proteolytic activation of other apoptotic effectors.

#### Aging and Senescence

Studies of the aging process or senescence have shown a number of characteristic cellular and molecular changes (Fauci et al. (1998) Harrison's Principles of Internal Medicine, McGraw-Hill, New  
35 York NY, p.37). These characteristics include increases in chromosome structural abnormalities, DNA cross-linking, incidence of single-stranded breaks in DNA, losses in DNA methylation, and

degradation of telomere regions. In addition to these DNA changes, post-translational alterations of proteins increase including, deamidation, oxidation, cross-linking, and nonenzymatic glycation. Still further molecular changes occur in the mitochondria of aging cells through deterioration of structure. These changes eventually contribute to decreased function in every organ of the body.

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### Biochemical Pathway Molecules

Biochemical pathways are responsible for regulating metabolism, growth and development, protein secretion and trafficking, environmental responses, and ecological interactions including immune response and response to parasites.

### 10 DNA replication

Deoxyribonucleic acid (DNA), the genetic material, is found in both the nucleus and mitochondria of human cells. The bulk of human DNA is nuclear, in the form of linear chromosomes, while mitochondrial DNA is circular. DNA replication begins at specific sites called origins of replication. Bidirectional synthesis occurs from the origin via two growing forks that move in opposite directions. Replication is semi-conservative, with each daughter duplex containing one old strand and its newly synthesized complementary partner. Proteins involved in DNA replication include DNA polymerases, DNA primase, telomerase, DNA helicase, topoisomerases, DNA ligases, replication factors, and DNA-binding proteins.

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### DNA Recombination and Repair

Cells are constantly faced with replication errors and environmental assault (such as ultraviolet irradiation) that can produce DNA damage. Damage to DNA consists of any change that modifies the structure of the molecule. Changes to DNA can be divided into two general classes, single base changes and structural distortions. Any damage to DNA can produce a mutation, and the mutation may produce a disorder, such as cancer.

20

Changes in DNA are recognized by repair systems within the cell. These repair systems act to correct the damage and thus prevent any deleterious effects of a mutational event. Repair systems can be divided into three general types, direct repair, excision repair, and retrieval systems. Proteins involved in DNA repair include DNA polymerase, excision repair proteins, excision and cross link repair proteins, recombination and repair proteins, RAD51 proteins, and BLN and WRN proteins that are homologs of RecQ helicase. When the repair systems are eliminated, cells become exceedingly sensitive to environmental mutagens, such as ultraviolet irradiation. Patients with disorders associated with a loss in DNA repair systems often exhibit a high sensitivity to environmental mutagens. Examples of such disorders include xeroderma pigmentosum (XP), Bloom's syndrome (BS), and Werner's syndrome (WS) (Yamagata, K. et al. (1998) Proc. Natl. Acad. Sci. USA 95:8733-8738), ataxia telangiectasia, Cockayne's syndrome, and Fanconi's anemia.

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Recombination is the process whereby new DNA sequences are generated by the movements

of large pieces of DNA. In homologous recombination, which occurs during meiosis and DNA repair, parent DNA duplexes align at regions of sequence similarity, and new DNA molecules form by the breakage and joining of homologous segments. Proteins involved include RAD51 recombinase. In site-specific recombination, two specific but not necessarily homologous DNA sequences are exchanged. In the immune system this process generates a diverse collection of antibody and T cell receptor genes. Proteins involved in site-specific recombination in the immune system include recombination activating genes 1 and 2 (RAG1 and RAG2). A defect in immune system site-specific recombination causes severe combined immunodeficiency disease in mice.

#### RNA Metabolism

10 Ribonucleic acid (RNA) is a linear single-stranded polymer of four nucleotides, ATP, CTP, UTP, and GTP. In most organisms, RNA is transcribed as a copy of DNA, the genetic material of the organism. In retroviruses RNA rather than DNA serves as the genetic material. RNA copies of the genetic material encode proteins or serve various structural, catalytic, or regulatory roles in organisms. RNA is classified according to its cellular localization and function. Messenger RNAs (mRNAs) encode polypeptides. Ribosomal RNAs (rRNAs) are assembled, along with ribosomal proteins, into ribosomes, which are cytoplasmic particles that translate mRNA into polypeptides. 15 Transfer RNAs (tRNAs) are cytosolic adaptor molecules that function in mRNA translation by recognizing both an mRNA codon and the amino acid that matches that codon. Heterogeneous nuclear RNAs (hnRNAs) include mRNA precursors and other nuclear RNAs of various sizes. Small nuclear RNAs (snRNAs) are a part of the nuclear spliceosome complex that removes intervening, non-coding sequences (introns) and rejoins exons in pre-mRNAs. 20

#### RNA Transcription

The transcription process synthesizes an RNA copy of DNA. Proteins involved include multi-subunit RNA polymerases, transcription factors IIA, IIB, IID, IIE, IIF, IIH, and IIJ. Many transcription factors incorporate DNA-binding structural motifs which comprise either  $\alpha$ -helices or  $\beta$ -sheets that bind to the major groove of DNA. Four well-characterized structural motifs are helix-turn-helix, zinc finger, leucine zipper, and helix-loop-helix. 25

#### RNA Processing

Various proteins are necessary for processing of transcribed RNAs in the nucleus. Pre-mRNA processing steps include capping at the 5' end with methylguanosine, polyadenylating the 3' end, and splicing to remove introns. The spliceosomal complex is comprised of five small nuclear ribonucleoprotein particles (snRNPs) designated U1, U2, U4, U5, and U6. Each snRNP contains a single species of snRNA and about ten proteins. The RNA components of some snRNPs recognize and base-pair with intron consensus sequences. The protein components mediate spliceosome assembly and the splicing reaction. Autoantibodies to snRNP proteins are found in the blood of patients with systemic lupus erythematosus (Stryer, L. (1995) Biochemistry W.H. Freeman and 35

Company, New York NY, p. 863).

Heterogeneous nuclear ribonucleoproteins (hnRNPs) have been identified that have roles in splicing, exporting of the mature RNAs to the cytoplasm, and mRNA translation (Biamonti, G. et al. (1998) Clin. Exp. Rheumatol. 16:317-326). Some examples of hnRNPs include the yeast proteins

5 Hrp1p, involved in cleavage and polyadenylation at the 3' end of the RNA; Cbp80p, involved in capping the 5' end of the RNA; and Npl3p, a homolog of mammalian hnRNP A1, involved in export of mRNA from the nucleus (Shen, E.C. et al. (1998) Genes Dev. 12:679-691). HnRNPs have been shown to be important targets of the autoimmune response in rheumatic diseases (Biamonti, *supra*).

Many snRNP proteins, hnRNP proteins, and alternative splicing factors are characterized by

10 an RNA recognition motif (RRM). (Reviewed in Birney, E. et al. (1993) Nucleic Acids Res. 21:5803-5816.) The RRM is about 80 amino acids in length and forms four  $\beta$ -strands and two  $\alpha$ -helices arranged in an  $\alpha/\beta$  sandwich. The RRM contains a core RNP-1 octapeptide motif along with surrounding conserved sequences.

#### RNA Stability and Degradation

15 RNA helicases alter and regulate RNA conformation and secondary structure by using energy derived from ATP hydrolysis to destabilize and unwind RNA duplexes. The most well-characterized and ubiquitous family of RNA helicases is the DEAD-box family, so named for the conserved B-type ATP-binding motif which is diagnostic of proteins in this family. Over 40 DEAD-box helicases have been identified in organisms as diverse as bacteria, insects, yeast, amphibians, mammals, and plants.

20 DEAD-box helicases function in diverse processes such as translation initiation, splicing, ribosome assembly, and RNA editing, transport, and stability. Some DEAD-box helicases play tissue- and stage-specific roles in spermatogenesis and embryogenesis. (Reviewed in Linder, P. et al. (1989) Nature 337:121-122.)

Overexpression of the DEAD-box 1 protein (DDX1) may play a role in the progression of

25 neuroblastoma (Nb) and retinoblastoma (Rb) tumors. Other DEAD-box helicases have been implicated either directly or indirectly in ultraviolet light-induced tumors, B cell lymphoma, and myeloid malignancies. (Reviewed in Godbout, R. et al. (1998) J. Biol. Chem. 273:21161-21168.)

Ribonucleases (RNases) catalyze the hydrolysis of phosphodiester bonds in RNA chains, thus cleaving the RNA. For example, RNase P is a ribonucleoprotein enzyme which cleaves the 5' end of

30 pre-tRNAs as part of their maturation process. RNase H digests the RNA strand of an RNA/DNA hybrid. Such hybrids occur in cells invaded by retroviruses, and RNase H is an important enzyme in the retroviral replication cycle. RNase H domains are often found as a domain associated with reverse transcriptases. RNase activity in serum and cell extracts is elevated in a variety of cancers and infectious diseases (Schein, C.H. (1997) Nat. Biotechnol. 15:529-536). Regulation of RNase

35 activity is being investigated as a means to control tumor angiogenesis, allergic reactions, viral infection and replication, and fungal infections.

### Protein Translation

The eukaryotic ribosome is composed of a 60S (large) subunit and a 40S (small) subunit, which together form the 80S ribosome. In addition to the 18S, 28S, 5S, and 5.8S rRNAs, the ribosome also contains more than fifty proteins. The ribosomal proteins have a prefix which denotes the subunit to which they belong, either L (large) or S (small). Three important sites are identified on the ribosome. The aminoacyl-tRNA site (A site) is where charged tRNAs (with the exception of the initiator-tRNA) bind on arrival at the ribosome. The peptidyl-tRNA site (P site) is where new peptide bonds are formed, as well as where the initiator tRNA binds. The exit site (E site) is where deacylated tRNAs bind prior to their release from the ribosome. (Translation is reviewed in Stryer, L. (1995) Biochemistry, W.H. Freeman and Company, New York NY, pp. 875-908; and Lodish, H. et al. (1995) Molecular Cell Biology, Scientific American Books, New York NY, pp. 119-138.)

### tRNA Charging

Protein biosynthesis depends on each amino acid forming a linkage with the appropriate tRNA. The aminoacyl-tRNA synthetases are responsible for the activation and correct attachment of an amino acid with its cognate tRNA. The 20 aminoacyl-tRNA synthetase enzymes can be divided into two structural classes, Class I and Class II. Autoantibodies against aminoacyl-tRNAs are generated by patients with dermatomyositis and polymyositis, and correlate strongly with complicating interstitial lung disease (ILD). These antibodies appear to be generated in response to viral infection, and coxsackie virus has been used to induce experimental viral myositis in animals.

### Translation Initiation

Initiation of translation can be divided into three stages. The first stage brings an initiator transfer RNA (Met-tRNA<sub>i</sub>) together with the 40S ribosomal subunit to form the 43S preinitiation complex. The second stage binds the 43S preinitiation complex to the mRNA, followed by migration of the complex to the correct AUG initiation codon. The third stage brings the 60S ribosomal subunit to the 40S subunit to generate an 80S ribosome at the initiation codon. Regulation of translation primarily involves the first and second stage in the initiation process (Pain, V.M. (1996) *Eur. J. Biochem.* 236:747-771).

Several initiation factors, many of which contain multiple subunits, are involved in bringing an initiator tRNA and 40S ribosomal subunit together. eIF2, a guanine nucleotide binding protein, recruits the initiator tRNA to the 40S ribosomal subunit. Only when eIF2 is bound to GTP does it associate with the initiator tRNA. eIF2B, a guanine nucleotide exchange protein, is responsible for converting eIF2 from the GDP-bound inactive form to the GTP-bound active form. Two other factors, eIF1A and eIF3 bind and stabilize the 40S subunit by interacting with 18S ribosomal RNA and specific ribosomal structural proteins. eIF3 is also involved in association of the 40S ribosomal subunit with mRNA. The Met-tRNA<sub>i</sub>, eIF1A, eIF3, and 40S ribosomal subunit together make up the 43S preinitiation complex (Pain, *supra*).

Additional factors are required for binding of the 43S preinitiation complex to an mRNA molecule, and the process is regulated at several levels. eIF4F is a complex consisting of three proteins: eIF4E, eIF4A, and eIF4G. eIF4E recognizes and binds to the mRNA 5'-terminal m<sup>7</sup>GTP cap, eIF4A is a bidirectional RNA-dependent helicase, and eIF4G is a scaffolding polypeptide.

- 5 eIF4G has three binding domains. The N-terminal third of eIF4G interacts with eIF4E, the central third interacts with eIF4A, and the C-terminal third interacts with eIF3 bound to the 43S preinitiation complex. Thus, eIF4G acts as a bridge between the 40S ribosomal subunit and the mRNA (Hentze, M.W. (1997) Science 275:500-501).

- The ability of eIF4F to initiate binding of the 43S preinitiation complex is regulated by structural features of the mRNA. The mRNA molecule has an untranslated region (UTR) between the 5' cap and the AUG start codon. In some mRNAs this region forms secondary structures that impede binding of the 43S preinitiation complex. The helicase activity of eIF4A is thought to function in removing this secondary structure to facilitate binding of the 43S preinitiation complex (Pain, supra).

15 Translation Elongation

- Elongation is the process whereby additional amino acids are joined to the initiator methionine to form the complete polypeptide chain. The elongation factors EF1 $\alpha$ , EF1 $\beta$   $\gamma$ , and EF2 are involved in elongating the polypeptide chain following initiation. EF1 $\alpha$  is a GTP-binding protein. In EF1 $\alpha$ 's GTP-bound form, it brings an aminoacyl-tRNA to the ribosome's A site. The amino acid attached to the newly arrived aminoacyl-tRNA forms a peptide bond with the initiator methionine. The GTP on EF1 $\alpha$  is hydrolyzed to GDP, and EF1 $\alpha$ -GDP dissociates from the ribosome. EF1 $\beta$   $\gamma$  binds EF1 $\alpha$ -GDP and induces the dissociation of GDP from EF1 $\alpha$ , allowing EF1 $\alpha$  to bind GTP and a new cycle to begin.

- As subsequent aminoacyl-tRNAs are brought to the ribosome, EF-G, another GTP-binding protein, catalyzes the translocation of tRNAs from the A site to the P site and finally to the E site of the ribosome. This allows the processivity of translation.

Translation Termination

The release factor eRF carries out termination of translation. eRF recognizes stop codons in the mRNA, leading to the release of the polypeptide chain from the ribosome.

30 Post-Translational Pathways

- Proteins may be modified after translation by the addition of phosphate, sugar, prenyl, fatty acid, and other chemical groups. These modifications are often required for proper protein activity. Enzymes involved in post-translational modification include kinases, phosphatases, glycosyltransferases, and prenyltransferases. The conformation of proteins may also be modified after translation by the introduction and rearrangement of disulfide bonds (rearrangement catalyzed by protein disulfide isomerase), the isomerization of proline sidechains by prolyl isomerase, and by

interactions with molecular chaperone proteins.

Proteins may also be cleaved by proteases. Such cleavage may result in activation, inactivation, or complete degradation of the protein. Proteases include serine proteases, cysteine proteases, aspartic proteases, and metalloproteases. Signal peptidase in the endoplasmic reticulum (ER) lumen cleaves the signal peptide from membrane or secretory proteins that are imported into the ER. Ubiquitin proteases are associated with the ubiquitin conjugation system (UCS), a major pathway for the degradation of cellular proteins in eukaryotic cells and some bacteria. The UCS mediates the elimination of abnormal proteins and regulates the half-lives of important regulatory proteins that control cellular processes such as gene transcription and cell cycle progression. In the UCS pathway, proteins targeted for degradation are conjugated to a ubiquitin, a small heat stable protein. Proteins involved in the UCS include ubiquitin-activating enzyme, ubiquitin-conjugating enzymes, ubiquitin-ligases, and ubiquitin C-terminal hydrolases. The ubiquitinated protein is then recognized and degraded by the proteasome, a large, multisubunit proteolytic enzyme complex, and ubiquitin is released for reutilization by ubiquitin protease.

#### 15 Lipid Metabolism

Lipids are water-insoluble, oily or greasy substances that are soluble in nonpolar solvents such as chloroform or ether. Neutral fats (triacylglycerols) serve as major fuels and energy stores. Polar lipids, such as phospholipids, sphingolipids, glycolipids, and cholesterol, are key structural components of cell membranes.

Lipid metabolism is involved in human diseases and disorders. In the arterial disease atherosclerosis, fatty lesions form on the inside of the arterial wall. These lesions promote the loss of arterial flexibility and the formation of blood clots (Guyton, A.C. Textbook of Medical Physiology (1991) W.B. Saunders Company, Philadelphia PA, pp.760-763). In Tay-Sachs disease, the GM<sub>2</sub> ganglioside (a sphingolipid) accumulates in lysosomes of the central nervous system due to a lack of the enzyme N-acetylhexosaminidase. Patients suffer nervous system degeneration leading to early death (Fauci, A.S. et al. (1998) Harrison's Principles of Internal Medicine McGraw-Hill, New York NY, p. 2171). The Niemann-Pick diseases are caused by defects in lipid metabolism. Niemann-Pick diseases types A and B are caused by accumulation of sphingomyelin (a sphingolipid) and other lipids in the central nervous system due to a defect in the enzyme sphingomyelinase, leading to neurodegeneration and lung disease. Niemann-Pick disease type C results from a defect in cholesterol transport, leading to the accumulation of sphingomyelin and cholesterol in lysosomes and a secondary reduction in sphingomyelinase activity. Neurological symptoms such as grand mal seizures, ataxia, and loss of previously learned speech, manifest 1-2 years after birth. A mutation in the NPC protein, which contains a putative cholesterol-sensing domain, was found in a mouse model of Niemann-Pick disease type C (Fauci, supra, p. 2175; Loftus, S.K. et al. (1997) Science 277:232-235). (Lipid metabolism is reviewed in Stryer, L. (1995) Biochemistry, W.H. Freeman and Company,



New York NY; Lehninger, A. (1982) Principles of Biochemistry Worth Publishers, Inc., New York NY; and ExPASy "Biochemical Pathways" index of Boehringer Mannheim World Wide Web site.)

#### Fatty Acid Synthesis

Fatty acids are long-chain organic acids with a single carboxyl group and a long non-polar hydrocarbon tail. Long-chain fatty acids are essential components of glycolipids, phospholipids, and cholesterol, which are building blocks for biological membranes, and of triglycerides, which are biological fuel molecules. Long-chain fatty acids are also substrates for eicosanoid production, and are important in the functional modification of certain complex carbohydrates and proteins. 16-carbon and 18-carbon fatty acids are the most common.

Fatty acid synthesis occurs in the cytoplasm. In the first step, acetyl-Coenzyme A (CoA) carboxylase (ACC) synthesizes malonyl-CoA from acetyl-CoA and bicarbonate. The enzymes which catalyze the remaining reactions are covalently linked into a single polypeptide chain, referred to as the multifunctional enzyme fatty acid synthase (FAS). FAS catalyzes the synthesis of palmitate from acetyl-CoA and malonyl-CoA. FAS contains acetyl transferase, malonyl transferase,  $\beta$ -ketoacetyl synthase, acyl carrier protein,  $\beta$ -ketoacyl reductase, dehydratase, enoyl reductase, and thioesterase activities. The final product of the FAS reaction is the 16-carbon fatty acid palmitate. Further elongation, as well as unsaturation, of palmitate by accessory enzymes of the ER produces the variety of long chain fatty acids required by the individual cell. These enzymes include a NADH-cytochrome  $b_5$  reductase, cytochrome  $b_5$ , and a desaturase.

#### Phospholipid and Triacylglycerol Synthesis

Triacylglycerols, also known as triglycerides and neutral fats, are major energy stores in animals. Triacylglycerols are esters of glycerol with three fatty acid chains. Glycerol-3-phosphate is produced from dihydroxyacetone phosphate by the enzyme glycerol phosphate dehydrogenase or from glycerol by glycerol kinase. Fatty acid-CoA's are produced from fatty acids by fatty acyl-CoA synthetases. Glycerol-3-phosphate is acylated with two fatty acyl-CoA's by the enzyme glycerol phosphate acyltransferase to give phosphatidate. Phosphatidate phosphatase converts phosphatidate to diacylglycerol, which is subsequently acylated to a triacylglycerol by the enzyme diglyceride acyltransferase. Phosphatidate phosphatase and diglyceride acyltransferase form a triacylglycerol synthetase complex bound to the ER membrane.

A major class of phospholipids are the phosphoglycerides, which are composed of a glycerol backbone, two fatty acid chains, and a phosphorylated alcohol. Phosphoglycerides are components of cell membranes. Principal phosphoglycerides are phosphatidyl choline, phosphatidyl ethanolamine, phosphatidyl serine, phosphatidyl inositol, and diphosphatidyl glycerol. Many enzymes involved in phosphoglyceride synthesis are associated with membranes (Meyers, R.A. (1995) Molecular Biology and Biotechnology, VCH Publishers Inc., New York NY, pp. 494-501). Phosphatidate is converted to CDP-diacylglycerol by the enzyme phosphatidate cytidyltransferase (ExPASy ENZYME EC

2.7.7.41). Transfer of the diacylglycerol group from CDP-diacylglycerol to serine to yield phosphatidyl serine, or to inositol to yield phosphatidyl inositol, is catalyzed by the enzymes CDP-diacylglycerol-serine O-phosphatidyltransferase and CDP-diacylglycerol-inositol 3-phosphatidyltransferase, respectively (ExPASy ENZYME EC 2.7.8.8; ExPASy ENZYME EC 2.7.8.11). The enzyme phosphatidyl serine decarboxylase catalyzes the conversion of phosphatidyl serine to phosphatidyl ethanolamine, using a pyruvate cofactor (Voelker, D.R. (1997) *Biochim. Biophys. Acta* 1348:236-244). Phosphatidyl choline is formed using diet-derived choline by the reaction of CDP-choline with 1,2-diacylglycerol, catalyzed by diacylglycerol cholinephosphotransferase (ExPASy ENZYME 2.7.8.2).

#### 10 Sterol, Steroid, and Isoprenoid Metabolism

Cholesterol, composed of four fused hydrocarbon rings with an alcohol at one end, moderates the fluidity of membranes in which it is incorporated. In addition, cholesterol is used in the synthesis of steroid hormones such as cortisol, progesterone, estrogen, and testosterone. Bile salts derived from cholesterol facilitate the digestion of lipids. Cholesterol in the skin forms a barrier that prevents excess water evaporation from the body. Farnesyl and geranylgeranyl groups, which are derived from cholesterol biosynthesis intermediates, are post-translationally added to signal transduction proteins such as ras and protein-targeting proteins such as rab. These modifications are important for the activities of these proteins (Guyton, *supra*; Stryer, *supra*, pp. 279-280, 691-702, 934).

Mammals obtain cholesterol derived from both *de novo* biosynthesis and the diet. The liver is the major site of cholesterol biosynthesis in mammals. Two acetyl-CoA molecules initially condense to form acetoacetyl-CoA, catalyzed by a thiolase. Acetoacetyl-CoA condenses with a third acetyl-CoA to form hydroxymethylglutaryl-CoA (HMG-CoA), catalyzed by HMG-CoA synthase. Conversion of HMG-CoA to cholesterol is accomplished via a series of enzymatic steps known as the mevalonate pathway. The rate-limiting step is the conversion of HMG-CoA to mevalonate by HMG-CoA reductase. The drug lovastatin, a potent inhibitor of HMG-CoA reductase, is given to patients to reduce their serum cholesterol levels. Other mevalonate pathway enzymes include mevalonate kinase, phosphomevalonate kinase, diphosphomevalonate decarboxylase, isopentenylidiphosphate isomerase, dimethylallyl transferase, geranyl transferase, farnesyl-diphosphate farnesyltransferase, squalene monooxygenase, lanosterol synthase, lathosterol oxidase, and 7-dehydrocholesterol reductase.

Cholesterol is used in the synthesis of steroid hormones such as cortisol, progesterone, aldosterone, estrogen, and testosterone. First, cholesterol is converted to pregnenolone by cholesterol monooxygenases. The other steroid hormones are synthesized from pregnenolone by a series of enzyme-catalyzed reactions including oxidations, isomerizations, hydroxylations, reductions, and demethylations. Examples of these enzymes include steroid  $\Delta$ -isomerase,  $3\beta$ -hydroxy- $\Delta^5$ -steroid dehydrogenase, steroid 21-monooxygenase, steroid 19-hydroxylase, and  $3\beta$ -hydroxysteroid

dehydrogenase. Cholesterol is also the precursor to vitamin D.

Numerous compounds contain 5-carbon isoprene units derived from the mevalonate pathway intermediate isopentenyl pyrophosphate. Isoprenoid groups are found in vitamin K, ubiquinone, retinal, dolichol phosphate (a carrier of oligosaccharides needed for N-linked glycosylation), and  
5 farnesyl and geranylgeranyl groups that modify proteins. Enzymes involved include farnesyl transferase, polyprenyl transferases, dolichyl phosphatase, and dolichyl kinase.

#### Sphingolipid Metabolism

Sphingolipids are an important class of membrane lipids that contain sphingosine, a long chain amino alcohol. They are composed of one long-chain fatty acid, one polar head alcohol, and  
10 sphingosine or sphingosine derivative. The three classes of sphingolipids are sphingomyelins, cerebroside, and gangliosides. Sphingomyelins, which contain phosphocholine or phosphoethanolamine as their head group, are abundant in the myelin sheath surrounding nerve cells. Galactocerebrosides, which contain a glucose or galactose head group, are characteristic of the brain. Other cerebroside are found in nonneural tissues. Gangliosides, whose head groups contain multiple  
15 sugar units, are abundant in the brain, but are also found in nonneural tissues.

Sphingolipids are built on a sphingosine backbone. Sphingosine is acylated to ceramide by the enzyme sphingosine acetyltransferase. Ceramide and phosphatidyl choline are converted to sphingomyelin by the enzyme ceramide choline phosphotransferase. Cerebrosides are synthesized by the linkage of glucose or galactose to ceramide by a transferase. Sequential addition of sugar  
20 residues to ceramide by transferase enzymes yields gangliosides.

#### Eicosanoid Metabolism

Eicosanoids, including prostaglandins, prostacyclin, thromboxanes, and leukotrienes, are 20-carbon molecules derived from fatty acids. Eicosanoids are signaling molecules which have roles in pain, fever, and inflammation. The precursor of all eicosanoids is arachidonate, which is generated  
25 from phospholipids by phospholipase A<sub>2</sub> and from diacylglycerols by diacylglycerol lipase. Leukotrienes are produced from arachidonate by the action of lipoxygenases. Prostaglandin synthase, reductases, and isomerases are responsible for the synthesis of the prostaglandins. Prostaglandins have roles in inflammation, blood flow, ion transport, synaptic transmission, and sleep. Prostacyclin and the thromboxanes are derived from a precursor prostaglandin by the action of prostacyclin  
30 synthase and thromboxane synthases, respectively.

#### Ketone Body Metabolism

Pairs of acetyl-CoA molecules derived from fatty acid oxidation in the liver can condense to form acetoacetyl-CoA, which subsequently forms acetoacetate, D-3-hydroxybutyrate, and acetone. These three products are known as ketone bodies. Enzymes involved in ketone body metabolism  
35 include HMG-CoA synthetase, HMG-CoA cleavage enzyme, D-3-hydroxybutyrate dehydrogenase, acetoacetate decarboxylase, and 3-ketoacyl-CoA transferase. Ketone bodies are a normal fuel supply

of the heart and renal cortex. Acetoacetate produced by the liver is transported to cells where the acetoacetate is converted back to acetyl-CoA and enters the citric acid cycle. In times of starvation, ketone bodies produced from stored triacylglycerols become an important fuel source, especially for the brain. Abnormally high levels of ketone bodies are observed in diabetics. Diabetic coma can  
5 result if ketone body levels become too great:

#### Lipid Mobilization

Within cells, fatty acids are transported by cytoplasmic fatty acid binding proteins (Online Mendelian Inheritance in Man (OMIM) \*134650 Fatty Acid-Binding Protein 1, Liver; FABP1). Diazepam binding inhibitor (DBI), also known as endozepine and acyl CoA-binding protein, is an  
10 endogenous  $\gamma$ -aminobutyric acid (GABA) receptor ligand which is thought to down-regulate the effects of GABA. DBI binds medium- and long-chain acyl-CoA esters with very high affinity and may function as an intracellular carrier of acyl-CoA esters (OMIM \*125950 Diazepam Binding Inhibitor; DBI; PROSITE PDOC00686 Acyl-CoA-binding protein signature).

Fat stored in liver and adipose triglycerides may be released by hydrolysis and transported in  
15 the blood. Free fatty acids are transported in the blood by albumin. Triacylglycerols and cholesterol esters in the blood are transported in lipoprotein particles. The particles consist of a core of hydrophobic lipids surrounded by a shell of polar lipids and apolipoproteins. The protein components serve in the solubilization of hydrophobic lipids and also contain cell-targeting signals. Lipoproteins include chylomicrons, chylomicron remnants, very-low-density lipoproteins (VLDL), intermediate-  
20 density lipoproteins (IDL), low-density lipoproteins (LDL), and high-density lipoproteins (HDL). There is a strong inverse correlation between the levels of plasma HDL and risk of premature coronary heart disease.

Triacylglycerols in chylomicrons and VLDL are hydrolyzed by lipoprotein lipases that line blood vessels in muscle and other tissues that use fatty acids. Cell surface LDL receptors bind LDL  
25 particles which are then internalized by endocytosis. Absence of the LDL receptor, the cause of the disease familial hypercholesterolemia, leads to increased plasma cholesterol levels and ultimately to atherosclerosis. Plasma cholesteryl ester transfer protein mediates the transfer of cholesteryl esters from HDL to apolipoprotein B-containing lipoproteins. Cholesteryl ester transfer protein is important in the reverse cholesterol transport system and may play a role in atherosclerosis (Yamashita, S. et al.  
30 (1997) Curr. Opin. Lipidol. 8:101-110). Macrophage scavenger receptors, which bind and internalize modified lipoproteins, play a role in lipid transport and may contribute to atherosclerosis (Greaves, D.R. et al. (1998) Curr. Opin. Lipidol. 9:425-432).

Proteins involved in cholesterol uptake and biosynthesis are tightly regulated in response to cellular cholesterol levels. The sterol regulatory element binding protein (SREBP) is a sterol-  
35 responsive transcription factor. Under normal cholesterol conditions, SREBP resides in the ER membrane. When cholesterol levels are low, a regulated cleavage of SREBP occurs which releases

the extracellular domain of the protein. This cleaved domain is then transported to the nucleus where it activates the transcription of the LDL receptor gene, and genes encoding enzymes of cholesterol synthesis, by binding the sterol regulatory element (SRE) upstream of the genes (Yang, J. et al. (1995) J. Biol. Chem. 270:12152-12161). Regulation of cholesterol uptake and biosynthesis also occurs via the oxysterol-binding protein (OSBP). OSBP is a high-affinity intracellular receptor for a variety of oxysterols that down-regulate cholesterol synthesis and stimulate cholesterol esterification (Lagace, T.A. et al. (1997) Biochem. J. 326:205-213).

#### Beta-oxidation

Mitochondrial and peroxisomal beta-oxidation enzymes degrade saturated and unsaturated fatty acids by sequential removal of two-carbon units from CoA-activated fatty acids. The main beta-oxidation pathway degrades both saturated and unsaturated fatty acids while the auxiliary pathway performs additional steps required for the degradation of unsaturated fatty acids.

The pathways of mitochondrial and peroxisomal beta-oxidation use similar enzymes, but have different substrate specificities and functions. Mitochondria oxidize short-, medium-, and long-chain fatty acids to produce energy for cells. Mitochondrial beta-oxidation is a major energy source for cardiac and skeletal muscle. In liver, it provides ketone bodies to the peripheral circulation when glucose levels are low as in starvation, endurance exercise, and diabetes (Eaton, S. et al. (1996) Biochem. J. 320:345-357). Peroxisomes oxidize medium-, long-, and very-long-chain fatty acids, dicarboxylic fatty acids, branched fatty acids, prostaglandins, xenobiotics, and bile acid intermediates. The chief roles of peroxisomal beta-oxidation are to shorten toxic lipophilic carboxylic acids to facilitate their excretion and to shorten very-long-chain fatty acids prior to mitochondrial beta-oxidation (Mannaerts, G.P. and P.P. van Veldhoven (1993) Biochimie 75:147-158).

Enzymes involved in beta-oxidation include acyl CoA synthetase, carnitine acyltransferase, acyl CoA dehydrogenases, enoyl CoA hydratases, L-3-hydroxyacyl CoA dehydrogenase,  $\beta$ -ketothiolase, 2,4-dienoyl CoA reductase, and isomerase.

#### Lipid Cleavage and Degradation

Triglycerides are hydrolyzed to fatty acids and glycerol by lipases. Lysophospholipases (LPLs) are widely distributed enzymes that metabolize intracellular lipids, and occur in numerous isoforms. Small isoforms, approximately 15-30 kD, function as hydrolases; large isoforms, those exceeding 60 kD, function both as hydrolases and transacylases. A particular substrate for LPLs, lysophosphatidylcholine, causes lysis of cell membranes when it is formed or imported into a cell. LPLs are regulated by lipid factors including acylcarnitine, arachidonic acid, and phosphatidic acid. These lipid factors are signaling molecules important in numerous pathways, including the inflammatory response. (Anderson, R. et al. (1994) Toxicol. Appl. Pharmacol. 125:176-183; Selle, H. et al. (1993); Eur. J. Biochem. 212:411-416.)

The secretory phospholipase A<sub>2</sub> (PLA<sub>2</sub>) superfamily comprises a number of heterogeneous enzymes whose common feature is to hydrolyze the sn-2 fatty acid acyl ester bond of phosphoglycerides. Hydrolysis of the glycerophospholipids releases free fatty acids and lysophospholipids. PLA<sub>2</sub> activity generates precursors for the biosynthesis of biologically active lipids, hydroxy fatty acids, and platelet-activating factor. PLA<sub>2</sub> hydrolysis of the sn-2 ester bond in phospholipids generates free fatty acids, such as arachidonic acid and lysophospholipids.

#### Carbon and Carbohydrate Metabolism

Carbohydrates, including sugars or saccharides, starch, and cellulose, are aldehyde or ketone compounds with multiple hydroxyl groups. The importance of carbohydrate metabolism is demonstrated by the sensitive regulatory system in place for maintenance of blood glucose levels. Two pancreatic hormones, insulin and glucagon, promote increased glucose uptake and storage by cells, and increased glucose release from cells, respectively. Carbohydrates have three important roles in mammalian cells. First, carbohydrates are used as energy stores, fuels, and metabolic intermediates. Carbohydrates are broken down to form energy in glycolysis and are stored as glycogen for later use. Second, the sugars deoxyribose and ribose form part of the structural support of DNA and RNA, respectively. Third, carbohydrate modifications are added to secreted and membrane proteins and lipids as they traverse the secretory pathway. Cell surface carbohydrate-containing macromolecules, including glycoproteins, glycolipids, and transmembrane proteoglycans, mediate adhesion with other cells and with components of the extracellular matrix. The extracellular matrix is comprised of diverse glycoproteins, glycosaminoglycans (GAGs), and carbohydrate-binding proteins which are secreted from the cell and assembled into an organized meshwork in close association with the cell surface. The interaction of the cell with the surrounding matrix profoundly influences cell shape, strength, flexibility, motility, and adhesion. These dynamic properties are intimately associated with signal transduction pathways controlling cell proliferation and differentiation, tissue construction, and embryonic development.

Carbohydrate metabolism is altered in several disorders including diabetes mellitus, hyperglycemia, hypoglycemia, galactosemia, galactokinase deficiency, and UDP-galactose-4-epimerase deficiency (Fauci, A.S. et al. (1998) Harrison's Principles of Internal Medicine, McGraw-Hill, New York NY, pp. 2208-2209). Altered carbohydrate metabolism is associated with cancer. Reduced GAG and proteoglycan expression is associated with human lung carcinomas (Nackaerts, K. et al. (1997) *Int. J. Cancer* 74:335-345). The carbohydrate determinants sialyl Lewis A and sialyl Lewis X are frequently expressed on human cancer cells (Kannagi, R. (1997) *Glycoconj. J.* 14:577-584). Alterations of the N-linked carbohydrate core structure of cell surface glycoproteins are linked to colon and pancreatic cancers (Schwarz, R.E. et al. (1996) *Cancer Lett.* 107:285-291). Reduced expression of the Sda blood group carbohydrate structure in cell surface glycolipids and glycoproteins is observed in gastrointestinal cancer (Dohi, T. et al. (1996) *Int. J. Cancer* 67:626-663). (Carbon and

carbohydrate metabolism is reviewed in Stryer, L. (1995) Biochemistry W.H. Freeman and Company, New York NY; Lehninger, A.L. (1982) Principles of Biochemistry Worth Publishers Inc., New York NY; and Lodish, H. et al. (1995) Molecular Cell Biology Scientific American Books, New York NY.)

#### Glycolysis

- 5 Enzymes of the glycolytic pathway convert the sugar glucose to pyruvate while simultaneously producing ATP. The pathway also provides building blocks for the synthesis of cellular components such as long-chain fatty acids. After glycolysis, pyruvate is converted to acetyl-Coenzyme A, which, in aerobic organisms, enters the citric acid cycle. Glycolytic enzymes include hexokinase, phosphoglucose isomerase, phosphofructokinase, aldolase, triose phosphate isomerase, 10 glyceraldehyde 3-phosphate dehydrogenase, phosphoglycerate kinase, phosphoglyceromutase, enolase, and pyruvate kinase. Of these, phosphofructokinase, hexokinase, and pyruvate kinase are important in regulating the rate of glycolysis.

#### Gluconeogenesis

- Gluconeogenesis is the synthesis of glucose from noncarbohydrate precursors such as lactate 15 and amino acids. The pathway, which functions mainly in times of starvation and intense exercise, occurs mostly in the liver and kidney. Responsible enzymes include pyruvate carboxylase, phosphoenolpyruvate carboxykinase, fructose 1,6-bisphosphatase, and glucose-6-phosphatase.

#### Pentose Phosphate Pathway

- Pentose phosphate pathway enzymes are responsible for generating the reducing agent 20 NADPH, while at the same time oxidizing glucose-6-phosphate to ribose-5-phosphate. Ribose-5-phosphate and its derivatives become part of important biological molecules such as ATP, Coenzyme A, NAD<sup>+</sup>, FAD, RNA, and DNA. The pentose phosphate pathway has both oxidative and non-oxidative branches. The oxidative branch steps, which are catalyzed by the enzymes glucose-6-phosphate dehydrogenase, lactonase, and 6-phosphogluconate dehydrogenase, convert glucose-6-phosphate and NADP<sup>+</sup> to ribulose-6-phosphate and NADPH. The non-oxidative branch steps, which 25 are catalyzed by the enzymes phosphopentose isomerase, phosphopentose epimerase, transketolase, and transaldolase, allow the interconversion of three-, four-, five-, six-, and seven-carbon sugars.

#### Glucuronate Metabolism

- Glucuronate is a monosaccharide which, in the form of D-glucuronic acid, is found in the 30 GAGs chondroitin and dermatan. D-glucuronic acid is also important in the detoxification and excretion of foreign organic compounds such as phenol. Enzymes involved in glucuronate metabolism include UDP-glucose dehydrogenase and glucuronate reductase.

#### Disaccharide Metabolism

- Disaccharides must be hydrolyzed to monosaccharides to be digested. Lactose, a 35 disaccharide found in milk, is hydrolyzed to galactose and glucose by the enzyme lactase. Maltose is derived from plant starch and is hydrolyzed to glucose by the enzyme maltase. Sucrose is derived

from plants and is hydrolyzed to glucose and fructose by the enzyme sucrase. Trehalose, a disaccharide found mainly in insects and mushrooms, is hydrolyzed to glucose by the enzyme trehalase (OMIM \*275360 Trehalase; Ruf, J. et al. (1990) J. Biol. Chem. 265:15034-15039). Lactase, maltase, sucrase, and trehalase are bound to mucosal cells lining the small intestine, where they participate in the digestion of dietary disaccharides. The enzyme lactose synthetase, composed of the catalytic subunit galactosyltransferase and the modifier subunit  $\alpha$ -lactalbumin, converts UDP-galactose and glucose to lactose in the mammary glands.

#### Glycogen, Starch, and Chitin Metabolism

Glycogen is the storage form of carbohydrates in mammals. Mobilization of glycogen maintains glucose levels between meals and during muscular activity. Glycogen is stored mainly in the liver and in skeletal muscle in the form of cytoplasmic granules. These granules contain enzymes that catalyze the synthesis and degradation of glycogen, as well as enzymes that regulate these processes. Enzymes that catalyze the degradation of glycogen include glycogen phosphorylase, a transferase,  $\alpha$ -1,6-glucosidase, and phosphoglucomutase. Enzymes that catalyze the synthesis of glycogen include UDP-glucose pyrophosphorylase, glycogen synthetase, a branching enzyme, and nucleoside diphosphokinase. The enzymes of glycogen synthesis and degradation are tightly regulated by the hormones insulin, glucagon, and epinephrine. Starch, a plant-derived polysaccharide, is hydrolyzed to maltose, maltotriose, and  $\alpha$ -dextrin by  $\alpha$ -amylase, an enzyme secreted by the salivary glands and pancreas. Chitin is a polysaccharide found in insects and crustacea. A chitotriosidase is secreted by macrophages and may play a role in the degradation of chitin-containing pathogens (Boot, R.G. et al. (1995) J. Biol. Chem. 270:26252-26256).

#### Peptidoglycans and Glycosaminoglycans

Glycosaminoglycans (GAGs) are anionic linear unbranched polysaccharides composed of repetitive disaccharide units. These repetitive units contain a derivative of an amino sugar, either glucosamine or galactosamine. GAGs exist free or as part of proteoglycans, large molecules composed of a core protein attached to one or more GAGs. GAGs are found on the cell surface, inside cells, and in the extracellular matrix. Changes in GAG levels are associated with several autoimmune diseases including autoimmune thyroid disease, autoimmune diabetes mellitus, and systemic lupus erythematosus (Hansen, C. et al. (1996) Clin. Exp. Rheum. 14 (Suppl. 15):S59-S67). GAGs include chondroitin sulfate, keratan sulfate, heparin, heparan sulfate, dermatan sulfate, and hyaluronan.

The GAG hyaluronan (HA) is found in the extracellular matrix of many cells, especially in soft connective tissues, and is abundant in synovial fluid (Pitsillides, A.A. et al. (1993) Int. J. Exp. Pathol. 74:27-34). HA seems to play important roles in cell regulation, development, and differentiation (Laurent, T.C. and J.R. Fraser (1992) FASEB J. 6:2397-2404). Hyaluronidase is an enzyme that degrades HA to oligosaccharides. Hyaluronidases may function in cell adhesion,



infection, angiogenesis, signal transduction, reproduction, cancer, and inflammation.

Proteoglycans, also known as peptidoglycans, are found in the extracellular matrix of connective tissues such as cartilage and are essential for distributing the load in weight-bearing joints. Cell-surface-attached proteoglycans anchor cells to the extracellular matrix. Both extracellular and cell-surface proteoglycans bind growth factors, facilitating their binding to cell-surface receptors and subsequent triggering of signal transduction pathways.

#### Amino Acid and Nitrogen Metabolism

$\text{NH}_4^+$  is assimilated into amino acids by the actions of two enzymes, glutamate dehydrogenase and glutamine synthetase. The carbon skeletons of amino acids come from the intermediates of glycolysis, the pentose phosphate pathway, or the citric acid cycle. Of the twenty amino acids used in proteins, humans can synthesize only thirteen (nonessential amino acids). The remaining nine must come from the diet (essential amino acids). Enzymes involved in nonessential amino acid biosynthesis include glutamate kinase dehydrogenase, pyrroline carboxylate reductase, asparagine synthetase, phenylalanine oxygenase, methionine adenosyltransferase, adenosylhomocysteinase, cystathionine  $\beta$ -synthase, cystathionine  $\gamma$ -lyase, phosphoglycerate dehydrogenase, phosphoserine transaminase, phosphoserine phosphatase, serine hydroxymethyltransferase, and glycine synthase.

Metabolism of amino acids takes place almost entirely in the liver, where the amino group is removed by aminotransferases (transaminases), for example, alanine aminotransferase. The amino group is transferred to  $\alpha$ -ketoglutarate to form glutamate. Glutamate dehydrogenase converts glutamate to  $\text{NH}_4^+$  and  $\alpha$ -ketoglutarate.  $\text{NH}_4^+$  is converted to urea by the urea cycle which is catalyzed by the enzymes arginase, ornithine transcarbamoylase, arginosuccinate synthetase, and arginosuccinase. Carbamoyl phosphate synthetase is also involved in urea formation. Enzymes involved in the metabolism of the carbon skeleton of amino acids include serine dehydratase, asparaginase, glutaminase, propionyl CoA carboxylase, methylmalonyl CoA mutase, branched-chain  $\alpha$ -keto dehydrogenase complex, isovaleryl CoA dehydrogenase,  $\beta$ -methylcrotonyl CoA carboxylase, phenylalanine hydroxylase, p-hydroxyphenylpyruvate hydroxylase, and homogentisate oxidase.

Polyamines, which include spermidine, putrescine, and spermine, bind tightly to nucleic acids and are abundant in rapidly proliferating cells. Enzymes involved in polyamine synthesis include ornithine decarboxylase.

Diseases involved in amino acid and nitrogen metabolism include hyperammonemia, carbamoyl phosphate synthetase deficiency, urea cycle enzyme deficiencies, methylmalonic aciduria, maple syrup disease, alcaptonuria, and phenylketonuria.

#### Energy Metabolism

Cells derive energy from metabolism of ingested compounds that may be roughly categorized as carbohydrates, fats, or proteins. Energy is also stored in polymers such as triglycerides (fats) and

glycogen (carbohydrates). Metabolism proceeds along separate reaction pathways connected by key intermediates such as acetyl coenzyme A (acetyl-CoA). Metabolic pathways feature anaerobic and aerobic degradation, coupled with the energy-requiring reactions such as phosphorylation of adenosine diphosphate (ADP) to the triphosphate (ATP) or analogous phosphorylations of guanosine  
 5 (GDP/GTP), uridine (UDP/UTP), or cytidine (CDP/CTP). Subsequent dephosphorylation of the triphosphate drives reactions needed for cell maintenance, growth, and proliferation.

Digestive enzymes convert carbohydrates and sugars to glucose; fructose and galactose are converted in the liver to glucose. Enzymes involved in these conversions include galactose-1-phosphate uridyl transferase and UDP-galactose-4 epimerase. In the cytoplasm, glycolysis converts  
 10 glucose to pyruvate in a series of reactions coupled to ATP synthesis.

Pyruvate is transported into the mitochondria and converted to acetyl-CoA for oxidation via the citric acid cycle, involving pyruvate dehydrogenase components, dihydrolipoyl transacetylase, and dihydrolipoyl dehydrogenase. Enzymes involved in the citric acid cycle include: citrate synthetase, aconitases, isocitrate dehydrogenase, alpha-ketoglutarate dehydrogenase complex  
 15 including transsuccinylases, succinyl CoA synthetase, succinate dehydrogenase, fumarases, and malate dehydrogenase. Acetyl CoA is oxidized to CO<sub>2</sub> with concomitant formation of NADH, FADH<sub>2</sub>, and GTP. In oxidative phosphorylation, the transport of electrons from NADH and FADH<sub>2</sub> to oxygen by dehydrogenases is coupled to the synthesis of ATP from ADP and P<sub>i</sub> by the F<sub>0</sub>F<sub>1</sub> ATPase complex in the mitochondrial inner membrane. Enzyme complexes responsible for electron  
 20 transport and ATP synthesis include the F<sub>0</sub>F<sub>1</sub> ATPase complex, ubiquinone(CoQ)-cytochrome c reductase, ubiquinone reductase, cytochrome b, cytochrome c<sub>1</sub>, FeS protein, and cytochrome c oxidase.

Triglycerides are hydrolyzed to fatty acids and glycerol by lipases. Glycerol is then phosphorylated to glycerol-3-phosphate by glycerol kinase and glycerol phosphate dehydrogenase,  
 25 and degraded by the glycolysis. Fatty acids are transported into the mitochondria as fatty acyl-carnitine esters and undergo oxidative degradation.

In addition to metabolic disorders such as diabetes and obesity, disorders of energy metabolism are associated with cancers (Dorward, A. et al. (1997) *J. Bioenerg. Biomembr.* 29:385-392), autism (Lombard, J. (1998) *Med. Hypotheses* 50:497-500), neurodegenerative disorders (Alexi,  
 30 T. et al. (1998) *Neuroreport* 9:R57-64), and neuromuscular disorders (DiMauro, S. et al. (1998) *Biochim. Biophys. Acta* 1366:199-210). The myocardium is heavily dependent on oxidative metabolism, so metabolic dysfunction often leads to heart disease (DiMauro, S. and M. Hirano (1998) *Curr. Opin. Cardiol.* 13:190-197).

For a review of energy metabolism enzymes and intermediates, see Stryer, L. et al. (1995) *Biochemistry*, W.H. Freeman and Co., San Francisco CA, pp. 443-652. For a review of energy  
 35 metabolism regulation, see Lodish, H. et al. (1995) *Molecular Cell Biology*, Scientific American

Books, New York NY, pp. 744-770.

### Cofactor Metabolism

Cofactors, including coenzymes and prosthetic groups, are small molecular weight inorganic or organic compounds that are required for the action of an enzyme. Many cofactors contain  
5 vitamins as a component. Cofactors include thiamine pyrophosphate, flavin adenine dinucleotide, flavin mononucleotide, nicotinamide adenine dinucleotide, pyridoxal phosphate, coenzyme A, tetrahydrofolate, lipoamide, and heme. The vitamins biotin and cobalamin are associated with enzymes as well. Heme, a prosthetic group found in myoglobin and hemoglobin, consists of  
10 protoporphyrin group bound to iron. Porphyrin groups contain four substituted pyrroles covalently joined in a ring, often with a bound metal atom. Enzymes involved in porphyrin synthesis include  $\delta$ -aminolevulinate synthase,  $\delta$ -aminolevulinate dehydrase, porphobilinogen deaminase, and cosynthase. Deficiencies in heme formation cause porphyrias. Heme is broken down as a part of erythrocyte turnover. Enzymes involved in heme degradation include heme oxygenase and biliverdin reductase.

Iron is a required cofactor for many enzymes. Besides the heme-containing enzymes, iron is  
15 found in iron-sulfur clusters in proteins including aconitase, succinate dehydrogenase, and NADH-Q reductase. Iron is transported in the blood by the protein transferrin. Binding of transferrin to the transferrin receptor on cell surfaces allows uptake by receptor mediated endocytosis. Cytosolic iron is bound to ferritin protein.

A molybdenum-containing cofactor (molybdopterin) is found in enzymes including sulfite  
20 oxidase, xanthine dehydrogenase, and aldehyde oxidase. Molybdopterin biosynthesis is performed by two molybdenum cofactor synthesizing enzymes. Deficiencies in these enzymes cause mental retardation and lens dislocation. Other diseases caused by defects in cofactor metabolism include pernicious anemia and methylmalonic aciduria.

### Secretion and Trafficking

Eukaryotic cells are bound by a lipid bilayer membrane and subdivided into functionally  
25 distinct, membrane bound compartments. The membranes maintain the essential differences between the cytosol, the extracellular environment, and the luminal space of each intracellular organelle. As lipid membranes are highly impermeable to most polar molecules, transport of essential nutrients, metabolic waste products, cell signaling molecules, macromolecules and proteins across lipid  
30 membranes and between organelles must be mediated by a variety of transport-associated molecules.

### Protein Trafficking

In eukaryotes, some proteins are synthesized on ER-bound ribosomes, co-translationally imported into the ER, delivered from the ER to the Golgi complex for post-translational processing and sorting, and transported from the Golgi to specific intracellular and extracellular destinations.  
35 All cells possess a constitutive transport process which maintains homeostasis between the cell and its environment. In many differentiated cell types, the basic machinery is modified to carry out

specific transport functions. For example, in endocrine glands, hormones and other secreted proteins are packaged into secretory granules for regulated exocytosis to the cell exterior. In macrophage, foreign extracellular material is engulfed (phagocytosis) and delivered to lysosomes for degradation. In fat and muscle cells, glucose transporters are stored in vesicles which fuse with the plasma

5 membrane only in response to insulin stimulation.

#### The Secretory Pathway

Synthesis of most integral membrane proteins, secreted proteins, and proteins destined for the lumen of a particular organelle occurs on ER-bound ribosomes. These proteins are co-translationally imported into the ER. The proteins leave the ER via membrane-bound vesicles which bud off the ER  
10 at specific sites and fuse with each other (homotypic fusion) to form the ER-Golgi Intermediate Compartment (ERGIC). The ERGIC matures progressively through the *cis*, *medial*, and *trans* cisternal stacks of the Golgi, modifying the enzyme composition by retrograde transport of specific Golgi enzymes. In this way, proteins moving through the Golgi undergo post-translational modification, such as glycosylation. The final Golgi compartment is the Trans-Golgi Network  
15 (TGN), where both membrane and luminal proteins are sorted for their final destination. Transport vesicles destined for intracellular compartments, such as the lysosome, bud off the TGN. What remains is a secretory vesicle which contains proteins destined for the plasma membrane, such as receptors, adhesion molecules, and ion channels, and secretory proteins, such as hormones, neurotransmitters, and digestive enzymes. Secretory vesicles eventually fuse with the plasma  
20 membrane (Glick, B.S. and V. Malhotra (1998) Cell 95:883-889).

The secretory process can be constitutive or regulated. Most cells have a constitutive pathway for secretion, whereby vesicles derived from maturation of the TGN require no specific signal to fuse with the plasma membrane. In many cells, such as endocrine cells, digestive cells, and neurons, vesicle pools derived from the TGN collect in the cytoplasm and do not fuse with the plasma  
25 membrane until they are directed to by a specific signal.

#### Endocytosis

Endocytosis, wherein cells internalize material from the extracellular environment, is essential for transmission of neuronal, metabolic, and proliferative signals; uptake of many essential nutrients; and defense against invading organisms. Most cells exhibit two forms of endocytosis. The  
30 first, phagocytosis, is an actin-driven process exemplified in macrophage and neutrophils. Material to be endocytosed contacts numerous cell surface receptors which stimulate the plasma membrane to extend and surround the particle, enclosing it in a membrane-bound phagosome. In the mammalian immune system, IgG-coated particles bind Fc receptors on the surface of phagocytic leukocytes. Activation of the Fc receptors initiates a signal cascade involving src-family cytosolic kinases and the  
35 monomeric GTP-binding (G) protein Rho. The resulting actin reorganization leads to phagocytosis of the particle. This process is an important component of the humoral immune response, allowing the

processing and presentation of bacterial-derived peptides to antigen-specific T-lymphocytes.

The second form of endocytosis, pinocytosis, is a more generalized uptake of material from the external milieu. Like phagocytosis, pinocytosis is activated by ligand binding to cell surface receptors. Activation of individual receptors stimulates an internal response that includes

5 coalescence of the receptor-ligand complexes and formation of clathrin-coated pits. Invagination of the plasma membrane at clathrin-coated pits produces an endocytic vesicle within the cell cytoplasm. These vesicles undergo homotypic fusion to form an early endosomal (EE) compartment. The tubulovesicular EE serves as a sorting site for incoming material. ATP-driven proton pumps in the EE membrane lowers the pH of the EE lumen (pH 6.3-6.8). The acidic environment causes many

10 ligands to dissociate from their receptors. The receptors, along with membrane and other integral membrane proteins, are recycled back to the plasma membrane by budding off the tubular extensions of the EE in recycling vesicles (RV). This selective removal of recycled components produces a carrier vesicle containing ligand and other material from the external environment. The carrier vesicle fuses with TGN-derived vesicles which contain hydrolytic enzymes. The acidic environment

15 of the resulting late endosome (LE) activates the hydrolytic enzymes which degrade the ligands and other material. As digestion takes place, the LE fuses with the lysosome where digestion is completed (Mellman, I. (1996) *Annu. Rev. Cell Dev. Biol.* 12:575-625).

Recycling vesicles may return directly to the plasma membrane. Receptors internalized and returned directly to the plasma membrane have a turnover rate of 2-3 minutes. Some RVs undergo

20 microtubule-directed relocation to a perinuclear site, from which they then return to the plasma membrane. Receptors following this route have a turnover rate of 5-10 minutes. Still other RVs are retained within the cell until an appropriate signal is received (Mellman, *supra*; and James, D.E. et al. (1994) *Trends Cell Biol.* 4:120-126).

#### Vesicle Formation

Several steps in the transit of material along the secretory and endocytic pathways require the formation of transport vesicles. Specifically, vesicles form at the transitional endoplasmic reticulum (tER), the rim of Golgi cisternae, the face of the Trans-Golgi Network (TGN), the plasma membrane (PM), and tubular extensions of the endosomes. The process begins with the budding of a vesicle out

25 of the donor membrane. The membrane-bound vesicle contains proteins to be transported and is surrounded by a protective coat made up of protein subunits recruited from the cytosol. The initial budding and coating processes are controlled by a cytosolic ras-like GTP-binding protein, ADP-ribosylating factor (Arf), and adapter proteins (AP). Different isoforms of both Arf and AP are involved at different sites of budding. Another small G-protein, dynamin, forms a ring complex

30 around the neck of the forming vesicle and may provide the mechanochemical force to accomplish the final step of the budding process. The coated vesicle complex is then transported through the cytosol. During the transport process, Arf-bound GTP is hydrolyzed to GDP and the coat dissociates from the

transport vesicle (West, M.A. et al. (1997) *J. Cell Biol.* 138:1239-1254). Two different classes of coat protein have also been identified. Clathrin coats form on the TGN and PM surfaces, whereas coatomer or COP coats form on the ER and Golgi. COP coats can further be distinguished as COPI, involved in retrograde traffic through the Golgi and from the Golgi to the ER, and COPII, involved in anterograde traffic from the ER to the Golgi (Mellman, *supra*). The COP coat consists of two major components, a G-protein (Arf or Sar) and coat protomer (coatomer). Coatomer is an equimolar complex of seven proteins, termed alpha-, beta-, beta'-, gamma-, delta-, epsilon- and zeta-COP. (Harter, C. and F.T. Wieland (1998) *Proc. Natl. Acad. Sci. USA* 95:11649-11654.)

#### Membrane Fusion

Transport vesicles undergo homotypic or heterotypic fusion in the secretory and endocytotic pathways. Molecules required for appropriate targeting and fusion of vesicles with their target membrane include proteins incorporated in the vesicle membrane, the target membrane, and proteins recruited from the cytosol. During budding of the vesicle from the donor compartment, an integral membrane protein, VAMP (vesicle-associated membrane protein) is incorporated into the vesicle. Soon after the vesicle uncoats, a cytosolic prenylated GTP-binding protein, Rab (a member of the Ras superfamily), is inserted into the vesicle membrane. GTP-bound Rab proteins are directed into nascent transport vesicles where they interact with VAMP. Following vesicle transport, GTPase activating proteins (GAPs) in the target membrane convert Rab proteins to the GDP-bound form. A cytosolic protein, guanine-nucleotide dissociation inhibitor (GDI) helps return GDP-bound Rab proteins to their membrane of origin. Several Rab isoforms have been identified and appear to associate with specific compartments within the cell. Rab proteins appear to play a role in mediating the function of a viral gene, Rev, which is essential for replication of HIV-1, the virus responsible for AIDS (Flavell, R.A. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:4421-4424).

Docking of the transport vesicle with the target membrane involves the formation of a complex between the vesicle SNAP receptor (v-SNARE), target membrane (t-) SNAREs, and certain other membrane and cytosolic proteins. Many of these other proteins have been identified although their exact functions in the docking complex remain uncertain (Tellam, J.T. et al. (1995) *J. Biol. Chem.* 270:5857-5863; and Hata, Y. and T.C. Sudhof (1995) *J. Biol. Chem.* 270:13022-13028). N-ethylmaleimide sensitive factor (NSF) and soluble NSF-attachment protein ( $\alpha$ -SNAP and  $\beta$ -SNAP) are two such proteins that are conserved from yeast to man and function in most intracellular membrane fusion reactions. Sec1 represents a family of yeast proteins that function at many different stages in the secretory pathway including membrane fusion. Recently, mammalian homologs of Sec1, called Munc-18 proteins, have been identified (Katagiri, H. et al. (1995) *J. Biol. Chem.* 270:4963-4966; Hata et al. *supra*).

The SNARE complex involves three SNARE molecules, one in the vesicular membrane and two in the target membrane. Synaptotagmin is an integral membrane protein in the synaptic vesicle

which associates with the t-SNARE syntaxin in the docking complex. Synaptotagmin binds calcium in a complex with negatively charged phospholipids, which allows the cytosolic SNAP protein to displace synaptotagmin from syntaxin and fusion to occur. Thus, synaptotagmin is a negative regulator of fusion in the neuron (Littleton, J.T. et al. (1993) Cell 74:1125-1134). The most abundant  
5 membrane protein of synaptic vesicles appears to be the glycoprotein synaptophysin, a 38 kDa protein with four transmembrane domains.

Specificity between a vesicle and its target is derived from the v-SNARE, t-SNAREs, and associated proteins involved. Different isoforms of SNAREs and Rabs show distinct cellular and subcellular distributions. VAMP-1/synaptobrevin, membrane-anchored synaptosome-associated  
10 protein of 25 kDa (SNAP-25), syntaxin-1, Rab3A, Rab15, and Rab23 are predominantly expressed in the brain and nervous system. Different syntaxin, VAMP, and Rab proteins are associated with distinct subcellular compartments and their vesicular carriers.

#### Nuclear Transport

Transport of proteins and RNA between the nucleus and the cytoplasm occurs through  
15 nuclear pore complexes (NPCs). NPC-mediated transport occurs in both directions through the nuclear envelope. All nuclear proteins are imported from the cytoplasm, their site of synthesis. tRNA and mRNA are exported from the nucleus, their site of synthesis, to the cytoplasm, their site of function. Processing of small nuclear RNAs involves export into the cytoplasm, assembly with proteins and modifications such as hypermethylation to produce small nuclear ribonuclear proteins  
20 (snRNPs), and subsequent import of the snRNPs back into the nucleus. The assembly of ribosomes requires the initial import of ribosomal proteins from the cytoplasm, their incorporation with RNA into ribosomal subunits, and export back to the cytoplasm. (Görllich, D. and I.W. Mattaj (1996) Science 271:1513-1518.)

The transport of proteins and mRNAs across the NPC is selective, dependent on nuclear  
25 localization signals, and generally requires association with nuclear transport factors. Nuclear localization signals (NLS) consist of short stretches of amino acids enriched in basic residues. NLS are found on proteins that are targeted to the nucleus, such as the glucocorticoid receptor. The NLS is recognized by the NLS receptor, importin, which then interacts with the monomeric GTP-binding protein Ran. This NLS protein/receptor/Ran complex navigates the nuclear pore with the help of the  
30 homodimeric protein nuclear transport factor 2 (NTF2). NTF2 binds the GDP-bound form of Ran and to multiple proteins of the nuclear pore complex containing FXFG repeat motifs, such as p62. (Paschal, B. et al. (1997) J. Biol. Chem. 272:21534-21539; and Wong, D.H. et al. (1997) Mol. Cell Biol. 17:3755-3767). Some proteins are dissociated before nuclear mRNAs are transported across the NPC while others are dissociated shortly after nuclear mRNA transport across the NPC and are  
35 reimported into the nucleus.

#### Disease Correlation

The etiology of numerous human diseases and disorders can be attributed to defects in the transport or secretion of proteins. For example, abnormal hormonal secretion is linked to disorders such as diabetes insipidus (vasopressin), hyper- and hypoglycemia (insulin, glucagon), Grave's disease and goiter (thyroid hormone), and Cushing's and Addison's diseases (adrenocorticotrophic hormone, ACTH). Moreover, cancer cells secrete excessive amounts of hormones or other biologically active peptides. Disorders related to excessive secretion of biologically active peptides by tumor cells include fasting hypoglycemia due to increased insulin secretion from insulinoma-islet cell tumors; hypertension due to increased epinephrine and norepinephrine secreted from pheochromocytomas of the adrenal medulla and sympathetic paraganglia; and carcinoid syndrome, which is characterized by abdominal cramps, diarrhea, and valvular heart disease caused by excessive amounts of vasoactive substances such as serotonin, bradykinin, histamine, prostaglandins, and polypeptide hormones, secreted from intestinal tumors. Biologically active peptides that are ectopically synthesized in and secreted from tumor cells include ACTH and vasopressin (lung and pancreatic cancers); parathyroid hormone (lung and bladder cancers); calcitonin (lung and breast cancers); and thyroid-stimulating hormone (medullary thyroid carcinoma). Such peptides may be useful as diagnostic markers for tumorigenesis (Schwartz, M.Z. (1997) *Semin. Pediatr. Surg.* 3:141-146; and Said, S.I. and G.R. Faloona (1975) *N. Engl. J. Med.* 293:155-160).

Defective nuclear transport may play a role in cancer. The BRCA1 protein contains three potential NLSs which interact with importin alpha, and is transported into the nucleus by the importin/NPC pathway. In breast cancer cells the BRCA1 protein is aberrantly localized in the cytoplasm. The mislocation of the BRCA1 protein in breast cancer cells may be due to a defect in the NPC nuclear import pathway (Chen, C.F. et al. (1996) *J. Biol. Chem.* 271:32863-32868).

It has been suggested that in some breast cancers, the tumor-suppressing activity of p53 is inactivated by the sequestration of the protein in the cytoplasm, away from its site of action in the cell nucleus. Cytoplasmic wild-type p53 was also found in human cervical carcinoma cell lines. (Moll, U.M. et al. (1992) *Proc. Natl. Acad. Sci. USA* 89:7262-7266; and Liang, X.H. et al. (1993) *Oncogene* 8:2645-2652.)

#### Environmental Responses

Organisms respond to the environment by a number of pathways. Heat shock proteins, including hsp 70, hsp60, hsp90, and hsp 40, assist organisms in coping with heat damage to cellular proteins.

Aquaporins (AQP) are channels that transport water and, in some cases, nonionic small solutes such as urea and glycerol. Water movement is important for a number of physiological processes including renal fluid filtration, aqueous humor generation in the eye, cerebrospinal fluid production in the brain, and appropriate hydration of the lung. Aquaporins are members of the major intrinsic protein (MIP) family of membrane transporters (King, L.S. and P. Agre (1996) *Annu. Rev.*



Physiol. 58:619-648; Ishibashi, K. et al. (1997) J. Biol. Chem. 272:20782-20786). The study of aquaporins may have relevance to understanding edema formation and fluid balance in both normal physiology and disease states (King, *supra*). Mutations in AQP2 cause autosomal recessive nephrogenic diabetes insipidus (OMIM \*107777 Aquaporin 2; AQP2). Reduced AQP4 expression in  
5 skeletal muscle may be associated with Duchenne muscular dystrophy (Frigeri, A. et al. (1998) J. Clin. Invest. 102:695-703). Mutations in AQP0 cause autosomal dominant cataracts in the mouse (OMIM \*154050 Major Intrinsic Protein of Lens Fiber; MIP).

The metallothioneins (MTs) are a group of small (61 amino acids), cysteine-rich proteins that bind heavy metals such as cadmium, zinc, mercury, lead, and copper and are thought to play a role in  
10 metal detoxification or the metabolism and homeostasis of metals. Arsenite-resistance proteins have been identified in hamsters that are resistant to toxic levels of arsenite (Rossman, T.G. et al. (1997) Mutat. Res. 386:307-314).

Humans respond to light and odors by specific protein pathways. Proteins involved in light perception include rhodopsin, transducin, and cGMP phosphodiesterase. Proteins involved in odor  
15 perception include multiple olfactory receptors. Other proteins are important in human Circadian rhythms and responses to wounds.

#### Immunity and Host Defense

All vertebrates have developed sophisticated and complex immune systems that provide protection from viral, bacterial, fungal and parasitic infections. Included in these systems are the  
20 processes of humoral immunity, the complement cascade and the inflammatory response (Paul, W.E. (1993) Fundamental Immunology, Raven Press, Ltd., New York NY, pp.1-20).

The cellular components of the humoral immune system include six different types of leukocytes: monocytes, lymphocytes, polymorphonuclear granulocytes (consisting of neutrophils, eosinophils, and basophils) and plasma cells. Additionally, fragments of megakaryocytes, a seventh  
25 type of white blood cell in the bone marrow, occur in large numbers in the blood as platelets.

Leukocytes are formed from two stem cell lineages in bone marrow. The myeloid stem cell line produces granulocytes and monocytes and, the lymphoid stem cell produces lymphocytes. Lymphoid cells travel to the thymus, spleen and lymph nodes, where they mature and differentiate into lymphocytes. Leukocytes are responsible for defending the body against invading pathogens.  
30 Neutrophils and monocytes attack invading bacteria, viruses, and other pathogens and destroy them by phagocytosis. Monocytes enter tissues and differentiate into macrophages which are extremely phagocytic. Lymphocytes and plasma cells are a part of the immune system which recognizes specific foreign molecules and organisms and inactivates them, as well as signals other cells to attack the invaders.

35 Granulocytes and monocytes are formed and stored in the bone marrow until needed. Megakaryocytes are produced in bone marrow, where they fragment into platelets and are released

into the bloodstream. The main function of platelets is to activate the blood clotting mechanism. Lymphocytes and plasma cells are produced in various lymphogenous organs, including the lymph nodes, spleen, thymus, and tonsils.

Both neutrophils and macrophages exhibit chemotaxis towards sites of inflammation. Tissue inflammation in response to pathogen invasion results in production of chemo-attractants for leukocytes, such as endotoxins or other bacterial products, prostaglandins, and products of leukocytes or platelets.

Basophils participate in the release of the chemicals involved in the inflammatory process. The main function of basophils is secretion of these chemicals to such a degree that they have been referred to as "unicellular endocrine glands." A distinct aspect of basophilic secretion is that the contents of granules go directly into the extracellular environment, not into vacuoles as occurs with neutrophils, eosinophils and monocytes. Basophils have receptors for the Fc fragment of immunoglobulin E (IgE) that are not present on other leukocytes. Crosslinking of membrane IgE with anti-IgE or other ligands triggers degranulation.

Eosinophils are bi- or multi-nucleated white blood cells which contain eosinophilic granules. Their plasma membrane is characterized by Ig receptors, particularly IgG and IgE. Generally, eosinophils are stored in the bone marrow until recruited for use at a site of inflammation or invasion. They have specific functions in parasitic infections and allergic reactions, and are thought to detoxify some of the substances released by mast cells and basophils which cause inflammation. Additionally, they phagocytize antigen-antibody complexes and further help prevent spread of the inflammation.

Macrophages are monocytes that have left the blood stream to settle in tissue. Once monocytes have migrated into tissues, they do not re-enter the bloodstream. The mononuclear phagocyte system is comprised of precursor cells in the bone marrow, monocytes in circulation, and macrophages in tissues. The system is capable of very fast and extensive phagocytosis. A macrophage may phagocytize over 100 bacteria, digest them and extrude residues, and then survive for many more months. Macrophages are also capable of ingesting large particles, including red blood cells and malarial parasites. They increase several-fold in size and transform into macrophages that are characteristic of the tissue they have entered, surviving in tissues for several months.

Mononuclear phagocytes are essential in defending the body against invasion by foreign pathogens, particularly intracellular microorganisms such as M. tuberculosis, listeria, leishmania and toxoplasma. Macrophages can also control the growth of tumorous cells, via both phagocytosis and secretion of hydrolytic enzymes. Another important function of macrophages is that of processing antigen and presenting them in a biochemically modified form to lymphocytes.

The immune system responds to invading microorganisms in two major ways: antibody production and cell mediated responses. Antibodies are immunoglobulin proteins produced by B-lymphocytes which bind to specific antigens and cause inactivation or promote destruction of the

antigen by other cells. Cell-mediated immune responses involve T-lymphocytes (T cells) that react with foreign antigen on the surface of infected host cells. Depending on the type of T cell, the infected cell is either killed or signals are secreted which activate macrophages and other cells to destroy the infected cell (Paul, *supra*).

5 T-lymphocytes originate in the bone marrow or liver in fetuses. Precursor cells migrate via the blood to the thymus, where they are processed to mature into T-lymphocytes. This processing is crucial because of positive and negative selection of T cells that will react with foreign antigen and not with self molecules. After processing, T cells continuously circulate in the blood and secondary lymphoid tissues, such as lymph nodes, spleen, certain epithelium-associated tissues in the  
10 gastrointestinal tract, respiratory tract and skin. When T-lymphocytes are presented with the complementary antigen, they are stimulated to proliferate and release large numbers of activated T cells into the lymph system and the blood system. These activated T cells can survive and circulate for several days. At the same time, T memory cells are created, which remain in the lymphoid tissue for months or years. Upon subsequent exposure to that specific antigen, these memory cells will  
15 respond more rapidly and with a stronger response than induced by the original antigen. This creates an "immunological memory" that can provide immunity for years.

There are two major types of T cells: cytotoxic T cells destroy infected host cells, and helper T cells activate other white blood cells via chemical signals. One class of helper cell,  $T_H1$ , activates macrophages to destroy ingested microorganisms, while another,  $T_H2$ , stimulates the production of  
20 antibodies by B cells.

Cytotoxic T cells directly attack the infected target cell. In virus-infected cells, peptides derived from viral proteins are generated by the proteasome. These peptides are transported into the ER by the transporter associated with antigen processing (TAP) (Pamer, E. and P. Cresswell (1998) *Annu. Rev. Immunol.* 16:323-358). Once inside the ER, the peptides bind MHC I chains, and the  
25 peptide/MHC I complex is transported to the cell surface. Receptors on the surface of T cells bind to antigen presented on cell surface MHC molecules. Once activated by binding to antigen, T cells secrete  $\gamma$ -interferon, a signal molecule that induces the expression of genes necessary for presenting viral (or other) antigens to cytotoxic T cells. Cytotoxic T cells kill the infected cell by stimulating programmed cell death.

30 Helper T cells constitute up to 75% of the total T cell population. They regulate the immune functions by producing a variety of lymphokines that act on other cells in the immune system and on bone marrow. Among these lymphokines are: interleukins-2,3,4,5,6; granulocyte-monocyte colony stimulating factor, and  $\gamma$ -interferon.

Helper T cells are required for most B cells to respond to antigen. When an activated helper  
35 cell contacts a B cell, its centrosome and Golgi apparatus become oriented toward the B cell, aiding the directing of signal molecules, such as transmembrane-bound protein called CD40 ligand, onto the

B cell surface to interact with the CD40 transmembrane protein. Secreted signals also help B cells to proliferate and mature and, in some cases, to switch the class of antibody being produced.

B-lymphocytes (B cells) produce antibodies which react with specific antigenic proteins presented by pathogens. Once activated, B cells become filled with extensive rough endoplasmic reticulum and are known as plasma cells. As with T cells, interaction of B cells with antigen stimulates proliferation of only those B cells which produce antibody specific to that antigen. There are five classes of antibodies, known as immunoglobulins, which together comprise about 20% of total plasma protein. Each class mediates a characteristic biological response after antigen binding. Upon activation by specific antigen B cells switch from making membrane-bound antibody to secretion of that antibody.

Antibodies, or immunoglobulins (Ig), are the founding members of the Ig superfamily and the central components of the humoral immune response. Antibodies are either expressed on the surface of B cells or secreted by B cells into the circulation. Antibodies bind and neutralize blood-borne foreign antigens. The prototypical antibody is a tetramer consisting of two identical heavy polypeptide chains (H-chains) and two identical light polypeptide chains (L-chains) interlinked by disulfide bonds. This arrangement confers the characteristic Y-shape to antibody molecules. Antibodies are classified based on their H-chain composition. The five antibody classes, IgA, IgD, IgE, IgG and IgM, are defined by the  $\alpha$ ,  $\delta$ ,  $\epsilon$ ,  $\gamma$ , and  $\mu$  H-chain types. There are two types of L-chains,  $\kappa$  and  $\lambda$ , either of which may associate as a pair with any H-chain pair. IgG, the most common class of antibody found in the circulation, is tetrameric, while the other classes of antibodies are generally variants or multimers of this basic structure.

H-chains and L-chains each contain an N-terminal variable region and a C-terminal constant region. Both H-chains and L-chains contain repeated Ig domains. For example, a typical H-chain contains four Ig domains, three of which occur within the constant region and one of which occurs within the variable region and contributes to the formation of the antigen recognition site. Likewise, a typical L-chain contains two Ig domains, one of which occurs within the constant region and one of which occurs within the variable region. In addition, H chains such as  $\mu$  have been shown to associate with other polypeptides during differentiation of the B cell.

Antibodies can be described in terms of their two main functional domains. Antigen recognition is mediated by the Fab (antigen binding fragment) region of the antibody, while effector functions are mediated by the Fc (crystallizable fragment) region. Binding of antibody to an antigen, such as a bacterium, triggers the destruction of the antigen by phagocytic white blood cells such as macrophages and neutrophils. These cells express surface receptors that specifically bind to the antibody Fc region and allow the phagocytic cells to engulf, ingest, and degrade the antibody-bound antigen. The Fc receptors expressed by phagocytic cells are single-pass transmembrane glycoproteins of about 300 to 400 amino acids (Sears, D.W. et al. (1990) J. Immunol. 144:371-378).

The extracellular portion of the Fc receptor typically contains two or three Ig domains.

Diseases which cause over- or under-abundance of any one type of leukocyte usually result in the entire immune defense system becoming involved. A well-known autoimmune disease is AIDS (Acquired Immunodeficiency Syndrome) where the number of helper T cells is depleted, leaving the patient susceptible to infection by microorganisms and parasites. Another widespread medical condition attributable to the immune system is that of allergic reactions to certain antigens. Allergic reactions include: hay fever, asthma, anaphylaxis, and urticaria (hives). Leukemias are an excess production of white blood cells, to the point where a major portion of the body's metabolic resources are directed solely at proliferation of white blood cells, leaving other tissues to starve. Leukopenia or agranulocytosis occurs when the bone marrow stops producing white blood cells. This leaves the body unprotected against foreign microorganisms, including those which normally inhabit skin, mucous membranes, and gastrointestinal tract. If all white blood cell production stops completely, infection will occur within two days and death may follow only 1 to 4 days later.

Impaired phagocytosis occurs in several diseases, including monocytic leukemia, systemic lupus, and granulomatous disease. In such a situation, macrophages can phagocytize normally, but the enveloped organism is not killed. A defect in the plasma membrane enzyme which converts oxygen to lethally reactive forms results in abscess formation in liver, lungs, spleen, lymph nodes, and beneath the skin. Eosinophilia is an excess of eosinophils commonly observed in patients with allergies (hay fever, asthma), allergic reactions to drugs, rheumatoid arthritis, and cancers (Hodgkin's disease, lung, and liver cancer) (Isselbacher, K.J. et al. (1994) Harrison's Principles of Internal Medicine, McGraw-Hill, Inc., New York NY).

Host defense is further augmented by the complement system. The complement system serves as an effector system and is involved in infectious agent recognition. It can function as an independent immune network or in conjunction with other humoral immune responses. The complement system is comprised of numerous plasma and membrane proteins that act in a cascade of reaction sequences whereby one component activates the next. The result is a rapid and amplified response to infection through either an inflammatory response or increased phagocytosis.

The complement system has more than 30 protein components which can be divided into functional groupings including modified serine proteases, membrane-binding proteins and regulators of complement activation. Activation occurs through two different pathways the classical and the alternative. Both pathways serve to destroy infectious agents through distinct triggering mechanisms that eventually merge with the involvement of the component C3.

The classical pathway requires antibody binding to infectious agent antigens. The antibodies serve to define the target and initiate the complement system cascade, culminating in the destruction of the infectious agent. In this pathway, since the antibody guides initiation of the process, the complement can be seen as an effector arm of the humoral immune system.

The alternative pathway of the complement system does not require the presence of pre-existing antibodies for targeting infectious agent destruction. Rather, this pathway, through low levels of an activated component, remains constantly primed and provides surveillance in the non-immune host to enable targeting and destruction of infectious agents. In this case foreign material triggers the cascade, thereby facilitating phagocytosis or lysis (Paul, *supra*, pp.918-919).

Another important component of host defense is the process of inflammation. Inflammatory responses are divided into four categories on the basis of pathology and include allergic inflammation, cytotoxic antibody mediated inflammation, immune complex mediated inflammation and monocyte mediated inflammation. Inflammation manifests as a combination of each of these forms with one predominating.

Allergic acute inflammation is observed in individuals wherein specific antigens stimulate IgE antibody production. Mast cells and basophils are subsequently activated by the attachment of antigen-IgE complexes, resulting in the release of cytoplasmic granule contents such as histamine. The products of activated mast cells can increase vascular permeability and constrict the smooth muscle of breathing passages, resulting in anaphylaxis or asthma. Acute inflammation is also mediated by cytotoxic antibodies and can result in the destruction of tissue through the binding of complement-fixing antibodies to cells. The responsible antibodies are of the IgG or IgM types. Resultant clinical disorders include autoimmune hemolytic anemia and thrombocytopenia as associated with systemic lupus erythematosus:

Immune complex mediated acute inflammation involves the IgG or IgM antibody types which combine with antigen to activate the complement cascade. When such immune complexes bind to neutrophils and macrophages they activate the respiratory burst to form protein- and vessel-damaging agents such as hydrogen peroxide, hydroxyl radical, hypochlorous acid, and chloramines. Clinical manifestations include rheumatoid arthritis and systemic lupus erythematosus.

In chronic inflammation or delayed-type hypersensitivity, macrophages are activated and process antigen for presentation to T cells that subsequently produce lymphokines and monokines. This type of inflammatory response is likely important for defense against intracellular parasites and certain viruses. Clinical associations include, granulomatous disease, tuberculosis, leprosy, and sarcoidosis (Paul, W.E., *supra*, pp.1017-1018).

### **Extracellular Information Transmission Molecules**

Intercellular communication is essential for the growth and survival of multicellular organisms, and in particular, for the function of the endocrine, nervous, and immune systems. In addition, intercellular communication is critical for developmental processes such as tissue construction and organogenesis, in which cell proliferation, cell differentiation, and morphogenesis must be spatially and temporally regulated in a precise and coordinated manner. Cells communicate

with one another through the secretion and uptake of diverse types of signaling molecules such as hormones, growth factors, neuropeptides, and cytokines.

### Hormones

Hormones are signaling molecules that coordinately regulate basic physiological processes from embryogenesis throughout adulthood. These processes include metabolism, respiration, reproduction, excretion, fetal tissue differentiation and organogenesis, growth and development, homeostasis, and the stress response. Hormonal secretions and the nervous system are tightly integrated and interdependent. Hormones are secreted by endocrine glands, primarily the hypothalamus and pituitary, the thyroid and parathyroid, the pancreas, the adrenal glands, and the ovaries and testes.

The secretion of hormones into the circulation is tightly controlled. Hormones are often secreted in diurnal, pulsatile, and cyclic patterns. Hormone secretion is regulated by perturbations in blood biochemistry, by other upstream-acting hormones, by neural impulses, and by negative feedback loops. Blood hormone concentrations are constantly monitored and adjusted to maintain optimal, steady-state levels. Once secreted, hormones act only on those target cells that express specific receptors.

Most disorders of the endocrine system are caused by either hyposecretion or hypersecretion of hormones. Hyposecretion often occurs when a hormone's gland of origin is damaged or otherwise impaired. Hypersecretion often results from the proliferation of tumors derived from hormone-secreting cells. Inappropriate hormone levels may also be caused by defects in regulatory feedback loops or in the processing of hormone precursors. Endocrine malfunction may also occur when the target cell fails to respond to the hormone.

Hormones can be classified biochemically as polypeptides, steroids, eicosanoids, or amines. Polypeptides, which include diverse hormones such as insulin and growth hormone, vary in size and function and are often synthesized as inactive precursors that are processed intracellularly into mature, active forms. Amines, which include epinephrine and dopamine, are amino acid derivatives that function in neuroendocrine signaling. Steroids, which include the cholesterol-derived hormones estrogen and testosterone, function in sexual development and reproduction. Eicosanoids, which include prostaglandins and prostacyclins, are fatty acid derivatives that function in a variety of processes. Most polypeptides and some amines are soluble in the circulation where they are highly susceptible to proteolytic degradation within seconds after their secretion. Steroids and lipids are insoluble and must be transported in the circulation by carrier proteins. The following discussion will focus primarily on polypeptide hormones.

Hormones secreted by the hypothalamus and pituitary gland play a critical role in endocrine function by coordinately regulating hormonal secretions from other endocrine glands in response to neural signals. Hypothalamic hormones include thyrotropin-releasing hormone, gonadotropin-

releasing hormone, somatostatin, growth-hormone releasing factor, corticotropin-releasing hormone, substance P, dopamine, and prolactin-releasing hormone. These hormones directly regulate the secretion of hormones from the anterior lobe of the pituitary. Hormones secreted by the anterior pituitary include adrenocorticotrophic hormone (ACTH), melanocyte-stimulating hormone, 5 somatotrophic hormones such as growth hormone and prolactin, glycoprotein hormones such as thyroid-stimulating hormone, luteinizing hormone (LH), and follicle-stimulating hormone (FSH),  $\beta$ -lipotropin, and  $\beta$ -endorphins. These hormones regulate hormonal secretions from the thyroid, pancreas, and adrenal glands, and act directly on the reproductive organs to stimulate ovulation and spermatogenesis. The posterior pituitary synthesizes and secretes antidiuretic hormone (ADH, 10 vasopressin) and oxytocin.

Disorders of the hypothalamus and pituitary often result from lesions such as primary brain tumors, adenomas, infarction associated with pregnancy, hypophysectomy, aneurysms, vascular malformations, thrombosis, infections, immunological disorders, and complications due to head trauma. Such disorders have profound effects on the function of other endocrine glands. Disorders 15 associated with hypopituitarism include hypogonadism, Sheehan syndrome, diabetes insipidus, Kallman's disease, Hand-Schuller-Christian disease, Letterer-Siwe disease, sarcoidosis, empty sella syndrome, and dwarfism. Disorders associated with hyperpituitarism include acromegaly, gigantism, and syndrome of inappropriate ADH secretion (SIADH), often caused by benign adenomas.

Hormones secreted by the thyroid and parathyroid primarily control metabolic rates and the 20 regulation of serum calcium levels, respectively. Thyroid hormones include calcitonin, somatostatin, and thyroid hormone. The parathyroid secretes parathyroid hormone. Disorders associated with hypothyroidism include goiter, myxedema, acute thyroiditis associated with bacterial infection, subacute thyroiditis associated with viral infection, autoimmune thyroiditis (Hashimoto's disease), and cretinism. Disorders associated with hyperthyroidism include thyrotoxicosis and its various 25 forms, Grave's disease, pretibial myxedema, toxic multinodular goiter, thyroid carcinoma, and Plummer's disease. Disorders associated with hyperparathyroidism include Conn disease (chronic hypercalcemia) leading to bone resorption and parathyroid hyperplasia.

Hormones secreted by the pancreas regulate blood glucose levels by modulating the rates of carbohydrate, fat, and protein metabolism. Pancreatic hormones include insulin, glucagon, amylin,  $\gamma$ - 30 aminobutyric acid, gastrin, somatostatin, and pancreatic polypeptide. The principal disorder associated with pancreatic dysfunction is diabetes mellitus caused by insufficient insulin activity. Diabetes mellitus is generally classified as either Type I (insulin-dependent, juvenile diabetes) or Type II (non-insulin-dependent, adult diabetes). The treatment of both forms by insulin replacement therapy is well known. Diabetes mellitus often leads to acute complications such as hypoglycemia 35 (insulin shock), coma, diabetic ketoacidosis, lactic acidosis, and chronic complications leading to disorders of the eye, kidney, skin, bone, joint, cardiovascular system, nervous system, and to



decreased resistance to infection.

The anatomy, physiology, and diseases related to hormonal function are reviewed in McCance, K.L. and S.E. Huether (1994) Pathophysiology: The Biological Basis for Disease in Adults and Children, Mosby-Year Book, Inc., St. Louis MO; Greenspan, F.S. and J.D. Baxter (1994) Basic and Clinical Endocrinology, Appleton and Lange, East Norwalk CT.

#### Growth Factors

Growth factors are secreted proteins that mediate intercellular communication. Unlike hormones, which travel great distances via the circulatory system, most growth factors are primarily local mediators that act on neighboring cells. Most growth factors contain a hydrophobic N-terminal signal peptide sequence which directs the growth factor into the secretory pathway. Most growth factors also undergo post-translational modifications within the secretory pathway. These modifications can include proteolysis, glycosylation, phosphorylation, and intramolecular disulfide bond formation. Once secreted, growth factors bind to specific receptors on the surfaces of neighboring target cells, and the bound receptors trigger intracellular signal transduction pathways. These signal transduction pathways elicit specific cellular responses in the target cells. These responses can include the modulation of gene expression and the stimulation or inhibition of cell division, cell differentiation, and cell motility.

Growth factors fall into at least two broad and overlapping classes. The broadest class includes the large polypeptide growth factors, which are wide-ranging in their effects. These factors include epidermal growth factor (EGF), fibroblast growth factor (FGF), transforming growth factor- $\beta$  (TGF- $\beta$ ), insulin-like growth factor (IGF), nerve growth factor (NGF), and platelet-derived growth factor (PDGF), each defining a family of numerous related factors. The large polypeptide growth factors, with the exception of NGF, act as mitogens on diverse cell types to stimulate wound healing, bone synthesis and remodeling, extracellular matrix synthesis, and proliferation of epithelial, epidermal, and connective tissues. Members of the TGF- $\beta$ , EGF, and FGF families also function as inductive signals in the differentiation of embryonic tissue. NGF functions specifically as a neurotrophic factor, promoting neuronal growth and differentiation.

Another class of growth factors includes the hematopoietic growth factors, which are narrow in their target specificity. These factors stimulate the proliferation and differentiation of blood cells such as B-lymphocytes, T-lymphocytes, erythrocytes, platelets, eosinophils, basophils, neutrophils, macrophages, and their stem cell precursors. These factors include the colony-stimulating factors (G-CSF, M-CSF, GM-CSF, and CSF1-3), erythropoietin, and the cytokines. The cytokines are specialized hematopoietic factors secreted by cells of the immune system and are discussed in detail below.

Growth factors play critical roles in neoplastic transformation of cells in vitro and in tumor progression in vivo. Overexpression of the large polypeptide growth factors promotes the

proliferation and transformation of cells in culture. Inappropriate expression of these growth factors by tumor cells in vivo may contribute to tumor vascularization and metastasis. Inappropriate activity of hematopoietic growth factors can result in anemias, leukemias, and lymphomas. Moreover, growth factors are both structurally and functionally related to oncoproteins, the potentially cancer-causing products of proto-oncogenes. Certain FGF and PDGF family members are themselves homologous to oncoproteins, whereas receptors for some members of the EGF, NGF, and FGF families are encoded by proto-oncogenes. Growth factors also affect the transcriptional regulation of both proto-oncogenes and oncosuppressor genes (Pimentel, E. (1994) Handbook of Growth Factors, CRC Press, Ann Arbor MI; McKay, I. and I. Leigh, eds. (1993) Growth Factors: A Practical Approach, Oxford University Press, New York NY; Habenicht, A., ed. (1990) Growth Factors, Differentiation Factors, and Cytokines, Springer-Verlag, New York NY).

In addition, some of the large polypeptide growth factors play crucial roles in the induction of the primordial germ layers in the developing embryo. This induction ultimately results in the formation of the embryonic mesoderm, ectoderm, and endoderm which in turn provide the framework for the entire adult body plan. Disruption of this inductive process would be catastrophic to embryonic development.

#### Small Peptide Factors - Neuropeptides and Vasomediators

Neuropeptides and vasomediators (NP/VM) comprise a family of small peptide factors, typically of 20 amino acids or less. These factors generally function in neuronal excitation and inhibition of vasoconstriction/vasodilation, muscle contraction, and hormonal secretions from the brain and other endocrine tissues. Included in this family are neuropeptides and neuropeptide hormones such as bombesin, neuropeptide Y, neurotensin, neuromedin N, melanocortins, opioids, galanin, somatostatin, tachykinins, urotensin II and related peptides involved in smooth muscle stimulation, vasopressin, vasoactive intestinal peptide, and circulatory system-borne signaling molecules such as angiotensin, complement, calcitonin, endothelins, formyl-methionyl peptides, glucagon, cholecystokinin, gastrin, and many of the peptide hormones discussed above. NP/VMs can transduce signals directly, modulate the activity or release of other neurotransmitters and hormones, and act as catalytic enzymes in signaling cascades. The effects of NP/VMs range from extremely brief to long-lasting. (Reviewed in Martin, C.R. et al. (1985) Endocrine Physiology, Oxford University Press, New York NY, pp. 57-62.)

#### Cytokines

Cytokines comprise a family of signaling molecules that modulate the immune system and the inflammatory response. Cytokines are usually secreted by leukocytes, or white blood cells, in response to injury or infection. Cytokines function as growth and differentiation factors that act primarily on cells of the immune system such as B- and T-lymphocytes, monocytes, macrophages, and granulocytes. Like other signaling molecules, cytokines bind to specific plasma membrane

receptors and trigger intracellular signal transduction pathways which alter gene expression patterns. There is considerable potential for the use of cytokines in the treatment of inflammation and immune system disorders.

Cytokine structure and function have been extensively characterized in vitro. Most cytokines  
5 are small polypeptides of about 30 kilodaltons or less. Over 50 cytokines have been identified from human and rodent sources. Examples of cytokine subfamilies include the interferons (IFN- $\alpha$ , - $\beta$ , and - $\gamma$ ), the interleukins (IL1-IL13), the tumor necrosis factors (TNF- $\alpha$  and - $\beta$ ), and the chemokines. Many cytokines have been produced using recombinant DNA techniques, and the activities of individual cytokines have been determined in vitro. These activities include regulation of leukocyte  
10 proliferation, differentiation, and motility.

The activity of an individual cytokine in vitro may not reflect the full scope of that cytokine's activity in vivo. Cytokines are not expressed individually in vivo but are instead expressed in combination with a multitude of other cytokines when the organism is challenged with a stimulus. Together, these cytokines collectively modulate the immune response in a manner appropriate for that  
15 particular stimulus. Therefore, the physiological activity of a cytokine is determined by the stimulus itself and by complex interactive networks among co-expressed cytokines which may demonstrate both synergistic and antagonistic relationships.

Chemokines comprise a cytokine subfamily with over 30 members. (Reviewed in Wells, T. N.C. and M.C. Peitsch (1997) *J. Leukoc. Biol.* 61:545-550.) Chemokines were initially identified as  
20 chemotactic proteins that recruit monocytes and macrophages to sites of inflammation. Recent evidence indicates that chemokines may also play key roles in hematopoiesis and HIV-1 infection. Chemokines are small proteins which range from about 6-15 kilodaltons in molecular weight. Chemokines are further classified as C, CC, CXC, or CX<sub>3</sub>C based on the number and position of critical cysteine residues. The CC chemokines, for example, each contain a conserved motif  
25 consisting of two consecutive cysteines followed by two additional cysteines which occur downstream at 24- and 16-residue intervals, respectively (ExPASy PROSITE database, documents PS00472 and PDOC00434). The presence and spacing of these four cysteine residues are highly conserved, whereas the intervening residues diverge significantly. However, a conserved tyrosine located about 15 residues downstream of the cysteine doublet seems to be important for chemotactic  
30 activity. Most of the human genes encoding CC chemokines are clustered on chromosome 17, although there are a few examples of CC chemokine genes that map elsewhere. Other chemokines include lymphotactin (C chemokine); macrophage chemotactic and activating factor (MCAF/MCP-1; CC chemokine); platelet factor 4 and IL-8 (CXC chemokines); and fractalkine and neurotactin (CX<sub>3</sub>C chemokines). (Reviewed in Luster, A.D. (1998) *N. Engl. J. Med.* 338:436-445.)

35

## Receptor Molecules

The term receptor describes proteins that specifically recognize other molecules. The category is broad and includes proteins with a variety of functions. The bulk of receptors are cell surface proteins which bind extracellular ligands and produce cellular responses in the areas of growth, differentiation, endocytosis, and immune response. Other receptors facilitate the selective transport of proteins out of the endoplasmic reticulum and localize enzymes to particular locations in the cell. The term may also be applied to proteins which act as receptors for ligands with known or unknown chemical composition and which interact with other cellular components. For example, the steroid hormone receptors bind to and regulate transcription of DNA.

Regulation of cell proliferation, differentiation, and migration is important for the formation and function of tissues. Regulatory proteins such as growth factors coordinately control these cellular processes and act as mediators in cell-cell signaling pathways. Growth factors are secreted proteins that bind to specific cell-surface receptors on target cells. The bound receptors trigger intracellular signal transduction pathways which activate various downstream effectors that regulate gene expression, cell division, cell differentiation, cell motility, and other cellular processes.

Cell surface receptors are typically integral plasma membrane proteins. These receptors recognize hormones such as catecholamines; peptide hormones; growth and differentiation factors; small peptide factors such as thyrotropin-releasing hormone; galanin, somatostatin, and tachykinins; and circulatory system-borne signaling molecules. Cell surface receptors on immune system cells recognize antigens, antibodies, and major histocompatibility complex (MHC)-bound peptides. Other cell surface receptors bind ligands to be internalized by the cell. This receptor-mediated endocytosis functions in the uptake of low density lipoproteins (LDL), transferrin, glucose- or mannose-terminal glycoproteins, galactose-terminal glycoproteins, immunoglobulins, phosphovitellogenins, fibrin, proteinase-inhibitor complexes, plasminogen activators, and thrombospondin (Lodish, H. et al. (1995) Molecular Cell Biology, Scientific American Books, New York NY, p. 723; Mikhailenko, I. et al. (1997) J. Biol. Chem. 272:6784-6791).

#### Receptor Protein Kinases

Many growth factor receptors, including receptors for epidermal growth factor, platelet-derived growth factor, fibroblast growth factor, as well as the growth modulator  $\alpha$ -thrombin, contain intrinsic protein kinase activities. When growth factor binds to the receptor, it triggers the autophosphorylation of a serine, threonine, or tyrosine residue on the receptor. These phosphorylated sites are recognition sites for the binding of other cytoplasmic signaling proteins. These proteins participate in signaling pathways that eventually link the initial receptor activation at the cell surface to the activation of a specific intracellular target molecule. In the case of tyrosine residue autophosphorylation, these signaling proteins contain a common domain referred to as a Src homology (SH) domain. SH2 domains and SH3 domains are found in phospholipase C- $\gamma$ , PI-3-K p85 regulatory subunit, Ras-GTPase activating protein, and pp60<sup>c-src</sup> (Lowenstein, E.J. et al. (1992) Cell

70:431-442). The cytokine family of receptors share a different common binding domain and include transmembrane receptors for growth hormone (GH), interleukins, erythropoietin, and prolactin.

Other receptors and second messenger-binding proteins have intrinsic serine/threonine protein kinase activity. These include activin/TGF- $\beta$ /BMP-superfamily receptors, calcium- and diacylglycerol-activated/phospholipid-dependant protein kinase (PK-C), and RNA-dependant protein kinase (PK-R). In addition, other serine/threonine protein kinases, including nematode Twitchin, have fibronectin-like, immunoglobulin C2-like domains.

#### G-Protein Coupled Receptors

G-protein coupled receptors (GPCRs) are integral membrane proteins characterized by the presence of seven hydrophobic transmembrane domains which span the plasma membrane and form a bundle of antiparallel alpha ( $\alpha$ ) helices. These proteins range in size from under 400 to over 1000 amino acids (Strosberg, A.D. (1991) Eur. J. Biochem. 196:1-10; Coughlin, S.R. (1994) Curr. Opin. Cell Biol. 6:191-197). The amino-terminus of the GPCR is extracellular, of variable length and often glycosylated; the carboxy-terminus is cytoplasmic and generally phosphorylated. Extracellular loops of the GPCR alternate with intracellular loops and link the transmembrane domains. The most conserved domains of GPCRs are the transmembrane domains and the first two cytoplasmic loops. The transmembrane domains account for structural and functional features of the receptor. In most cases, the bundle of  $\alpha$  helices forms a binding pocket. In addition, the extracellular N-terminal segment or one or more of the three extracellular loops may also participate in ligand binding. Ligand binding activates the receptor by inducing a conformational change in intracellular portions of the receptor. The activated receptor, in turn, interacts with an intracellular heterotrimeric guanine nucleotide binding (G) protein complex which mediates further intracellular signaling activities, generally the production of second messengers such as cyclic AMP (cAMP), phospholipase C, inositol triphosphate, or interactions with ion channel proteins (Baldwin, J.M. (1994) Curr. Opin. Cell Biol. 6:180-190).

GPCRs include those for acetylcholine, adenosine, epinephrine and norepinephrine, bombesin, bradykinin, chemokines, dopamine, endothelin,  $\gamma$ -aminobutyric acid (GABA), follicle-stimulating hormone (FSH), glutamate, gonadotropin-releasing hormone (GnRH), hepatocyte growth factor, histamine, leukotrienes, melanocortins, neuropeptide Y, opioid peptides, opsins, prostanoids, serotonin, somatostatin, tachykinins, thrombin, thyrotropin-releasing hormone (TRH), vasoactive intestinal polypeptide family, vasopressin and oxytocin, and orphan receptors.

GPCR mutations, which may cause loss of function or constitutive activation, have been associated with numerous human diseases (Coughlin, supra). For instance, retinitis pigmentosa may arise from mutations in the rhodopsin gene. Rhodopsin is the retinal photoreceptor which is located within the discs of the eye rod cell. Parma, J. et al. (1993, Nature 365:649-651) report that somatic activating mutations in the thyrotropin receptor cause hyperfunctioning thyroid adenomas and suggest

that certain GPCRs susceptible to constitutive activation may behave as protooncogenes.

#### Nuclear Receptors

Nuclear receptors bind small molecules such as hormones or second messengers, leading to increased receptor-binding affinity to specific chromosomal DNA elements. In addition the affinity  
5 for other nuclear proteins may also be altered. Such binding and protein-protein interactions may regulate and modulate gene expression. Examples of such receptors include the steroid hormone receptors family, the retinoic acid receptors family, and the thyroid hormone receptors family.

#### Ligand-Gated Receptor Ion Channels

Ligand-gated receptor ion channels fall into two categories. The first category, extracellular  
10 ligand-gated receptor ion channels (ELGs), rapidly transduce neurotransmitter-binding events into electrical signals, such as fast synaptic neurotransmission. ELG function is regulated by post-translational modification. The second category, intracellular ligand-gated receptor ion channels (ILGs), are activated by many intracellular second messengers and do not require post-translational modification(s) to effect a channel-opening response.

15 ELGs depolarize excitable cells to the threshold of action potential generation. In non-excitable cells, ELGs permit a limited calcium ion-influx during the presence of agonist. ELGs include channels directly gated by neurotransmitters such as acetylcholine, L-glutamate, glycine, ATP, serotonin, GABA, and histamine. ELG genes encode proteins having strong structural and functional similarities. ILGs are encoded by distinct and unrelated gene families and include  
20 receptors for cAMP, cGMP, calcium ions, ATP, and metabolites of arachidonic acid.

#### Macrophage Scavenger Receptors

Macrophage scavenger receptors with broad ligand specificity may participate in the binding of low density lipoproteins (LDL) and foreign antigens. Scavenger receptors types I and II are  
25 trimeric membrane proteins with each subunit containing a small N-terminal intracellular domain, a transmembrane domain, a large extracellular domain, and a C-terminal cysteine-rich domain. The extracellular domain contains a short spacer domain, an  $\alpha$ -helical coiled-coil domain, and a triple helical collagenous domain. These receptors have been shown to bind a spectrum of ligands, including chemically modified lipoproteins and albumin, polyribonucleotides, polysaccharides, phospholipids, and asbestos (Matsumoto, A. et al. (1990) Proc. Natl. Acad. Sci. USA 87:9133-9137;  
30 Elomaa, O. et al. (1995) Cell 80:603-609). The scavenger receptors are thought to play a key role in atherogenesis by mediating uptake of modified LDL in arterial walls, and in host defense by binding bacterial endotoxins, bacteria, and protozoa.

#### T-Cell Receptors

T cells play a dual role in the immune system as effectors and regulators, coupling antigen  
35 recognition with the transmission of signals that induce cell death in infected cells and stimulate proliferation of other immune cells. Although a population of T cells can recognize a wide range of

different antigens, an individual T cell can only recognize a single antigen and only when it is presented to the T cell receptor (TCR) as a peptide complexed with a major histocompatibility molecule (MHC) on the surface of an antigen presenting cell. The TCR on most T cells consists of immunoglobulin-like integral membrane glycoproteins containing two polypeptide subunits,  $\alpha$  and  $\beta$ , of similar molecular weight. Both TCR subunits have an extracellular domain containing both variable and constant regions, a transmembrane domain that traverses the membrane once, and a short intracellular domain (Saito, H. et al. (1984) *Nature* 309:757-762). The genes for the TCR subunits are constructed through somatic rearrangement of different gene segments. Interaction of antigen in the proper MHC context with the TCR initiates signaling cascades that induce the proliferation, maturation, and function of cellular components of the immune system (Weiss, A. (1991) *Annu. Rev. Genet.* 25:487-510). Rearrangements in TCR genes and alterations in TCR expression have been noted in lymphomas, leukemias, autoimmune disorders, and immunodeficiency disorders (Aisenberg, A.C. et al. (1985) *N. Engl. J. Med.* 313:529-533; Weiss, *supra*).

#### 15 Intracellular Signaling Molecules

Intracellular signaling is the general process by which cells respond to extracellular signals (hormones, neurotransmitters, growth and differentiation factors, etc.) through a cascade of biochemical reactions that begins with the binding of a signaling molecule to a cell membrane receptor and ends with the activation of an intracellular target molecule. Intermediate steps in the process involve the activation of various cytoplasmic proteins by phosphorylation via protein kinases, and their deactivation by protein phosphatases, and the eventual translocation of some of these activated proteins to the cell nucleus where the transcription of specific genes is triggered. The intracellular signaling process regulates all types of cell functions including cell proliferation, cell differentiation, and gene transcription, and involves a diversity of molecules including protein kinases and phosphatases, and second messenger molecules, such as cyclic nucleotides, calcium-calmodulin, inositol, and various mitogens, that regulate protein phosphorylation.

##### Protein Phosphorylation

Protein kinases and phosphatases play a key role in the intracellular signaling process by controlling the phosphorylation and activation of various signaling proteins. The high energy phosphate for this reaction is generally transferred from the adenosine triphosphate molecule (ATP) to a particular protein by a protein kinase and removed from that protein by a protein phosphatase. Protein kinases are roughly divided into two groups: those that phosphorylate tyrosine residues (protein tyrosine kinases, PTK) and those that phosphorylate serine or threonine residues (serine/threonine kinases, STK). A few protein kinases have dual specificity for serine/threonine and tyrosine residues. Almost all kinases contain a conserved 250-300 amino acid catalytic domain containing specific residues and sequence motifs characteristic of the kinase family (Hardie, G. and

S. Hanks (1995) The Protein Kinase Facts Books, Vol 1:7-20, Academic Press, San Diego CA).

STKs include the second messenger dependent protein kinases such as the cyclic-AMP dependent protein kinases (PKA), involved in mediating hormone-induced cellular responses; calcium-calmodulin (CaM) dependent protein kinases, involved in regulation of smooth muscle contraction, glycogen breakdown, and neurotransmission; and the mitogen-activated protein kinases (MAP) which mediate signal transduction from the cell surface to the nucleus via phosphorylation cascades. Altered PKA expression is implicated in a variety of disorders and diseases including cancer, thyroid disorders, diabetes, atherosclerosis, and cardiovascular disease (Isselbacher, K.J. et al. (1994) Harrison's Principles of Internal Medicine, McGraw-Hill, New York NY, pp. 416-431, 1887).

PTKs are divided into transmembrane, receptor PTKs and nontransmembrane, non-receptor PTKs. Transmembrane PTKs are receptors for most growth factors. Non-receptor PTKs lack transmembrane regions and, instead, form complexes with the intracellular regions of cell surface receptors. Receptors that function through non-receptor PTKs include those for cytokines and hormones (growth hormone and prolactin) and antigen-specific receptors on T and B lymphocytes. Many of these PTKs were first identified as the products of mutant oncogenes in cancer cells in which their activation was no longer subject to normal cellular controls. In fact, about one third of the known oncogenes encode PTKs, and it is well known that cellular transformation (oncogenesis) is often accompanied by increased tyrosine phosphorylation activity (Charbonneau, H. and N.K. Tonks (1992) *Annu. Rev. Cell Biol.* 8:463-493).

An additional family of protein kinases previously thought to exist only in procaryotes is the histidine protein kinase family (HPK). HPKs bear little homology with mammalian STKs or PTKs but have distinctive sequence motifs of their own (Davie, J.R. et al. (1995) *J. Biol. Chem.* 270:19861-19867). A histidine residue in the N-terminal half of the molecule (region I) is an autophosphorylation site. Three additional motifs located in the C-terminal half of the molecule include an invariant asparagine residue in region II and two glycine-rich loops characteristic of nucleotide binding domains in regions III and IV. Recently a branched chain alpha-ketoacid dehydrogenase kinase has been found with characteristics of HPK in rat (Davie, supra).

Protein phosphatases regulate the effects of protein kinases by removing phosphate groups from molecules previously activated by kinases. The two principal categories of protein phosphatases are the protein (serine/threonine) phosphatases (PPs) and the protein tyrosine phosphatases (PTPs). PPs dephosphorylate phosphoserine/threonine residues and are important regulators of many cAMP-mediated hormone responses (Cohen, P. (1989) *Annu. Rev. Biochem.* 58:453-508). PTPs reverse the effects of protein tyrosine kinases and play a significant role in cell cycle and cell signaling processes (Charbonneau, supra). As previously noted, many PTKs are encoded by oncogenes, and oncogenesis is often accompanied by increased tyrosine phosphorylation activity. It is therefore possible that PTPs may prevent or reverse cell transformation and the growth



of various cancers by controlling the levels of tyrosine phosphorylation in cells. This hypothesis is supported by studies showing that overexpression of PTPs can suppress transformation in cells, and that specific inhibition of PTPs can enhance cell transformation (Charbonneau, supra).

#### Phospholipid and Inositol-Phosphate Signaling

5 Inositol phospholipids (phosphoinositides) are involved in an intracellular signaling pathway that begins with binding of a signaling molecule to a G-protein linked receptor in the plasma membrane. This leads to the phosphorylation of phosphatidylinositol (PI) residues on the inner side of the plasma membrane to the biphosphate state (PIP<sub>2</sub>) by inositol kinases. Simultaneously, the G-protein linked receptor binding stimulates a trimeric G-protein which in turn activates a  
10 phosphoinositide-specific phospholipase C-β. Phospholipase C-β then cleaves PIP<sub>2</sub> into two products, inositol triphosphate (IP<sub>3</sub>) and diacylglycerol. These two products act as mediators for separate signaling events. IP<sub>3</sub> diffuses through the plasma membrane to induce calcium release from the endoplasmic reticulum (ER), while diacylglycerol remains in the membrane and helps activate protein kinase C, an STK that phosphorylates selected proteins in the target cell. The calcium  
15 response initiated by IP<sub>3</sub> is terminated by the dephosphorylation of IP<sub>3</sub> by specific inositol phosphatases. Cellular responses that are mediated by this pathway are glycogen breakdown in the liver in response to vasopressin, smooth muscle contraction in response to acetylcholine, and thrombin-induced platelet aggregation.

#### Cyclic Nucleotide Signaling

20 Cyclic nucleotides (cAMP and cGMP) function as intracellular second messengers to transduce a variety of extracellular signals including hormones, light, and neurotransmitters. In particular, cyclic-AMP dependent protein kinases (PKA) are thought to account for all of the effects of cAMP in most mammalian cells, including various hormone-induced cellular responses. Visual excitation and the phototransmission of light signals in the eye is controlled by cyclic-GMP  
25 regulated, Ca<sup>2+</sup>-specific channels. Because of the importance of cellular levels of cyclic nucleotides in mediating these various responses, regulating the synthesis and breakdown of cyclic nucleotides is an important matter. Thus adenylyl cyclase, which synthesizes cAMP from AMP, is activated to increase cAMP levels in muscle by binding of adrenaline to β-andrenergic receptors, while activation of guanylate cyclase and increased cGMP levels in photoreceptors leads to reopening of the  
30 Ca<sup>2+</sup>-specific channels and recovery of the dark state in the eye. In contrast, hydrolysis of cyclic nucleotides by cAMP and cGMP-specific phosphodiesterases (PDEs) produces the opposite of these and other effects mediated by increased cyclic nucleotide levels. PDEs appear to be particularly important in the regulation of cyclic nucleotides, considering the diversity found in this family of proteins. At least seven families of mammalian PDEs (PDE1-7) have been identified based on  
35 substrate specificity and affinity, sensitivity to cofactors, and sensitivity to inhibitory drugs (Beavo, J.A. (1995) Physiological Reviews 75:725-748). PDE inhibitors have been found to be particularly

useful in treating various clinical disorders. Rolipram, a specific inhibitor of PDE4, has been used in the treatment of depression, and similar inhibitors are undergoing evaluation as anti-inflammatory agents. Theophylline is a nonspecific PDE inhibitor used in the treatment of bronchial asthma and other respiratory diseases (Banner, K.H. and C.P. Page (1995) Eur. Respir. J. 8:996-1000).

#### 5 G-Protein Signaling

Guanine nucleotide binding proteins (G-proteins) are critical mediators of signal transduction between a particular class of extracellular receptors, the G-protein coupled receptors (GPCR), and intracellular second messengers such as cAMP and  $\text{Ca}^{2+}$ . G-proteins are linked to the cytosolic side of a GPCR such that activation of the GPCR by ligand binding stimulates binding of the G-protein to  
10 GTP, inducing an "active" state in the G-protein. In the active state, the G-protein acts as a signal to trigger other events in the cell such as the increase of cAMP levels or the release of  $\text{Ca}^{2+}$  into the cytosol from the ER, which, in turn, regulate phosphorylation and activation of other intracellular proteins. Recycling of the G-protein to the inactive state involves hydrolysis of the bound GTP to GDP by a GTPase activity in the G-protein. (See Alberts, B. et al. (1994) Molecular Biology of the  
15 Cell, Garland Publishing, Inc., New York NY, pp.734-759.) Two structurally distinct classes of G-proteins are recognized: heterotrimeric G-proteins, consisting of three different subunits, and monomeric, low molecular weight (LMW), G-proteins consisting of a single polypeptide chain.

The three polypeptide subunits of heterotrimeric G-proteins are the  $\alpha$ ,  $\beta$ , and  $\gamma$  subunits. The  $\alpha$  subunit binds and hydrolyzes GTP. The  $\beta$  and  $\gamma$  subunits form a tight complex that anchors the  
20 protein to the inner side of the plasma membrane. The  $\beta$  subunits, also known as G- $\beta$  proteins or  $\beta$  transducins, contain seven tandem repeats of the WD-repeat sequence motif, a motif found in many proteins with regulatory functions. Mutations and variant expression of  $\beta$  transducin proteins are linked with various disorders (Neer, E.J. et al. (1994) Nature 371:297-300; Margottin, F. et al. (1998) Mol. Cell 1:565-574).

LMW GTP-proteins are GTPases which regulate cell growth, cell cycle control, protein  
25 secretion, and intracellular vesicle interaction. They consist of single polypeptides which, like the  $\alpha$  subunit of the heterotrimeric G-proteins, are able to bind and hydrolyze GTP, thus cycling between an inactive and an active state. At least sixty members of the LMW G-protein superfamily have been identified and are currently grouped into the six subfamilies of ras, rho, arf, sar1, ran, and rab.  
30 Activated ras genes were initially found in human cancers, and subsequent studies confirmed that ras function is critical in determining whether cells continue to grow or become differentiated. Other members of the LMW G-protein superfamily have roles in signal transduction that vary with the function of the activated genes and the locations of the G-proteins.

Guanine nucleotide exchange factors regulate the activities of LMW G-proteins by  
35 determining whether GTP or GDP is bound. GTPase-activating protein (GAP) binds to GTP-ras and

induces it to hydrolyze GTP to GDP. In contrast, guanine nucleotide releasing protein (GNRP) binds to GDP-ras and induces the release of GDP and the binding of GTP.

Other regulators of G-protein signaling (RGS) also exist that act primarily by negatively regulating the G-protein pathway by an unknown mechanism (Druey, K.M. et al. (1996) Nature 379:742-746). Some 15 members of the RGS family have been identified. RGS family members are related structurally through similarities in an approximately 120 amino acid region termed the RGS domain and functionally by their ability to inhibit the interleukin (cytokine) induction of MAP kinase in cultured mammalian 293T cells (Druey, supra).

#### Calcium Signaling Molecules

Ca<sup>2+</sup> is another second messenger molecule that is even more widely used as an intracellular mediator than cAMP. Two pathways exist by which Ca<sup>2+</sup> can enter the cytosol in response to extracellular signals: One pathway acts primarily in nerve signal transduction where Ca<sup>2+</sup> enters a nerve terminal through a voltage-gated Ca<sup>2+</sup> channel. The second is a more ubiquitous pathway in which Ca<sup>2+</sup> is released from the ER into the cytosol in response to binding of an extracellular signaling molecule to a receptor. Ca<sup>2+</sup> directly activates regulatory enzymes, such as protein kinase C, which trigger signal transduction pathways. Ca<sup>2+</sup> also binds to specific Ca<sup>2+</sup>-binding proteins (CBPs) such as calmodulin (CaM) which then activate multiple target proteins in the cell including enzymes, membrane transport pumps, and ion channels. CaM interactions are involved in a multitude of cellular processes including, but not limited to, gene regulation, DNA synthesis, cell cycle progression, mitosis, cytokinesis, cytoskeletal organization, muscle contraction, signal transduction, ion homeostasis, exocytosis, and metabolic regulation (Celio, M.R. et al. (1996) Guidebook to Calcium-binding Proteins, Oxford University Press, Oxford, UK, pp. 15-20). Some CBPs can serve as a storage depot for Ca<sup>2+</sup> in an inactive state. Calsequestrin is one such CBP that is expressed in isoforms specific to cardiac muscle and skeletal muscle. It is suggested that calsequestrin binds Ca<sup>2+</sup> in a rapidly exchangeable state that is released during Ca<sup>2+</sup>-signaling conditions (Celio, M.R. et al. (1996) Guidebook to Calcium-binding Proteins, Oxford University Press, New York NY, pp. 222-224).

#### Cyclins

Cell division is the fundamental process by which all living things grow and reproduce. In most organisms, the cell cycle consists of three principle steps; interphase, mitosis, and cytokinesis. Interphase, involves preparations for cell division, replication of the DNA and production of essential proteins. In mitosis, the nuclear material is divided and separates to opposite sides of the cell. Cytokinesis is the final division and fission of the cell cytoplasm to produce the daughter cells.

The entry and exit of a cell from mitosis is regulated by the synthesis and destruction of a family of activating proteins called cyclins. Cyclins act by binding to and activating a group of cyclin-dependent protein kinases (Cdks) which then phosphorylate and activate selected proteins

involved in the mitotic process. Several types of cyclins exist. (Ciechanover, A. (1994) Cell 79:13-21.) Two principle types are mitotic cyclin, or cyclin B, which controls entry of the cell into mitosis, and G1 cyclin, which controls events that drive the cell out of mitosis.

#### Signal Complex Scaffolding Proteins

5           Certain proteins in intracellular signaling pathways serve to link or cluster other proteins involved in the signaling cascade. A conserved protein domain called the PDZ domain has been identified in various membrane-associated signaling proteins. This domain has been implicated in receptor and ion channel clustering and in the targeting of multiprotein signaling complexes to specialized functional regions of the cytosolic face of the plasma membrane. (For a review of PDZ  
10 domain-containing proteins, see Ponting, C.P. et al. (1997) Bioessays 19:469-479.) A large proportion of PDZ domains are found in the eukaryotic MAGUK (membrane-associated guanylate kinase) protein family, members of which bind to the intracellular domains of receptors and channels. However, PDZ domains are also found in diverse membrane-localized proteins such as protein tyrosine phosphatases, serine/threonine kinases, G-protein cofactors, and synapse-associated proteins  
15 such as syntrophins and neuronal nitric oxide synthase (nNOS). Generally, about one to three PDZ domains are found in a given protein, although up to nine PDZ domains have been identified in a single protein.

#### **Membrane Transport Molecules**

20           The plasma membrane acts as a barrier to most molecules. Transport between the cytoplasm and the extracellular environment, and between the cytoplasm and luminal spaces of cellular organelles requires specific transport proteins. Each transport protein carries a particular class of molecule, such as ions, sugars, or amino acids, and often is specific to a certain molecular species of the class. A variety of human inherited diseases are caused by a mutation in a transport protein. For  
25 example, cystinuria is an inherited disease that results from the inability to transport cystine, the disulfide-linked dimer of cysteine, from the urine into the blood. Accumulation of cystine in the urine leads to the formation of cystine stones in the kidneys.

Transport proteins are multi-pass transmembrane proteins, which either actively transport molecules across the membrane or passively allow them to cross. Active transport involves  
30 directional pumping of a solute across the membrane, usually against an electrochemical gradient. Active transport is tightly coupled to a source of metabolic energy, such as ATP hydrolysis or an electrochemically favorable ion gradient. Passive transport involves the movement of a solute down its electrochemical gradient. Transport proteins can be further classified as either carrier proteins or channel proteins. Carrier proteins, which can function in active or passive transport, bind to a  
35 specific solute to be transported and undergo a conformational change which transfers the bound solute across the membrane. Channel proteins, which only function in passive transport, form

hydrophilic pores across the membrane. When the pores open, specific solutes, such as inorganic ions, pass through the membrane and down the electrochemical gradient of the solute.

Carrier proteins which transport a single solute from one side of the membrane to the other are called uniporters. In contrast, coupled transporters link the transfer of one solute with simultaneous or sequential transfer of a second solute, either in the same direction (symport) or in the opposite direction (antiport). For example, intestinal and kidney epithelium contains a variety of symporter systems driven by the sodium gradient that exists across the plasma membrane. Sodium moves into the cell down its electrochemical gradient and brings the solute into the cell with it. The sodium gradient that provides the driving force for solute uptake is maintained by the ubiquitous  $\text{Na}^+/\text{K}^+$  ATPase. Sodium-coupled transporters include the mammalian glucose transporter (SGLT1), iodide transporter (NIS), and multivitamin transporter (SMVT). All three transporters have twelve putative transmembrane segments, extracellular glycosylation sites, and cytoplasmically-oriented N- and C-termini. NIS plays a crucial role in the evaluation, diagnosis, and treatment of various thyroid pathologies because it is the molecular basis for radioiodide thyroid-imaging techniques and for specific targeting of radioisotopes to the thyroid gland (Levy, O. et al. (1997) *Proc. Natl. Acad. Sci. USA* 94:5568-5573). SMVT is expressed in the intestinal mucosa, kidney, and placenta, and is implicated in the transport of the water-soluble vitamins, e.g., biotin and pantothenate (Prasad, P.D. et al. (1998) *J. Biol. Chem.* 273:7501-7506).

Transporters play a major role in the regulation of pH, excretion of drugs, and the cellular  $\text{K}^+/\text{Na}^+$  balance. Monocarboxylate anion transporters are proton-coupled symporters with a broad substrate specificity that includes L-lactate, pyruvate, and the ketone bodies acetate, acetoacetate, and beta-hydroxybutyrate. At least seven isoforms have been identified to date. The isoforms are predicted to have twelve transmembrane (TM) helical domains with a large intracellular loop between TM6 and TM7, and play a critical role in maintaining intracellular pH by removing the protons that are produced stoichiometrically with lactate during glycolysis. The best characterized  $\text{H}^+$ -monocarboxylate transporter is that of the erythrocyte membrane, which transports L-lactate and a wide range of other aliphatic monocarboxylates. Other cells possess  $\text{H}^+$ -linked monocarboxylate transporters with differing substrate and inhibitor selectivities. In particular, cardiac muscle and tumor cells have transporters that differ in their  $K_m$  values for certain substrates, including stereoselectivity for L- over D-lactate, and in their sensitivity to inhibitors. There are  $\text{Na}^+$ -monocarboxylate cotransporters on the luminal surface of intestinal and kidney epithelia, which allow the uptake of lactate, pyruvate, and ketone bodies in these tissues. In addition, there are specific and selective transporters for organic cations and organic anions in organs including the kidney, intestine and liver. Organic anion transporters are selective for hydrophobic, charged molecules with electron-attracting side groups. Organic cation transporters, such as the ammonium transporter, mediate the secretion of a variety of drugs and endogenous metabolites, and contribute to

the maintenance of intercellular pH. (Poole, R.C. and A.P. Halestrap (1993) *Am. J. Physiol.* 264:C761-C782; Price, N.T. et al. (1998) *Biochem. J.* 329:321-328; and Martinelle, K. and I. Haggstrom (1993) *J. Biotechnol.* 30: 339-350.)

The largest and most diverse family of transport proteins known is the ATP-binding cassette (ABC) transporters. As a family, ABC transporters can transport substances that differ markedly in chemical structure and size, ranging from small molecules such as ions, sugars, amino acids, peptides, and phospholipids, to lipopeptides, large proteins, and complex hydrophobic drugs. ABC proteins consist of four modules: two nucleotide-binding domains (NBD), which hydrolyze ATP to supply the energy required for transport, and two membrane-spanning domains (MSD), each containing six putative transmembrane segments. These four modules may be encoded by a single gene, as is the case for the cystic fibrosis transmembrane regulator (CFTR), or by separate genes. When encoded by separate genes, each gene product contains a single NBD and MSD. These "half-molecules" form homo- and heterodimers, such as Tap1 and Tap2, the endoplasmic reticulum-based major histocompatibility (MHC) peptide transport system. Several genetic diseases are attributed to defects in ABC transporters, such as the following diseases and their corresponding proteins: cystic fibrosis (CFTR, an ion channel), adrenoleukodystrophy (adrenoleukodystrophy protein, ALDP), Zellweger syndrome (peroxisomal membrane protein-70, PMP70), and hyperinsulinemic hypoglycemia (sulfonylurea receptor, SUR). Overexpression of the multidrug resistance (MDR) protein, another ABC transporter, in human cancer cells makes the cells resistant to a variety of cytotoxic drugs used in chemotherapy (Taglicht, D. and S. Michaelis (1998) *Meth. Enzymol.* 292:131-163).

Transport of fatty acids across the plasma membrane can occur by diffusion, a high capacity, low affinity process. However, under normal physiological conditions a significant fraction of fatty acid transport appears to occur via a high affinity, low capacity protein-mediated transport process. Fatty acid transport protein (FATP), an integral membrane protein with four transmembrane segments, is expressed in tissues exhibiting high levels of plasma membrane fatty acid flux, such as muscle, heart, and adipose. Expression of FATP is upregulated in 3T3-L1 cells during adipose conversion, and expression in COS7 fibroblasts elevates uptake of long-chain fatty acids (Hui, T.Y. et al. (1998) *J. Biol. Chem.* 273:27420-27429).

#### Ion Channels

The electrical potential of a cell is generated and maintained by controlling the movement of ions across the plasma membrane. The movement of ions requires ion channels, which form an ion-selective pore within the membrane. There are two basic types of ion channels, ion transporters and gated ion channels. Ion transporters utilize the energy obtained from ATP hydrolysis to actively transport an ion against the ion's concentration gradient. Gated ion channels allow passive flow of an ion down the ion's electrochemical gradient under restricted conditions. Together, these types of ion channels generate, maintain, and utilize an electrochemical gradient that is used in 1) electrical

impulse conduction down the axon of a nerve cell, 2) transport of molecules into cells against concentration gradients, 3) initiation of muscle contraction, and 4) endocrine cell secretion.

Ion transporters generate and maintain the resting electrical potential of a cell. Utilizing the energy derived from ATP hydrolysis, they transport ions against the ion's concentration gradient.

5 These transmembrane ATPases are divided into three families. The phosphorylated (P) class ion transporters, including  $\text{Na}^+$ - $\text{K}^+$  ATPase,  $\text{Ca}^{2+}$ -ATPase, and  $\text{H}^+$ -ATPase, are activated by a phosphorylation event. P-class ion transporters are responsible for maintaining resting potential distributions such that cytosolic concentrations of  $\text{Na}^+$  and  $\text{Ca}^{2+}$  are low and cytosolic concentration of  $\text{K}^+$  is high. The vacuolar (V) class of ion transporters includes  $\text{H}^+$  pumps on intracellular  
10 organelles, such as lysosomes and Golgi. V-class ion transporters are responsible for generating the low pH within the lumen of these organelles that is required for function. The coupling factor (F) class consists of  $\text{H}^+$  pumps in the mitochondria. F-class ion transporters utilize a proton gradient to generate ATP from ADP and inorganic phosphate ( $\text{P}_i$ ).

The resting potential of the cell is utilized in many processes involving carrier proteins and  
15 gated ion channels. Carrier proteins utilize the resting potential to transport molecules into and out of the cell. Amino acid and glucose transport into many cells is linked to sodium ion co-transport (symport) so that the movement of  $\text{Na}^+$  down an electrochemical gradient drives transport of the other molecule up a concentration gradient. Similarly, cardiac muscle links transfer of  $\text{Ca}^{2+}$  out of the cell with transport of  $\text{Na}^+$  into the cell (antiport).

20 Ion channels share common structural and mechanistic themes. The channel consists of four or five subunits or protein monomers that are arranged like a barrel in the plasma membrane. Each subunit typically consists of six potential transmembrane segments (S1, S2, S3, S4, S5, and S6). The center of the barrel forms a pore lined by  $\alpha$ -helices or  $\beta$ -strands. The side chains of the amino acid residues comprising the  $\alpha$ -helices or  $\beta$ -strands establish the charge (cation or anion) selectivity of the  
25 channel. The degree of selectivity, or what specific ions are allowed to pass through the channel, depends on the diameter of the narrowest part of the pore.

Gated ion channels control ion flow by regulating the opening and closing of pores. These channels are categorized according to the manner of regulating the gating function. Mechanically-gated channels open pores in response to mechanical stress, voltage-gated channels open pores in  
30 response to changes in membrane potential, and ligand-gated channels open pores in the presence of a specific ion, nucleotide, or neurotransmitter.

Voltage-gated  $\text{Na}^+$  and  $\text{K}^+$  channels are necessary for the function of electrically excitable cells, such as nerve and muscle cells. Action potentials, which lead to neurotransmitter release and muscle contraction, arise from large, transient changes in the permeability of the membrane to  $\text{Na}^+$   
35 and  $\text{K}^+$  ions. Depolarization of the membrane beyond the threshold level opens voltage-gated  $\text{Na}^+$  channels. Sodium ions flow into the cell, further depolarizing the membrane and opening more

voltage-gated  $\text{Na}^+$  channels, which propagates the depolarization down the length of the cell. Depolarization also opens voltage-gated potassium channels. Consequently, potassium ions flow outward, which leads to repolarization of the membrane. Voltage-gated channels utilize charged residues in the fourth transmembrane segment (S4) to sense voltage change. The open state lasts only about 1 millisecond, at which time the channel spontaneously converts into an inactive state that cannot be opened irrespective of the membrane potential. Inactivation is mediated by the channel's N-terminus, which acts as a plug that closes the pore. The transition from an inactive to a closed state requires a return to resting potential.

Voltage-gated  $\text{Na}^+$  channels are heterotrimeric complexes composed of a 260 kDa pore forming  $\alpha$  subunit that associates with two smaller auxiliary subunits,  $\beta 1$  and  $\beta 2$ . The  $\beta 2$  subunit is an integral membrane glycoprotein that contains an extracellular Ig domain, and its association with  $\alpha$  and  $\beta 1$  subunits correlates with increased functional expression of the channel, a change in its gating properties, and an increase in whole cell capacitance due to an increase in membrane surface area. (Isom, L.L. et al. (1995) Cell 83:433-442.)

Voltage-gated  $\text{Ca}^{2+}$  channels are involved in presynaptic neurotransmitter release, and heart and skeletal muscle contraction. The voltage-gated  $\text{Ca}^{2+}$  channels from skeletal muscle (L-type) and brain (N-type) have been purified, and though their functions differ dramatically, they have similar subunit compositions. The channels are composed of three subunits. The  $\alpha_1$  subunit forms the membrane pore and voltage sensor, while the  $\alpha_2\delta$  and  $\beta$  subunits modulate the voltage-dependence, gating properties, and the current amplitude of the channel. These subunits are encoded by at least six  $\alpha_1$ , one  $\alpha_2\delta$ , and four  $\beta$  genes. A fourth subunit,  $\gamma$ , has been identified in skeletal muscle. (Walker, D. et al. (1998) J. Biol. Chem. 273:2361-2367; and Jay, S.D. et al. (1990) Science 248:490-492.)

Chloride channels are necessary in endocrine secretion and in regulation of cytosolic and organelle pH. In secretory epithelial cells,  $\text{Cl}^-$  enters the cell across a basolateral membrane through an  $\text{Na}^+$ ,  $\text{K}^+/\text{Cl}^-$  cotransporter, accumulating in the cell above its electrochemical equilibrium concentration. Secretion of  $\text{Cl}^-$  from the apical surface, in response to hormonal stimulation, leads to flow of  $\text{Na}^+$  and water into the secretory lumen. The cystic fibrosis transmembrane conductance regulator (CFTR) is a chloride channel encoded by the gene for cystic fibrosis, a common fatal genetic disorder in humans. Loss of CFTR function decreases transepithelial water secretion and, as a result, the layers of mucus that coat the respiratory tree, pancreatic ducts, and intestine are dehydrated and difficult to clear. The resulting blockage of these sites leads to pancreatic insufficiency, "meconium ileus", and devastating "chronic obstructive pulmonary disease" (Al-Awqati, Q. et al. (1992) J. Exp. Biol. 172:245-266).

Many intracellular organelles contain  $\text{H}^+$ -ATPase pumps that generate transmembrane pH and electrochemical differences by moving protons from the cytosol to the organelle lumen. If the



membrane of the organelle is permeable to other ions, then the electrochemical gradient can be abrogated without affecting the pH differential. In fact, removal of the electrochemical barrier allows more  $H^+$  to be pumped across the membrane, increasing the pH differential.  $Cl^-$  is the sole counterion of  $H^+$  translocation in a number of organelles, including chromaffin granules, Golgi vesicles, lysosomes, and endosomes. Functions that require a low vacuolar pH include uptake of small molecules such as biogenic amines in chromaffin granules, processing of vacuolar constituents such as pro-hormones by proteolytic enzymes, and protein degradation in lysosomes (Al-Awqati, supra).

Ligand-gated channels open their pores when an extracellular or intracellular mediator binds to the channel. Neurotransmitter-gated channels are channels that open when a neurotransmitter binds to their extracellular domain. These channels exist in the postsynaptic membrane of nerve or muscle cells. There are two types of neurotransmitter-gated channels. Sodium channels open in response to excitatory neurotransmitters, such as acetylcholine, glutamate, and serotonin. This opening causes an influx of  $Na^+$  and produces the initial localized depolarization that activates the voltage-gated channels and starts the action potential. Chloride channels open in response to inhibitory neurotransmitters, such as  $\gamma$ -aminobutyric acid (GABA) and glycine, leading to hyperpolarization of the membrane and the subsequent generation of an action potential.

Ligand-gated channels can be regulated by intracellular second messengers. Calcium-activated  $K^+$  channels are gated by internal calcium ions. In nerve cells, an influx of calcium during depolarization opens  $K^+$  channels to modulate the magnitude of the action potential (Ishi, T.M. et al. (1997) Proc. Natl. Acad. Sci. USA 94:11651-11656). Cyclic nucleotide-gated (CNG) channels are gated by cytosolic cyclic nucleotides. The best examples of these are the cAMP-gated  $Na^+$  channels involved in olfaction and the cGMP-gated cation channels involved in vision. Both systems involve ligand-mediated activation of a G-protein coupled receptor which then alters the level of cyclic nucleotide within the cell.

Ion channels are expressed in a number of tissues where they are implicated in a variety of processes. CNG channels, while abundantly expressed in photoreceptor and olfactory sensory cells, are also found in kidney, lung, pineal, retinal ganglion cells, testis, aorta, and brain. Calcium-activated  $K^+$  channels may be responsible for the vasodilatory effects of bradykinin in the kidney and for shunting excess  $K^+$  from brain capillary endothelial cells into the blood. They are also implicated in repolarizing granulocytes after agonist-stimulated depolarization (Ishi, supra). Ion channels have been the target for many drug therapies. Neurotransmitter-gated channels have been targeted in therapies for treatment of insomnia, anxiety, depression, and schizophrenia. Voltage-gated channels have been targeted in therapies for arrhythmia, ischemic stroke, head trauma, and neurodegenerative disease (Taylor, C.P. and L.S. Narasimhan (1997) Adv. Pharmacol. 39:47-98).

#### Disease Correlation

The etiology of numerous human diseases and disorders can be attributed to defects in the transport of molecules across membranes. Defects in the trafficking of membrane-bound transporters and ion channels are associated with several disorders, e.g. cystic fibrosis, glucose-galactose malabsorption syndrome, hypercholesterolemia, von Gierke disease, and certain forms of diabetes mellitus. Single-gene defect diseases resulting in an inability to transport small molecules across membranes include, e.g., cystinuria, iminoglycinuria, Hartup disease, and Fanconi disease (van't Hoff, W.G. (1996) *Exp. Nephrol.* 4:253-262; Talente, G.M. et al. (1994) *Ann. Intern. Med.* 120:218-226; and Chillon, M. et al. (1995) *New Engl. J. Med.* 332:1475-1480).

## 10 Protein Modification and Maintenance Molecules

The cellular processes regulating modification and maintenance of protein molecules coordinate their conformation, stabilization, and degradation. Each of these processes is mediated by key enzymes or proteins such as proteases, protease inhibitors, transferases, isomerases, and molecular chaperones.

### 15 Proteases

Proteases cleave proteins and peptides at the peptide bond that forms the backbone of the peptide and protein chain. Proteolytic processing is essential to cell growth, differentiation, remodeling, and homeostasis as well as inflammation and immune response. Typical protein half-lives range from hours to a few days, so that within all living cells, precursor proteins are being  
 20 cleaved to their active form, signal sequences proteolytically removed from targeted proteins, and aged or defective proteins degraded by proteolysis. Proteases function in bacterial, parasitic, and viral invasion and replication within a host. Four principal categories of mammalian proteases have been identified based on active site structure, mechanism of action, and overall three-dimensional structure. (Beynon, R.J. and J.S. Bond (1994) Proteolytic Enzymes: A Practical Approach, Oxford  
 25 University Press, New York NY, pp. 1-5).

The serine proteases (SPs) have a serine residue, usually within a conserved sequence, in an active site composed of the serine, an aspartate, and a histidine residue. SPs include the digestive enzymes trypsin and chymotrypsin, components of the complement cascade and the blood-clotting cascade, and enzymes that control extracellular protein degradation. The main SP sub-families are  
 30 trypases, which cleave after arginine or lysine; aspartases, which cleave after aspartate; chymases, which cleave after phenylalanine or leucine; metases, which cleavage after methionine; and serases which cleave after serine. Enterokinase, the initiator of intestinal digestion, is a serine protease found in the intestinal brush border, where it cleaves the acidic propeptide from trypsinogen to yield active trypsin (Kitamoto, Y. et al. (1994) *Proc. Natl. Acad. Sci. USA* 91:7588-7592).  
 35 Prolylcarboxypeptidase, a lysosomal serine peptidase that cleaves peptides such as angiotensin II and III and [des-Arg9] bradykinin, shares sequence homology with members of both the serine

carboxypeptidase and prolylendopeptidase families (Tan, F. et al. (1993) *J. Biol. Chem.* 268:16631-16638).

Cysteine proteases (CPs) have a cysteine as the major catalytic residue at an active site where catalysis proceeds via an intermediate thiol ester and is facilitated by adjacent histidine and aspartic acid residues. CPs are involved in diverse cellular processes ranging from the processing of precursor proteins to intracellular degradation. Mammalian CPs include lysosomal cathepsins and cytosolic calcium activated proteases, calpains. CPs are produced by monocytes, macrophages and other cells of the immune system which migrate to sites of inflammation and secrete molecules involved in tissue repair. Overabundance of these repair molecules plays a role in certain disorders. In autoimmune diseases such as rheumatoid arthritis, secretion of the cysteine peptidase cathepsin C degrades collagen, laminin, elastin and other structural proteins found in the extracellular matrix of bones.

Aspartic proteases are members of the cathepsin family of lysosomal proteases and include pepsin A, gastricsin, chymosin, renin, and cathepsins D and E. Aspartic proteases have a pair of aspartic acid residues in the active site, and are most active in the pH 2 - 3 range, in which one of the aspartate residues is ionized, the other un-ionized. Aspartic proteases include bacterial penicillopepsin, mammalian pepsin, renin, chymosin, and certain fungal proteases. Abnormal regulation and expression of cathepsins is evident in various inflammatory disease states. In cells isolated from inflamed synovia, the mRNA for stromelysin, cytokines, TIMP-1, cathepsin, gelatinase, and other molecules is preferentially expressed. Expression of cathepsins L and D is elevated in synovial tissues from patients with rheumatoid arthritis and osteoarthritis. Cathepsin L expression may also contribute to the influx of mononuclear cells which exacerbates the destruction of the rheumatoid synovium. (Keyszer, G.M. (1995) *Arthritis Rheum.* 38:976-984.) The increased expression and differential regulation of the cathepsins are linked to the metastatic potential of a variety of cancers and as such are of therapeutic and prognostic interest (Chambers, A.F. et al. (1993) *Crit. Rev. Oncog.* 4:95-114).

Metalloproteases have active sites that include two glutamic acid residues and one histidine residue that serve as binding sites for zinc. Carboxypeptidases A and B are the principal mammalian metalloproteases. Both are exoproteases of similar structure and active sites. Carboxypeptidase A, like chymotrypsin, prefers C-terminal aromatic and aliphatic side chains of hydrophobic nature, whereas carboxypeptidase B is directed toward basic arginine and lysine residues. Glycoprotease (GCP), or O-sialoglycoprotein endopeptidase, is a metallopeptidase which specifically cleaves O-sialoglycoproteins such as glycophorin A. Another metallopeptidase, placental leucine aminopeptidase (P-LAP) degrades several peptide hormones such as oxytocin and vasopressin, suggesting a role in maintaining homeostasis during pregnancy, and is expressed in several tissues (Rogi, T. et al. (1996) *J. Biol. Chem.* 271:56-61).

Ubiquitin proteases are associated with the ubiquitin conjugation system (UCS), a major pathway for the degradation of cellular proteins in eukaryotic cells and some bacteria. The UCS mediates the elimination of abnormal proteins and regulates the half-lives of important regulatory proteins that control cellular processes such as gene transcription and cell cycle progression. In the UCS pathway, proteins targeted for degradation are conjugated to a ubiquitin, a small heat stable protein. The ubiquitinated protein is then recognized and degraded by proteasome, a large, multisubunit proteolytic enzyme complex, and ubiquitin is released for reutilization by ubiquitin protease. The UCS is implicated in the degradation of mitotic cyclic kinases, oncoproteins, tumor suppressor genes such as p53, viral proteins, cell surface receptors associated with signal transduction, transcriptional regulators, and mutated or damaged proteins (Ciechanover, A. (1994) Cell 79:13-21). A murine proto-oncogene, Unp, encodes a nuclear ubiquitin protease whose overexpression leads to oncogenic transformation of NIH3T3 cells, and the human homolog of this gene is consistently elevated in small cell tumors and adenocarcinomas of the lung (Gray, D.A. (1995) Oncogene 10:2179-2183).

#### 15 Signal Peptidases

The mechanism for the translocation process into the endoplasmic reticulum (ER) involves the recognition of an N-terminal signal peptide on the elongating protein. The signal peptide directs the protein and attached ribosome to a receptor on the ER membrane. The polypeptide chain passes through a pore in the ER membrane into the lumen while the N-terminal signal peptide remains attached at the membrane surface. The process is completed when signal peptidase located inside the ER cleaves the signal peptide from the protein and releases the protein into the lumen.

#### Protease Inhibitors

Protease inhibitors and other regulators of protease activity control the activity and effects of proteases. Protease inhibitors have been shown to control pathogenesis in animal models of proteolytic disorders (Murphy, G. (1991) Agents Actions Suppl. 35:69-76). Low levels of the cystatins, low molecular weight inhibitors of the cysteine proteases, correlate with malignant progression of tumors. (Calkins, C. et al (1995) Biol. Biochem. Hoppe Seyler 376:71-80). Serpins are inhibitors of mammalian plasma serine proteases. Many serpins serve to regulate the blood clotting cascade and/or the complement cascade in mammals. Sp32 is a positive regulator of the mammalian acrosomal protease, acrosin, that binds the proenzyme, proacrosin, and thereby aides in packaging the enzyme into the acrosomal matrix (Baba, T. et al. (1994) J. Biol. Chem. 269:10133-10140). The Kunitz family of serine protease inhibitors are characterized by one or more "Kunitz domains" containing a series of cysteine residues that are regularly spaced over approximately 50 amino acid residues and form three intrachain disulfide bonds. Members of this family include aprotinin, tissue factor pathway inhibitor (TFPI-1 and TFPI-2), inter- $\alpha$ -trypsin inhibitor, and bikunin. (Marlor, C.W. et al. (1997) J. Biol. Chem. 272:12202-12208.) Members of this family are potent

inhibitors (in the nanomolar range) against serine proteases such as kallikrein and plasmin. Aprotinin has clinical utility in reduction of perioperative blood loss.

A major portion of all proteins synthesized in eukaryotic cells are synthesized on the cytosolic surface of the endoplasmic reticulum (ER). Before these immature proteins are distributed  
5 to other organelles in the cell or are secreted, they must be transported into the interior lumen of the ER where post-translational modifications are performed. These modifications include protein folding and the formation of disulfide bonds, and N-linked glycosylations.

#### Protein Isomerases

Protein folding in the ER is aided by two principal types of protein isomerases, protein  
10 disulfide isomerase (PDI), and peptidyl-prolyl isomerase (PPI). PDI catalyzes the oxidation of free sulfhydryl groups in cysteine residues to form intramolecular disulfide bonds in proteins. PPI, an enzyme that catalyzes the isomerization of certain proline imidic bonds in oligopeptides and proteins, is considered to govern one of the rate limiting steps in the folding of many proteins to their final functional conformation. The cyclophilins represent a major class of PPI that was originally  
15 identified as the major receptor for the immunosuppressive drug cyclosporin A (Handschumacher, R.E. et al. (1984) Science 226: 544-547).

#### Protein Glycosylation

The glycosylation of most soluble secreted and membrane-bound proteins by oligosaccharides linked to asparagine residues in proteins is also performed in the ER. This reaction  
20 is catalyzed by a membrane-bound enzyme, oligosaccharyl transferase. Although the exact purpose of this "N-linked" glycosylation is unknown, the presence of oligosaccharides tends to make a glycoprotein resistant to protease digestion. In addition, oligosaccharides attached to cell-surface proteins called selectins are known to function in cell-cell adhesion processes (Alberts, B. et al. (1994) Molecular Biology of the Cell, Garland Publishing Co., New York NY, p.608). "O-linked"  
25 glycosylation of proteins also occurs in the ER by the addition of N-acetylgalactosamine to the hydroxyl group of a serine or threonine residue followed by the sequential addition of other sugar residues to the first. This process is catalysed by a series of glycosyltransferases each specific for a particular donor sugar nucleotide and acceptor molecule (Lodish, H. et al. (1995) Molecular Cell Biology, W.H. Freeman and Co., New York NY, pp.700-708). In many cases, both N- and O-linked  
30 oligosaccharides appear to be required for the secretion of proteins or the movement of plasma membrane glycoproteins to the cell surface.

An additional glycosylation mechanism operates in the ER specifically to target lysosomal enzymes to lysosomes and prevent their secretion. Lysosomal enzymes in the ER receive an N-linked oligosaccharide, like plasma membrane and secreted proteins, but are then phosphorylated on  
35 one or two mannose residues. The phosphorylation of mannose residues occurs in two steps, the first step being the addition of an N-acetylglucosamine phosphate residue by N-acetylglucosamine

phosphotransferase, and the second the removal of the N-acetylglucosamine group by phosphodiesterase. The phosphorylated mannose residue then targets the lysosomal enzyme to a mannose 6-phosphate receptor which transports it to a lysosome vesicle (Lodish, supra, pp. 708-711).

#### Chaperones

5 Molecular chaperones are proteins that aid in the proper folding of immature proteins and refolding of improperly folded ones, the assembly of protein subunits, and in the transport of unfolded proteins across membranes. Chaperones are also called heat-shock proteins (hsp) because of their tendency to be expressed in dramatically increased amounts following brief exposure of cells to elevated temperatures. This latter property most likely reflects their need in the refolding of  
10 proteins that have become denatured by the high temperatures. Chaperones may be divided into several classes according to their location, function, and molecular weight, and include hsp60, TCP1, hsp70, hsp40 (also called DnaJ), and hsp90. For example, hsp90 binds to steroid hormone receptors, represses transcription in the absence of the ligand, and provides proper folding of the ligand-binding domain of the receptor in the presence of the hormone (Burston, S.G. and A.R. Clarke (1995) *Essays*  
15 *Biochem.* 29:125-136). Hsp60 and hsp70 chaperones aid in the transport and folding of newly synthesized proteins. Hsp70 acts early in protein folding, binding a newly synthesized protein before it leaves the ribosome and transporting the protein to the mitochondria or ER before releasing the folded protein. Hsp60, along with hsp10, binds misfolded proteins and gives them the opportunity to refold correctly. All chaperones share an affinity for hydrophobic patches on incompletely folded  
20 proteins and the ability to hydrolyze ATP. The energy of ATP hydrolysis is used to release the hsp-bound protein in its properly folded state (Alberts, supra, pp 214, 571-572).

#### **Nucleic Acid Synthesis and Modification Molecules**

##### Polymerases

25 DNA and RNA replication are critical processes for cell replication and function. DNA and RNA replication are mediated by the enzymes DNA and RNA polymerase, respectively, by a "templating" process in which the nucleotide sequence of a DNA or RNA strand is copied by complementary base-pairing into a complementary nucleic acid sequence of either DNA or RNA. However, there are fundamental differences between the two processes.

30 DNA polymerase catalyzes the stepwise addition of a deoxyribonucleotide to the 3'-OH end of a polynucleotide strand (the primer strand) that is paired to a second (template) strand. The new DNA strand therefore grows in the 5' to 3' direction (Alberts, B. et al. (1994) The Molecular Biology of the Cell, Garland Publishing Inc., New York NY, pp. 251-254). The substrates for the polymerization reaction are the corresponding deoxynucleotide triphosphates which must base-pair  
35 with the correct nucleotide on the template strand in order to be recognized by the polymerase. Because DNA exists as a double-stranded helix, each of the two strands may serve as a template for

the formation of a new complementary strand. Each of the two daughter cells of the dividing cell therefore inherits a new DNA double helix containing one old and one new strand. Thus, DNA is said to be replicated "semiconservatively" by DNA polymerase. In addition to the synthesis of new DNA, DNA polymerase is also involved in the repair of damaged DNA as discussed below under

5 "Ligases."

In contrast to DNA polymerase, RNA polymerase uses a DNA template strand to "transcribe" DNA into RNA using ribonucleotide triphosphates as substrates. Like DNA polymerization, RNA polymerization proceeds in a 5' to 3' direction by addition of a ribonucleoside monophosphate to the 3'-OH end of a growing RNA chain. DNA transcription generates messenger RNAs (mRNA) that

10 carry information for protein synthesis, as well as the transfer, ribosomal, and other RNAs that have structural or catalytic functions. In eukaryotes, three discrete RNA polymerases synthesize the three different types of RNA (Alberts, *supra*, pp. 367-368). RNA polymerase I makes the large ribosomal RNAs, RNA polymerase II makes the mRNAs that will be translated into proteins, and RNA polymerase III makes a variety of small, stable RNAs, including 5S ribosomal RNA and the transfer

15 RNAs (tRNA). In all cases, RNA synthesis is initiated by binding of the RNA polymerase to a promoter region on the DNA and synthesis begins at a start site within the promoter. Synthesis is completed at a broad, general stop or termination region in the DNA where both the polymerase and the completed RNA chain are released.

#### Ligases

DNA repair is the process by which accidental base changes, such as those produced by oxidative damage, hydrolytic attack, or uncontrolled methylation of DNA are corrected before replication or transcription of the DNA can occur. Because of the efficiency of the DNA repair process, fewer than one in one thousand accidental base changes causes a mutation (Alberts, *supra*, pp. 245-249). The three steps common to most types of DNA repair are (1) excision of the damaged

20 or altered base or nucleotide by DNA nucleases, leaving a gap; (2) insertion of the correct nucleotide in this gap by DNA polymerase using the complementary strand as the template; and (3) sealing the break left between the inserted nucleotide(s) and the existing DNA strand by DNA ligase. In the last reaction, DNA ligase uses the energy from ATP hydrolysis to activate the 5' end of the broken phosphodiester bond before forming the new bond with the 3'-OH of the DNA strand. In Bloom's

30 syndrome, an inherited human disease, individuals are partially deficient in DNA ligation and consequently have an increased incidence of cancer (Alberts, *supra*, p. 247).

#### Nucleases

Nucleases comprise both enzymes that hydrolyze DNA (DNase) and RNA (RNase). They serve different purposes in nucleic acid metabolism. Nucleases hydrolyze the phosphodiester bonds

35 between adjacent nucleotides either at internal positions (endonucleases) or at the terminal 3' or 5' nucleotide positions (exonucleases). A DNA exonuclease activity in DNA polymerase, for example,

serves to remove improperly paired nucleotides attached to the 3'-OH end of the growing DNA strand by the polymerase and thereby serves a "proofreading" function. As mentioned above, DNA endonuclease activity is involved in the excision step of the DNA repair process.

RNases also serve a variety of functions. For example, RNase P is a ribonucleoprotein enzyme which cleaves the 5' end of pre-tRNAs as part of their maturation process. RNase H digests the RNA strand of an RNA/DNA hybrid. Such hybrids occur in cells invaded by retroviruses, and RNase H is an important enzyme in the retroviral replication cycle. Pancreatic RNase secreted by the pancreas into the intestine hydrolyzes RNA present in ingested foods. RNase activity in serum and cell extracts is elevated in a variety of cancers and infectious diseases (Schein, C.H. (1997) Nat. Biotechnol. 15:529-536). Regulation of RNase activity is being investigated as a means to control tumor angiogenesis, allergic reactions, viral infection and replication, and fungal infections.

#### Methylases

Methylation of specific nucleotides occurs in both DNA and RNA, and serves different functions in the two macromolecules. Methylation of cytosine residues to form 5-methyl cytosine in DNA occurs specifically at CG sequences which are base-paired with one another in the DNA double-helix. This pattern of methylation is passed from generation to generation during DNA replication by an enzyme called "maintenance methylase" that acts preferentially on those CG sequences that are base-paired with a CG sequence that is already methylated. Such methylation appears to distinguish active from inactive genes by preventing the binding of regulatory proteins that "turn on" the gene, but permit the binding of proteins that inactivate the gene (Alberts, *supra*, pp. 448-451). In RNA metabolism, "tRNA methylase" produces one of several nucleotide modifications in tRNA that affect the conformation and base-pairing of the molecule and facilitate the recognition of the appropriate mRNA codons by specific tRNAs. The primary methylation pattern is the dimethylation of guanine residues to form N,N-dimethyl guanine.

#### Helicases and Single-Stranded Binding Proteins

Helicases are enzymes that destabilize and unwind double helix structures in both DNA and RNA. Since DNA replication occurs more or less simultaneously on both strands, the two strands must first separate to generate a replication "fork" for DNA polymerase to act on. Two types of replication proteins contribute to this process, DNA helicases and single-stranded binding proteins. DNA helicases hydrolyze ATP and use the energy of hydrolysis to separate the DNA strands. Single-stranded binding proteins (SSBs) then bind to the exposed DNA strands without covering the bases, thereby temporarily stabilizing them for templating by the DNA polymerase (Alberts, *supra*, pp. 255-256).

RNA helicases also alter and regulate RNA conformation and secondary structure. Like the DNA helicases, RNA helicases utilize energy derived from ATP hydrolysis to destabilize and unwind RNA duplexes. The most well-characterized and ubiquitous family of RNA helicases is the DEAD-



box family, so named for the conserved B-type ATP-binding motif which is diagnostic of proteins in this family. Over 40 DEAD-box helicases have been identified in organisms as diverse as bacteria, insects, yeast, amphibians, mammals, and plants. DEAD-box helicases function in diverse processes such as translation initiation, splicing, ribosome assembly, and RNA editing, transport, and stability.

- 5 Some DEAD-box helicases play tissue- and stage-specific roles in spermatogenesis and embryogenesis. Overexpression of the DEAD-box 1 protein (DDX1) may play a role in the progression of neuroblastoma (Nb) and retinoblastoma (Rb) tumors (Godbout, R. et al. (1998) J. Biol. Chem. 273:21161-21168). These observations suggest that DDX1 may promote or enhance tumor progression by altering the normal secondary structure and expression levels of RNA in cancer cells.
- 10 Other DEAD-box helicases have been implicated either directly or indirectly in tumorigenesis (Discussed in Godbout, supra). For example, murine p68 is mutated in ultraviolet light-induced tumors, and human DDX6 is located at a chromosomal breakpoint associated with B-cell lymphoma. Similarly, a chimeric protein comprised of DDX10 and NUP98, a nucleoporin protein, may be involved in the pathogenesis of certain myeloid malignancies.

15 Topoisomerases

- Besides the need to separate DNA strands prior to replication, the two strands must be "unwound" from one another prior to their separation by DNA helicases. This function is performed by proteins known as DNA topoisomerases. DNA topoisomerase effectively acts as a reversible nuclease that hydrolyzes a phosphodiesterase bond in a DNA strand, permitting the two strands to
- 20 rotate freely about one another to remove the strain of the helix, and then rejoins the original phosphodiester bond between the two strands. Two types of DNA topoisomerase exist, types I and II. DNA Topoisomerase I causes a single-strand break in a DNA helix to allow the rotation of the two strands of the helix about the remaining phosphodiester bond in the opposite strand. DNA topoisomerase II causes a transient break in both strands of a DNA helix where two double helices
- 25 cross over one another. This type of topoisomerase can efficiently separate two interlocked DNA circles (Alberts, supra, pp.260-262). Type II topoisomerases are largely confined to proliferating cells in eukaryotes, such as cancer cells. For this reason they are targets for anticancer drugs. Topoisomerase II has been implicated in multi-drug resistance (MDR) as it appears to aid in the repair of DNA damage inflicted by DNA binding agents such as doxorubicin and vincristine.

30 Recombinases

- Genetic recombination is the process of rearranging DNA sequences within an organism's genome to provide genetic variation for the organism in response to changes in the environment. DNA recombination allows variation in the particular combination of genes present in an individual's genome, as well as the timing and level of expression of these genes (see Alberts, supra, pp. 263-
- 35 273). Two broad classes of genetic recombination are commonly recognized, general recombination and site-specific recombination. General recombination involves genetic exchange between any

homologous pair of DNA sequences usually located on two copies of the same chromosome. The process is aided by enzymes called recombinases that "nick" one strand of a DNA duplex more or less randomly and permit exchange with the complementary strand of another duplex. The process does not normally change the arrangement of genes on a chromosome. In site-specific  
5 recombination, the recombinase recognizes specific nucleotide sequences present in one or both of the recombining molecules. Base-pairing is not involved in this form of recombination and therefore does not require DNA homology between the recombining molecules. Unlike general recombination, this form of recombination can alter the relative positions of nucleotide sequences in chromosomes.

#### Splicing Factors

10 Various proteins are necessary for processing of transcribed RNAs in the nucleus. Pre-mRNA processing steps include capping at the 5' end with methylguanosine, polyadenylating the 3' end, and splicing to remove introns. The primary RNA transcript from DNA is a faithful copy of the gene containing both exon and intron sequences, and the latter sequences must be cut out of the RNA transcript to produce an mRNA that codes for a protein. This "splicing" of the mRNA sequence takes  
15 place in the nucleus with the aid of a large, multicomponent ribonucleoprotein complex known as a spliceosome. The spliceosomal complex is composed of five small nuclear ribonucleoprotein particles (snRNPs) designated U1, U2, U4, U5, and U6, and a number of additional proteins. Each snRNP contains a single species of snRNA and about ten proteins. The RNA components of some snRNPs recognize and base pair with intron consensus sequences. The protein components mediate  
20 spliceosome assembly and the splicing reaction. Autoantibodies to snRNP proteins are found in the blood of patients with systemic lupus erythematosus (Stryer, L. (1995) Biochemistry, W.H. Freeman and Company, New York NY, p. 863).

#### **Adhesion Molecules**

25 The surface of a cell is rich in transmembrane proteoglycans, glycoproteins, glycolipids, and receptors. These macromolecules mediate adhesion with other cells and with components of the extracellular matrix (ECM). The interaction of the cell with its surroundings profoundly influences cell shape, strength, flexibility, motility, and adhesion. These dynamic properties are intimately associated with signal transduction pathways controlling cell proliferation and differentiation, tissue  
30 construction, and embryonic development.

#### Cadherins

Cadherins comprise a family of calcium-dependent glycoproteins that function in mediating cell-cell adhesion in virtually all solid tissues of multicellular organisms. These proteins share multiple repeats of a cadherin-specific motif, and the repeats form the folding units of the cadherin  
35 extracellular domain. Cadherin molecules cooperate to form focal contacts, or adhesion plaques, between adjacent epithelial cells. The cadherin family includes the classical cadherins and

protocadherins. Classical cadherins include the E-cadherin, N-cadherin, and P-cadherin subfamilies. E-cadherin is present on many types of epithelial cells and is especially important for embryonic development. N-cadherin is present on nerve, muscle, and lens cells and is also critical for embryonic development. P-cadherin is present on cells of the placenta and epidermis. Recent studies  
5 report that protocadherins are involved in a variety of cell-cell interactions (Suzuki, S.T. (1996) J. Cell Sci. 109:2609-2611). The intracellular anchorage of cadherins is regulated by their dynamic association with catenins, a family of cytoplasmic signal transduction proteins associated with the actin cytoskeleton. The anchorage of cadherins to the actin cytoskeleton appears to be regulated by protein tyrosine phosphorylation, and the cadherins are the target of phosphorylation-induced  
10 junctional disassembly (Aberle, H. et al. (1996) J. Cell. Biochem. 61:514-523).

#### Integrins

Integrins are ubiquitous transmembrane adhesion molecules that link the ECM to the internal cytoskeleton. Integrins are composed of two noncovalently associated transmembrane glycoprotein subunits called  $\alpha$  and  $\beta$ . Integrins function as receptors that play a role in signal transduction. For  
15 example, binding of integrin to its extracellular ligand may stimulate changes in intracellular calcium levels or protein kinase activity (Sjaastad, M.D. and W.J. Nelson (1997) BioEssays 19:47-55). At least ten cell surface receptors of the integrin family recognize the ECM component fibronectin, which is involved in many different biological processes including cell migration and embryogenesis (Johansson, S. et al. (1997) Front. Biosci. 2:D126-D146).

#### Lectins

Lectins comprise a ubiquitous family of extracellular glycoproteins which bind cell surface carbohydrates specifically and reversibly, resulting in the agglutination of cells (reviewed in Drickamer, K. and M.E. Taylor (1993) Annu. Rev. Cell Biol. 9:237-264). This function is particularly important for activation of the immune response. Lectins mediate the agglutination and  
25 mitogenic stimulation of lymphocytes at sites of inflammation (Lasky, L.A. (1991) J. Cell. Biochem. 45:139-146; Paietta, E. et al. (1989) J. Immunol. 143:2850-2857).

Lectins are further classified into subfamilies based on carbohydrate-binding specificity and other criteria. The galectin subfamily, in particular, includes lectins that bind  $\beta$ -galactoside carbohydrate moieties in a thiol-dependent manner (reviewed in Hadari, Y.R. et al. (1998) J. Biol. Chem. 270:3447-3453). Galectins are widely expressed and developmentally regulated. Because all  
30 galectins lack an N-terminal signal peptide, it is suggested that galectins are externalized through an atypical secretory mechanism. Two classes of galectins have been defined based on molecular weight and oligomerization properties. Small galectins form homodimers and are about 14 to 16 kilodaltons in mass, while large galectins are monomeric and about 29-37 kilodaltons.

35 Galectins contain a characteristic carbohydrate recognition domain (CRD). The CRD is about 140 amino acids and contains several stretches of about 1 - 10 amino acids which are highly

conserved among all galectins. A particular 6-amino acid motif within the CRD contains conserved tryptophan and arginine residues which are critical for carbohydrate binding. The CRD of some galectins also contains cysteine residues which may be important for disulfide bond formation. Secondary structure predictions indicate that the CRD forms several  $\beta$ -sheets.

- 5 Galectins play a number of roles in diseases and conditions associated with cell-cell and cell-matrix interactions. For example, certain galectins associate with sites of inflammation and bind to cell surface immunoglobulin E molecules. In addition, galectins may play an important role in cancer metastasis. Galectin overexpression is correlated with the metastatic potential of cancers in humans and mice. Moreover, anti-galectin antibodies inhibit processes associated with cell
- 10 transformation, such as cell aggregation and anchorage-independent growth (See, for example, Su, Z.-Z. et al. (1996) Proc. Natl. Acad. Sci. USA 93:7252-7257).

#### Selectins

- Selectins, or LEC-CAMs, comprise a specialized lectin subfamily involved primarily in inflammation and leukocyte adhesion (Reviewed in Lasky, *supra*). Selectins mediate the recruitment
- 15 of leukocytes from the circulation to sites of acute inflammation and are expressed on the surface of vascular endothelial cells in response to cytokine signaling. Selectins bind to specific ligands on the leukocyte cell membrane and enable the leukocyte to adhere to and migrate along the endothelial surface. Binding of selectin to its ligand leads to polarized rearrangement of the actin cytoskeleton and stimulates signal transduction within the leukocyte (Brenner, B. et al. (1997) Biochem. Biophys.
- 20 Res. Commun. 231:802-807; Hidari, K.I. et al. (1997) J. Biol. Chem. 272:28750-28756). Members of the selectin family possess three characteristic motifs: a lectin or carbohydrate recognition domain; an epidermal growth factor-like domain; and a variable number of short consensus repeats (scr or "sushi" repeats) which are also present in complement regulatory proteins. The selectins include lymphocyte adhesion molecule-1 (Lam-1 or L-selectin), endothelial leukocyte adhesion
- 25 molecule-1 (ELAM-1 or E-selectin), and granule membrane protein-140 (GMP-140 or P-selectin) (Johnston, G.I. et al. (1989) Cell 56:1033-1044).

#### **Antigen Recognition Molecules**

- All vertebrates have developed sophisticated and complex immune systems that provide
- 30 protection from viral, bacterial, fungal, and parasitic infections. A key feature of the immune system is its ability to distinguish foreign molecules, or antigens, from "self" molecules. This ability is mediated primarily by secreted and transmembrane proteins expressed by leukocytes (white blood cells) such as lymphocytes, granulocytes, and monocytes. Most of these proteins belong to the immunoglobulin (Ig) superfamily, members of which contain one or more repeats of a conserved
- 35 structural domain. This Ig domain is comprised of antiparallel  $\beta$  sheets joined by a disulfide bond in an arrangement called the Ig fold. Members of the Ig superfamily include T-cell receptors, major

histocompatibility (MHC) proteins, antibodies, and immune cell-specific surface markers such as CD4, CD8, and CD28.

MHC proteins are cell surface markers that bind to and present foreign antigens to T cells. MHC molecules are classified as either class I or class II. Class I MHC molecules (MHC I) are  
5 expressed on the surface of almost all cells and are involved in the presentation of antigen to cytotoxic T cells. For example, a cell infected with virus will degrade intracellular viral proteins and express the protein fragments bound to MHC I molecules on the cell surface. The MHC I/antigen complex is recognized by cytotoxic T-cells which destroy the infected cell and the virus within. Class II MHC molecules are expressed primarily on specialized antigen-presenting cells of the  
10 immune system, such as B-cells and macrophages. These cells ingest foreign proteins from the extracellular fluid and express MHC II/antigen complex on the cell surface. This complex activates helper T-cells, which then secrete cytokines and other factors that stimulate the immune response. MHC molecules also play an important role in organ rejection following transplantation. Rejection occurs when the recipient's T-cells respond to foreign MHC molecules on the transplanted organ in  
15 the same way as to self MHC molecules bound to foreign antigen. (Reviewed in Alberts, B. et al. (1994) Molecular Biology of the Cell, Garland Publishing, New York NY, pp. 1229-1246.)

Antibodies, or immunoglobulins, are either expressed on the surface of B-cells or secreted by B-cells into the circulation. Antibodies bind and neutralize foreign antigens in the blood and other extracellular fluids. The prototypical antibody is a tetramer consisting of two identical heavy  
20 polypeptide chains (H-chains) and two identical light polypeptide chains (L-chains) interlinked by disulfide bonds. This arrangement confers the characteristic Y-shape to antibody molecules. Antibodies are classified based on their H-chain composition. The five antibody classes, IgA, IgD, IgE, IgG and IgM, are defined by the  $\alpha$ ,  $\delta$ ,  $\epsilon$ ,  $\gamma$ , and  $\mu$  H-chain types. There are two types of L-chains,  $\kappa$  and  $\lambda$ , either of which may associate as a pair with any H-chain pair. IgG, the most  
25 common class of antibody found in the circulation, is tetrameric, while the other classes of antibodies are generally variants or multimers of this basic structure.

H-chains and L-chains each contain an N-terminal variable region and a C-terminal constant region. The constant region consists of about 110 amino acids in L-chains and about 330 or 440 amino acids in H-chains. The amino acid sequence of the constant region is nearly identical among  
30 H- or L-chains of a particular class. The variable region consists of about 110 amino acids in both H- and L-chains. However, the amino acid sequence of the variable region differs among H- or L-chains of a particular class. Within each H- or L-chain variable region are three hypervariable regions of extensive sequence diversity, each consisting of about 5 to 10 amino acids. In the antibody molecule, the H- and L-chain hypervariable regions come together to form the antigen recognition site.  
35 (Reviewed in Alberts, supra, pp. 1206-1213 and 1216-1217.)

Both H-chains and L-chains contain repeated Ig domains. For example, a typical H-chain

contains four Ig domains, three of which occur within the constant region and one of which occurs within the variable region and contributes to the formation of the antigen recognition site. Likewise, a typical L-chain contains two Ig domains, one of which occurs within the constant region and one of which occurs within the variable region.

5           The immune system is capable of recognizing and responding to any foreign molecule that enters the body. Therefore, the immune system must be armed with a full repertoire of antibodies against all potential antigens. Such antibody diversity is generated by somatic rearrangement of gene segments encoding variable and constant regions. These gene segments are joined together by site-specific recombination which occurs between highly conserved DNA sequences that flank each gene  
10 segment. Because there are hundreds of different gene segments, millions of unique genes can be generated combinatorially. In addition, imprecise joining of these segments and an unusually high rate of somatic mutation within these segments further contribute to the generation of a diverse antibody population.

          T-cell receptors are both structurally and functionally related to antibodies. (Reviewed in  
15   Alberts, supra, pp. 1228-1229.) T-cell receptors are cell surface proteins that bind foreign antigens and mediate diverse aspects of the immune response. A typical T-cell receptor is a heterodimer comprised of two disulfide-linked polypeptide chains called  $\alpha$  and  $\beta$ . Each chain is about 280 amino acids in length and contains one variable region and one constant region. Each variable or constant region folds into an Ig domain. The variable regions from the  $\alpha$  and  $\beta$  chains come together in the  
20 heterodimer to form the antigen recognition site. T-cell receptor diversity is generated by somatic rearrangement of gene segments encoding the  $\alpha$  and  $\beta$  chains. T-cell receptors recognize small peptide antigens that are expressed on the surface of antigen-presenting cells and pathogen-infected cells. These peptide antigens are presented on the cell surface in association with major histocompatibility proteins which provide the proper context for antigen recognition.

25

#### **Secreted and Extracellular Matrix Molecules**

          Protein secretion is essential for cellular function. Protein secretion is mediated by a signal peptide located at the amino terminus of the protein to be secreted. The signal peptide is comprised of about ten to twenty hydrophobic amino acids which target the nascent protein from the ribosome to  
30 the endoplasmic reticulum (ER). Proteins targeted to the ER may either proceed through the secretory pathway or remain in any of the secretory organelles such as the ER, Golgi apparatus, or lysosomes. Proteins that transit through the secretory pathway are either secreted into the extracellular space or retained in the plasma membrane. Secreted proteins are often synthesized as inactive precursors that are activated by post-translational processing events during transit through  
35 the secretory pathway. Such events include glycosylation, proteolysis, and removal of the signal peptide by a signal peptidase. Other events that may occur during protein transport include

chaperone-dependent unfolding and folding of the nascent protein and interaction of the protein with a receptor or pore complex. Examples of secreted proteins with amino terminal signal peptides include receptors, extracellular matrix molecules, cytokines, hormones, growth and differentiation factors, neuropeptides, vasomediators, ion channels, transporters/pumps, and proteases. (Reviewed in  
5   Alberts, B. et al. (1994) Molecular Biology of The Cell, Garland Publishing, New York NY, pp. 557-560, 582-592.)

The extracellular matrix (ECM) is a complex network of glycoproteins, polysaccharides, proteoglycans, and other macromolecules that are secreted from the cell into the extracellular space. The ECM remains in close association with the cell surface and provides a supportive meshwork that  
10   profoundly influences cell shape, motility, strength, flexibility, and adhesion. In fact, adhesion of a cell to its surrounding matrix is required for cell survival except in the case of metastatic tumor cells, which have overcome the need for cell-ECM anchorage. This phenomenon suggests that the ECM plays a critical role in the molecular mechanisms of growth control and metastasis. (Reviewed in  
15   Ruoslahti, E. (1996) *Sci. Am.* 275:72-77.) Furthermore, the ECM determines the structure and physical properties of connective tissue and is particularly important for morphogenesis and other processes associated with embryonic development and pattern formation.

The collagens comprise a family of ECM proteins that provide structure to bone, teeth, skin, ligaments, tendons, cartilage, blood vessels, and basement membranes. Multiple collagen proteins have been identified. Three collagen molecules fold together in a triple helix stabilized by interchain  
20   disulfide bonds. Bundles of these triple helices then associate to form fibrils. Collagen primary structure consists of hundreds of (Gly-X-Y) repeats where about a third of the X and Y residues are Pro. Glycines are crucial to helix formation as the bulkier amino acid sidechains cannot fold into the triple helical conformation. Because of these strict sequence requirements, mutations in collagen genes have severe consequences. Osteogenesis imperfecta patients have brittle bones that fracture  
25   easily; in severe cases patients die *in utero* or at birth. Ehlers-Danlos syndrome patients have hyperelastic skin, hypermobile joints, and susceptibility to aortic and intestinal rupture. Chondrodysplasia patients have short stature and ocular disorders. Alport syndrome patients have hematuria, sensorineural deafness, and eye lens deformation. (Isselbacher, K.J. et al. (1994) Harrison's Principles of Internal Medicine, McGraw-Hill, Inc., New York NY, pp. 2105-2117; and  
30   Creighton, T.E. (1984) Proteins, Structures and Molecular Principles, W.H. Freeman and Company, New York NY, pp. 191-197.)

Elastin and related proteins confer elasticity to tissues such as skin, blood vessels, and lungs. Elastin is a highly hydrophobic protein of about 750 amino acids that is rich in proline and glycine residues. Elastin molecules are highly cross-linked, forming an extensive extracellular network of  
35   fibers and sheets. Elastin fibers are surrounded by a sheath of microfibrils which are composed of a number of glycoproteins, including fibrillin. Mutations in the gene encoding fibrillin are responsible

for Marfan's syndrome, a genetic disorder characterized by defects in connective tissue. In severe cases, the aortas of afflicted individuals are prone to rupture. (Reviewed in Alberts, supra, pp. 984-986.)

Fibronectin is a large ECM glycoprotein found in all vertebrates. Fibronectin exists as a dimer of two subunits, each containing about 2,500 amino acids. Each subunit folds into a rod-like structure containing multiple domains. The domains each contain multiple repeated modules, the most common of which is the type III fibronectin repeat. The type III fibronectin repeat is about 90 amino acids in length and is also found in other ECM proteins and in some plasma membrane and cytoplasmic proteins. Furthermore, some type III fibronectin repeats contain a characteristic tripeptide consisting of Arginine-Glycine-Aspartic acid (RGD). The RGD sequence is recognized by the integrin family of cell surface receptors and is also found in other ECM proteins. Disruption of both copies of the gene encoding fibronectin causes early embryonic lethality in mice. The mutant embryos display extensive morphological defects, including defects in the formation of the notochord, somites, heart, blood vessels, neural tube, and extraembryonic structures. (Reviewed in Alberts, supra, pp. 986-987.)

Laminin is a major glycoprotein component of the basal lamina which underlies and supports epithelial cell sheets. Laminin is one of the first ECM proteins synthesized in the developing embryo. Laminin is an 850 kilodalton protein composed of three polypeptide chains joined in the shape of a cross by disulfide bonds. Laminin is especially important for angiogenesis and in particular, for guiding the formation of capillaries. (Reviewed in Alberts, supra, pp. 990-991.)

There are many other types of proteinaceous ECM components, most of which can be classified as proteoglycans. Proteoglycans are composed of unbranched polysaccharide chains (glycosaminoglycans) attached to protein cores. Common proteoglycans include aggrecan, betaglycan, decorin, perlecan, serglycin, and syndecan-1. Some of these molecules not only provide mechanical support, but also bind to extracellular signaling molecules, such as fibroblast growth factor and transforming growth factor  $\beta$ , suggesting a role for proteoglycans in cell-cell communication and cell growth. (Reviewed in Alberts, supra, pp. 973-978.) Likewise, the glycoproteins tenascin-C and tenascin-R are expressed in developing and lesioned neural tissue and provide stimulatory and anti-adhesive (inhibitory) properties, respectively, for axonal growth. (Faissner, A. (1997) Cell Tissue Res. 290:331-341.)

### Cytoskeletal Molecules

The cytoskeleton is a cytoplasmic network of protein fibers that mediate cell shape, structure, and movement. The cytoskeleton supports the cell membrane and forms tracks along which organelles and other elements move in the cytosol. The cytoskeleton is a dynamic structure that allows cells to adopt various shapes and to carry out directed movements. Major cytoskeletal fibers



include the microtubules, the microfilaments, and the intermediate filaments. Motor proteins, including myosin, dynein, and kinesin, drive movement of or along the fibers. The motor protein dynamin drives the formation of membrane vesicles. Accessory or associated proteins modify the structure or activity of the fibers while cytoskeletal membrane anchors connect the fibers to the cell membrane.

#### Tubulins

Microtubules, cytoskeletal fibers with a diameter of about 24 nm, have multiple roles in the cell. Bundles of microtubules form cilia and flagella, which are whip-like extensions of the cell membrane that are necessary for sweeping materials across an epithelium and for swimming of sperm, respectively. Marginal bands of microtubules in red blood cells and platelets are important for these cells' pliability. Organelles, membrane vesicles, and proteins are transported in the cell along tracks of microtubules. For example, microtubules run through nerve cell axons, allowing bi-directional transport of materials and membrane vesicles between the cell body and the nerve terminal. Failure to supply the nerve terminal with these vesicles blocks the transmission of neural signals. Microtubules are also critical to chromosomal movement during cell division. Both stable and short-lived populations of microtubules exist in the cell.

Microtubules are polymers of GTP-binding tubulin protein subunits. Each subunit is a heterodimer of  $\alpha$ - and  $\beta$ - tubulin, multiple isoforms of which exist. The hydrolysis of GTP is linked to the addition of tubulin subunits at the end of a microtubule. The subunits interact head to tail to form protofilaments; the protofilaments interact side to side to form a microtubule. A microtubule is polarized, one end ringed with  $\alpha$ -tubulin and the other with  $\beta$ -tubulin, and the two ends differ in their rates of assembly. Generally, each microtubule is composed of 13 protofilaments although 11 or 15 protofilament-microtubules are sometimes found. Cilia and flagella contain doublet microtubules. Microtubules grow from specialized structures known as centrosomes or microtubule-organizing centers (MTOCs). MTOCs may contain one or two centrioles, which are pinwheel arrays of triplet microtubules. The basal body, the organizing center located at the base of a cilium or flagellum, contains one centriole. Gamma tubulin present in the MTOC is important for nucleating the polymerization of  $\alpha$ - and  $\beta$ - tubulin heterodimers but does not polymerize into microtubules.

#### Microtubule-Associated Proteins

Microtubule-associated proteins (MAPs) have roles in the assembly and stabilization of microtubules. One major family of MAPs, assembly MAPs, can be identified in neurons as well as non-neuronal cells. Assembly MAPs are responsible for cross-linking microtubules in the cytosol. These MAPs are organized into two domains: a basic microtubule-binding domain and an acidic projection domain. The projection domain is the binding site for membranes, intermediate filaments, or other microtubules. Based on sequence analysis, assembly MAPs can be further grouped into two types: Type I and Type II. Type I MAPs, which include MAP1A and MAP1B, are large, filamentous

molecules that co-purify with microtubules and are abundantly expressed in brain and testes. Type I MAPs contain several repeats of a positively-charged amino acid sequence motif that binds and neutralizes negatively charged tubulin, leading to stabilization of microtubules. MAP1A and MAP1B are each derived from a single precursor polypeptide that is subsequently proteolytically processed to  
5 generate one heavy chain and one light chain.

Another light chain, LC3, is a 16.4 kDa molecule that binds MAP1A, MAP1B, and microtubules. It is suggested that LC3 is synthesized from a source other than the MAP1A or MAP1B transcripts, and that the expression of LC3 may be important in regulating the microtubule binding activity of MAP1A and MAP1B during cell proliferation (Mann, S.S. et al. (1994) J. Biol.  
10 Chem. 269:11492-11497).

Type II MAPs, which include MAP2a, MAP2b, MAP2c, MAP4, and Tau, are characterized by three to four copies of an 18-residue sequence in the microtubule-binding domain. MAP2a, MAP2b, and MAP2c are found only in dendrites, MAP4 is found in non-neuronal cells, and Tau is found in axons and dendrites of nerve cells. Alternative splicing of the Tau mRNA leads to the  
15 existence of multiple forms of Tau protein. Tau phosphorylation is altered in neurodegenerative disorders such as Alzheimer's disease, Pick's disease, progressive supranuclear palsy, corticobasal degeneration, and familial frontotemporal dementia and Parkinsonism linked to chromosome 17. The altered Tau phosphorylation leads to a collapse of the microtubule network and the formation of intraneuronal Tau aggregates (Spillantini, M.G. and M. Goedert (1998) Trends Neurosci. 21:428-  
20 433).

The protein pericentrin is found in the MTOC and has a role in microtubule assembly.

#### Actins

Microfilaments, cytoskeletal filaments with a diameter of about 7-9 nm, are vital to cell locomotion, cell shape, cell adhesion, cell division, and muscle contraction. Assembly and  
25 disassembly of the microfilaments allow cells to change their morphology. Microfilaments are the polymerized form of actin, the most abundant intracellular protein in the eukaryotic cell. Human cells contain six isoforms of actin. The three  $\alpha$ -actins are found in different kinds of muscle, nonmuscle  $\beta$ -actin and nonmuscle  $\gamma$ -actin are found in nonmuscle cells, and another  $\gamma$ -actin is found in intestinal smooth muscle cells. G-actin, the monomeric form of actin, polymerizes into polarized,  
30 helical F-actin filaments, accompanied by the hydrolysis of ATP to ADP. Actin filaments associate to form bundles and networks, providing a framework to support the plasma membrane and determine cell shape. These bundles and networks are connected to the cell membrane. In muscle cells, thin filaments containing actin slide past thick filaments containing the motor protein myosin during contraction. A family of actin-related proteins exist that are not part of the actin cytoskeleton,  
35 but rather associate with microtubules and dynein.

#### Actin-Associated Proteins

Actin-associated proteins have roles in cross-linking, severing, and stabilization of actin filaments and in sequestering actin monomers. Several of the actin-associated proteins have multiple functions. Bundles and networks of actin filaments are held together by actin cross-linking proteins. These proteins have two actin-binding sites, one for each filament. Short cross-linking proteins promote bundle formation while longer, more flexible cross-linking proteins promote network formation. Calmodulin-like calcium-binding domains in actin cross-linking proteins allow calcium regulation of cross-linking. Group I cross-linking proteins have unique actin-binding domains and include the 30 kD protein, EF-1a, fascin, and scruin. Group II cross-linking proteins have a 7,000-MW actin-binding domain and include villin and dematin. Group III cross-linking proteins have pairs of a 26,000-MW actin-binding domain and include fimbrin, spectrin, dystrophin, ABP 120, and filamin.

Severing proteins regulate the length of actin filaments by breaking them into short pieces or by blocking their ends. Severing proteins include gCAP39, severin (fragmin), gelsolin, and villin. Capping proteins can cap the ends of actin filaments, but cannot break filaments. Capping proteins include CapZ and tropomodulin. The proteins thymosin and profilin sequester actin monomers in the cytosol, allowing a pool of unpolymerized actin to exist. The actin-associated proteins tropomyosin, troponin, and caldesmon regulate muscle contraction in response to calcium.

#### Intermediate Filaments and Associated Proteins

Intermediate filaments (IFs) are cytoskeletal fibers with a diameter of about 10 nm, intermediate between that of microfilaments and microtubules. IFs serve structural roles in the cell, reinforcing cells and organizing cells into tissues. IFs are particularly abundant in epidermal cells and in neurons. IFs are extremely stable, and, in contrast to microfilaments and microtubules, do not function in cell motility.

Five types of IF proteins are known in mammals. Type I and Type II proteins are the acidic and basic keratins, respectively. Heterodimers of the acidic and basic keratins are the building blocks of keratin IFs. Keratins are abundant in soft epithelia such as skin and cornea, hard epithelia such as nails and hair, and in epithelia that line internal body cavities. Mutations in keratin genes lead to epithelial diseases including epidermolysis bullosa simplex, bullous congenital ichthyosiform erythroderma (epidermolytic hyperkeratosis), non-epidermolytic and epidermolytic palmoplantar keratoderma, ichthyosis bullosa of Siemens, pachyonychia congenita, and white sponge nevus. Some of these diseases result in severe skin blistering. (See, e.g., Wawersik, M. et al. (1997) J. Biol. Chem. 272:32557-32565; and Corden L.D. and W.H. McLean (1996) Exp. Dermatol. 5:297-307.)

Type III IF proteins include desmin, glial fibrillary acidic protein, vimentin, and peripherin. Desmin filaments in muscle cells link myofibrils into bundles and stabilize sarcomeres in contracting muscle. Glial fibrillary acidic protein filaments are found in the glial cells that surround neurons and astrocytes. Vimentin filaments are found in blood vessel endothelial cells, some epithelial cells, and

mesenchymal cells such as fibroblasts, and are commonly associated with microtubules. Vimentin filaments may have roles in keeping the nucleus and other organelles in place in the cell. Type IV IFs include the neurofilaments and nestin. Neurofilaments, composed of three polypeptides NF-L, NF-M, and NF-H, are frequently associated with microtubules in axons. Neurofilaments are responsible for  
5 the radial growth and diameter of an axon, and ultimately for the speed of nerve impulse transmission. Changes in phosphorylation and metabolism of neurofilaments are observed in neurodegenerative diseases including amyotrophic lateral sclerosis, Parkinson's disease, and Alzheimer's disease (Julien, J.P. and W.E. Mushynski (1998) Prog. Nucleic Acid Res. Mol. Biol. 61:1-23). Type V IFs, the lamins, are found in the nucleus where they support the nuclear membrane.

10 IFs have a central  $\alpha$ -helical rod region interrupted by short nonhelical linker segments. The rod region is bracketed, in most cases, by non-helical head and tail domains. The rod regions of intermediate filament proteins associate to form a coiled-coil dimer. A highly ordered assembly process leads from the dimers to the IFs. Neither ATP nor GTP is needed for IF assembly, unlike that of microfilaments and microtubules.

15 IF-associated proteins (IFAPs) mediate the interactions of IFs with one another and with other cell structures. IFAPs cross-link IFs into a bundle, into a network, or to the plasma membrane, and may cross-link IFs to the microfilament and microtubule cytoskeleton. Microtubules and IFs are in particular closely associated. IFAPs include BPAG1, plakoglobin, desmoplakin I, desmoplakin II, plectin, ankyrin, filaggrin, and lamin B receptor.

#### 20 Cytoskeletal-Membrane Anchors

Cytoskeletal fibers are attached to the plasma membrane by specific proteins. These attachments are important for maintaining cell shape and for muscle contraction. In erythrocytes, the spectrin-actin cytoskeleton is attached to cell membrane by three proteins, band 4.1, ankyrin, and adducin. Defects in this attachment result in abnormally shaped cells which are more rapidly  
25 degraded by the spleen, leading to anemia. In platelets, the spectrin-actin cytoskeleton is also linked to the membrane by ankyrin; a second actin network is anchored to the membrane by filamin. In muscle cells the protein dystrophin links actin filaments to the plasma membrane; mutations in the dystrophin gene lead to Duchenne muscular dystrophy. In adherens junctions and adhesion plaques the peripheral membrane proteins  $\alpha$ -actinin and vinculin attach actin filaments to the cell membrane.

30 IFs are also attached to membranes by cytoskeletal-membrane anchors. The nuclear lamina is attached to the inner surface of the nuclear membrane by the lamin B receptor. Vimentin IFs are attached to the plasma membrane by ankyrin and plectin. Desmosome and hemidesmosome membrane junctions hold together epithelial cells of organs and skin. These membrane junctions allow shear forces to be distributed across the entire epithelial cell layer, thus providing strength and  
35 rigidity to the epithelium. IFs in epithelial cells are attached to the desmosome by plakoglobin and desmoplakins. The proteins that link IFs to hemidesmosomes are not known. Desmin IFs surround

the sarcomere in muscle and are linked to the plasma membrane by paranemin, synemin, and ankyrin.

#### Myosin-related Motor Proteins

Myosins are actin-activated ATPases, found in eukaryotic cells, that couple hydrolysis of ATP with motion. Myosin provides the motor function for muscle contraction and intracellular movements such as phagocytosis and rearrangement of cell contents during mitotic cell division (cytokinesis). The contractile unit of skeletal muscle, termed the sarcomere, consists of highly ordered arrays of thin actin-containing filaments and thick myosin-containing filaments. Crossbridges form between the thick and thin filaments, and the ATP-dependent movement of myosin heads within the thick filaments pulls the thin filaments, shortening the sarcomere and thus the muscle fiber.

Myosins are composed of one or two heavy chains and associated light chains. Myosin heavy chains contain an amino-terminal motor or head domain, a neck that is the site of light-chain binding, and a carboxy-terminal tail domain. The tail domains may associate to form an  $\alpha$ -helical coiled coil. Conventional myosins, such as those found in muscle tissue, are composed of two myosin heavy-chain subunits, each associated with two light-chain subunits that bind at the neck region and play a regulatory role. Unconventional myosins, believed to function in intracellular motion, may contain either one or two heavy chains and associated light chains. There is evidence for about 25 myosin heavy chain genes in vertebrates, more than half of them unconventional.

#### Dynein-related Motor Proteins

Dyneins are (-) end-directed motor proteins which act on microtubules. Two classes of dyneins, cytosolic and axonemal, have been identified. Cytosolic dyneins are responsible for translocation of materials along cytoplasmic microtubules, for example, transport from the nerve terminal to the cell body and transport of endocytic vesicles to lysosomes. Cytoplasmic dyneins are also reported to play a role in mitosis. Axonemal dyneins are responsible for the beating of flagella and cilia. Dynein on one microtubule doublet walks along the adjacent microtubule doublet. This sliding force produces bending forces that cause the flagellum or cilium to beat. Dyneins have a native mass between 1000 and 2000 kDa and contain either two or three force-producing heads driven by the hydrolysis of ATP. The heads are linked via stalks to a basal domain which is composed of a highly variable number of accessory intermediate and light chains.

#### Kinesin-related Motor Proteins

Kinesins are (+) end-directed motor proteins which act on microtubules. The prototypical kinesin molecule is involved in the transport of membrane-bound vesicles and organelles. This function is particularly important for axonal transport in neurons. Kinesin is also important in all cell types for the transport of vesicles from the Golgi complex to the endoplasmic reticulum. This role is critical for maintaining the identity and functionality of these secretory organelles.

Kinesins define a ubiquitous, conserved family of over 50 proteins that can be classified into

at least 8 subfamilies based on primary amino acid sequence, domain structure, velocity of movement, and cellular function. (Reviewed in Moore, J.D. and S.A. Endow (1996) *Bioessays* 18:207-219; and Hoyt, A.M. (1994) *Curr. Opin. Cell Biol.* 6:63-68.) The prototypical kinesin molecule is a heterotetramer comprised of two heavy polypeptide chains (KHCs) and two light polypeptide chains (KLCs). The KHC subunits are typically referred to as "kinesin." KHC is about 1000 amino acids in length, and KLC is about 550 amino acids in length. Two KHCs dimerize to form a rod-shaped molecule with three distinct regions of secondary structure. At one end of the molecule is a globular motor domain that functions in ATP hydrolysis and microtubule binding. Kinesin motor domains are highly conserved and share over 70% identity. Beyond the motor domain is an  $\alpha$ -helical coiled-coil region which mediates dimerization. At the other end of the molecule is a fan-shaped tail that associates with molecular cargo. The tail is formed by the interaction of the KHC C-termini with the two KLCs.

Members of the more divergent subfamilies of kinesins are called kinesin-related proteins (KRPs), many of which function during mitosis in eukaryotes (Hoyt, *supra*). Some KRPs are required for assembly of the mitotic spindle. *In vivo* and *in vitro* analyses suggest that these KRPs exert force on microtubules that comprise the mitotic spindle, resulting in the separation of spindle poles. Phosphorylation of KRP is required for this activity. Failure to assemble the mitotic spindle results in abortive mitosis and chromosomal aneuploidy, the latter condition being characteristic of cancer cells. In addition, a unique KRP, centromere protein E, localizes to the kinetochore of human mitotic chromosomes and may play a role in their segregation to opposite spindle poles.

#### Dynamin-related Motor Proteins

Dynamin is a large GTPase motor protein that functions as a "molecular pinchase," generating a mechanochemical force used to sever membranes. This activity is important in forming clathrin-coated vesicles from coated pits in endocytosis and in the biogenesis of synaptic vesicles in neurons. Binding of dynamin to a membrane leads to dynamin's self-assembly into spirals that may act to constrict a flat membrane surface into a tubule. GTP hydrolysis induces a change in conformation of the dynamin polymer that pinches the membrane tubule, leading to severing of the membrane tubule and formation of a membrane vesicle. Release of GDP and inorganic phosphate leads to dynamin disassembly. Following disassembly the dynamin may either dissociate from the membrane or remain associated to the vesicle and be transported to another region of the cell. Three homologous dynamin genes have been discovered, in addition to several dynamin-related proteins. Conserved dynamin regions are the N-terminal GTP-binding domain, a central pleckstrin homology domain that binds membranes, a central coiled-coil region that may activate dynamin's GTPase activity, and a C-terminal proline-rich domain that contains several motifs that bind SH3 domains on other proteins. Some dynamin-related proteins do not contain the pleckstrin homology domain or the proline-rich domain. (See McNiven, M.A. (1998) *Cell* 94:151-154; Scaife, R.M. and R.L. Margolis

(1997) Cell. Signal. 9:395-401.)

The cytoskeleton is reviewed in Lodish, H. et al. (1995) Molecular Cell Biology, Scientific American Books, New York NY.

## 5 Ribosomal Molecules

Ribosomal RNAs (rRNAs) are assembled, along with ribosomal proteins, into ribosomes, which are cytoplasmic particles that translate messenger RNA into polypeptides. The eukaryotic ribosome is composed of a 60S (large) subunit and a 40S (small) subunit, which together form the 80S ribosome. In addition to the 18S, 28S, 5S, and 5.8S rRNAs, the ribosome also contains more  
10 than fifty proteins. The ribosomal proteins have a prefix which denotes the subunit to which they belong, either L (large) or S (small). Ribosomal protein activities include binding rRNA and organizing the conformation of the junctions between rRNA helices (Woodson, S.A. and N.B. Leontis (1998) Curr. Opin. Struct. Biol. 8:294-300; Ramakrishnan, V. and S.W. White (1998) Trends Biochem. Sci. 23:208-212.) Three important sites are identified on the ribosome. The aminoacyl-  
15 tRNA site (A site) is where charged tRNAs (with the exception of the initiator-tRNA) bind on arrival at the ribosome. The peptidyl-tRNA site (P site) is where new peptide bonds are formed, as well as where the initiator tRNA binds. The exit site (E site) is where deacylated tRNAs bind prior to their release from the ribosome. (The ribosome is reviewed in Stryer, L. (1995) Biochemistry W.H. Freeman and Company, New York NY, pp. 888-908; and Lodish, H. et al. (1995) Molecular Cell  
20 Biology Scientific American Books, New York NY. pp. 119-138.)

## Chromatin Molecules

The nuclear DNA of eukaryotes is organized into chromatin. Two types of chromatin are observed: euchromatin, some of which may be transcribed, and heterochromatin so densely packed  
25 that much of it is inaccessible to transcription. Chromatin packing thus serves to regulate protein expression in eukaryotes. Bacteria lack chromatin and the chromatin-packing level of gene regulation.

The fundamental unit of chromatin is the nucleosome of 200 DNA base pairs associated with two copies each of histones H2A, H2B, H3, and H4. Adjacent nucleosomes are linked by another  
30 class of histones, H1. Low molecular weight non-histone proteins called the high mobility group (HMG), associated with chromatin, may function in the unwinding of DNA and stabilization of single-stranded DNA. Chromodomain proteins function in compaction of chromatin into its transcriptionally silent heterochromatin form.

During mitosis, all DNA is compacted into heterochromatin and transcription ceases.  
35 Transcription in interphase begins with the activation of a region of chromatin. Active chromatin is decondensed. Decondensation appears to be accompanied by changes in binding coefficient,

phosphorylation and acetylation states of chromatin histones. HMG proteins HMG13 and HMG17 selectively bind activated chromatin. Topoisomerases remove superhelical tension on DNA. The activated region decondenses, allowing gene regulatory proteins and transcription factors to assemble on the DNA.

5        Patterns of chromatin structure can be stably inherited, producing heritable patterns of gene expression. In mammals, one of the two X chromosomes in each female cell is inactivated by condensation to heterochromatin during zygote development. The inactive state of this chromosome is inherited, so that adult females are mosaics of clusters of paternal-X and maternal-X clonal cell groups. The condensed X chromosome is reactivated in meiosis.

10       Chromatin is associated with disorders of protein expression such as thalassemia, a genetic anemia resulting from the removal of the locus control region (LCR) required for decondensation of the globin gene locus.

For a review of chromatin structure and function see Alberts, B. et al. (1994) Molecular Cell Biology, third edition, Garland Publishing, Inc., New York NY, pp. 351-354, 433-439.

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#### **Electron Transfer Associated Molecules**

Electron carriers such as cytochromes accept electrons from NADH or FADH<sub>2</sub> and donate them to other electron carriers. Most electron-transferring proteins, except ubiquinone, are prosthetic groups such as flavins, heme, FeS clusters, and copper, bound to inner membrane proteins.

20       Adrenodoxin, for example, is an FeS protein that forms a complex with NADPH:adrenodoxin reductase and cytochrome p450. Cytochromes contain a heme prosthetic group, a porphyrin ring containing a tightly bound iron atom. Electron transfer reactions play a crucial role in cellular energy production.

Energy is produced by the oxidation of glucose and fatty acids. Glucose is initially converted  
25       to pyruvate in the cytoplasm. Fatty acids and pyruvate are transported to the mitochondria for complete oxidation to CO<sub>2</sub> coupled by enzymes to the transport of electrons from NADH and FADH<sub>2</sub> to oxygen and to the synthesis of ATP (oxidative phosphorylation) from ADP and P<sub>i</sub>.

Pyruvate is transported into the mitochondria and converted to acetyl-CoA for oxidation via the citric acid cycle, involving pyruvate dehydrogenase components, dihydrolipoyl transacetylase,  
30       and dihydrolipoyl dehydrogenase. Enzymes involved in the citric acid cycle include: citrate synthetase, aconitases, isocitrate dehydrogenase, alpha-ketoglutarate dehydrogenase complex including transsuccinylases, succinyl CoA synthetase, succinate dehydrogenase, fumarases, and malate dehydrogenase. Acetyl CoA is oxidized to CO<sub>2</sub> with concomitant formation of NADH, FADH<sub>2</sub>, and GTP. In oxidative phosphorylation, the transfer of electrons from NADH and FADH<sub>2</sub> to  
35       oxygen by dehydrogenases is coupled to the synthesis of ATP from ADP and P<sub>i</sub> by the F<sub>0</sub>F<sub>1</sub> ATPase complex in the mitochondrial inner membrane. Enzyme complexes responsible for electron transport



and ATP synthesis include the  $F_0F_1$  ATPase complex, ubiquinone(CoQ)-cytochrome c reductase, ubiquinone reductase, cytochrome b, cytochrome c<sub>1</sub>, FeS protein, and cytochrome c oxidase.

ATP synthesis requires membrane transport enzymes including the phosphate transporter and the ATP-ADP antiport protein. The ATP-binding cassette (ABC) superfamily has also been suggested  
5 as belonging to the mitochondrial transport group (Hogue, D.L. et al. (1999) J. Mol. Biol. 285:379-389). Brown fat uncoupling protein dissipates oxidative energy as heat, and may be involved the fever response to infection and trauma (Cannon, B. et al. (1998) Ann. NY Acad. Sci. 856:171-187).

Mitochondria are oval-shaped organelles comprising an outer membrane, a tightly folded inner membrane, an intermembrane space between the outer and inner membranes, and a matrix  
10 inside the inner membrane. The outer membrane contains many porin molecules that allow ions and charged molecules to enter the intermembrane space, while the inner membrane contains a variety of transport proteins that transfer only selected molecules. Mitochondria are the primary sites of energy production in cells.

Mitochondria contain a small amount of DNA. Human mitochondrial DNA encodes 13  
15 proteins, 22 tRNAs, and 2 rRNAs. Mitochondrial-DNA encoded proteins include NADH-Q reductase, a cytochrome reductase subunit, cytochrome oxidase subunits, and ATP synthase subunits.

Electron-transfer reactions also occur outside the mitochondria in locations such as the endoplasmic reticulum, which plays a crucial role in lipid and protein biosynthesis. Cytochrome b5 is a central electron donor for various reductive reactions occurring on the cytoplasmic surface of  
20 liver endoplasmic reticulum. Cytochrome b5 has been found in Golgi, plasma, endoplasmic reticulum (ER), and microbody membranes.

For a review of mitochondrial metabolism and regulation, see Lodish, H. et al. (1995) Molecular Cell Biology, Scientific American Books, New York NY, pp. 745-797 and Stryer (1995) Biochemistry, W.H. Freeman and Co., San Francisco CA, pp 529-558, 988-989.

25 The majority of mitochondrial proteins are encoded by nuclear genes, are synthesized on cytosolic ribosomes, and are imported into the mitochondria. Nuclear-encoded proteins which are destined for the mitochondrial matrix typically contain positively-charged amino terminal signal sequences. Import of these preproteins from the cytoplasm requires a multisubunit protein complex in the outer membrane known as the translocase of outer mitochondrial membrane (TOM; previously  
30 designated MOM; Pfanner, N. et al. (1996) Trends Biochem. Sci. 21:51-52) and at least three inner membrane proteins which comprise the translocase of inner mitochondrial membrane (TIM; previously designated MIM; Pfanner, supra). An inside-negative membrane potential across the inner mitochondrial membrane is also required for preprotein import. Preproteins are recognized by surface receptor components of the TOM complex and are translocated through a proteinaceous pore  
35 formed by other TOM components. Proteins targeted to the matrix are then recognized by the import machinery of the TIM complex. The import systems of the outer and inner membranes can function

independently (Segui-Real, B. et al. (1993) EMBO J. 12:2211-2218).

Once precursor proteins are in the mitochondria, the leader peptide is cleaved by a signal peptidase to generate the mature protein. Most leader peptides are removed in a one step process by a protease termed mitochondrial processing peptidase (MPP) (Paces, V. et al. (1993) Proc. Natl. Acad. Sci. USA 90:5355-5358). In some cases a two-step process occurs in which MPP generates an intermediate precursor form which is cleaved by a second enzyme, mitochondrial intermediate peptidase, to generate the mature protein.

Mitochondrial dysfunction leads to impaired calcium buffering, generation of free radicals that may participate in deleterious intracellular and extracellular processes, changes in mitochondrial permeability and oxidative damage which is observed in several neurodegenerative diseases. Neurodegenerative diseases linked to mitochondrial dysfunction include some forms of Alzheimer's disease, Friedreich's ataxia, familial amyotrophic lateral sclerosis, and Huntington's disease (Beal, M.F. (1998) Biochim. Biophys. Acta 1366:211-213). The myocardium is heavily dependent on oxidative metabolism, so mitochondrial dysfunction often leads to heart disease (DiMauro, S. and M. Hirano (1998) Curr. Opin. Cardiol 13:190-197). Mitochondria are implicated in disorders of cell proliferation, since they play an important role in a cell's decision to proliferate or self-destruct through apoptosis. The oncoprotein Bcl-2, for example, promotes cell proliferation by stabilizing mitochondrial membranes so that apoptosis signals are not released (Susin, S.A. (1998) Biochim. Biophys. Acta 1366:151-165).

#### Transcription Factor Molecules

Multicellular organisms are comprised of diverse cell types that differ dramatically both in structure and function. The identity of a cell is determined by its characteristic pattern of gene expression, and different cell types express overlapping but distinctive sets of genes throughout development. Spatial and temporal regulation of gene expression is critical for the control of cell proliferation, cell differentiation, apoptosis, and other processes that contribute to organismal development. Furthermore, gene expression is regulated in response to extracellular signals that mediate cell-cell communication and coordinate the activities of different cell types. Appropriate gene regulation also ensures that cells function efficiently by expressing only those genes whose functions are required at a given time.

Transcriptional regulatory proteins are essential for the control of gene expression. Some of these proteins function as transcription factors that initiate, activate, repress, or terminate gene transcription. Transcription factors generally bind to the promoter, enhancer, and upstream regulatory regions of a gene in a sequence-specific manner, although some factors bind regulatory elements within or downstream of a gene's coding region. Transcription factors may bind to a specific region of DNA singly or as a complex with other accessory factors. (Reviewed in Lewin, B.

(1990) Genes IV, Oxford University Press, New York NY, and Cell Press, Cambridge MA, pp. 554-570.)

The double helix structure and repeated sequences of DNA create topological and chemical features which can be recognized by transcription factors. These features are hydrogen bond donor  
5 and acceptor groups, hydrophobic patches, major and minor grooves, and regular, repeated stretches of sequence which induce distinct bends in the helix. Typically, transcription factors recognize specific DNA sequence motifs of about 20 nucleotides in length. Multiple, adjacent transcription factor-binding motifs may be required for gene regulation.

Many transcription factors incorporate DNA-binding structural motifs which comprise either  
10  $\alpha$  helices or  $\beta$  sheets that bind to the major groove of DNA. Four well-characterized structural motifs are helix-turn-helix, zinc finger, leucine zipper, and helix-loop-helix. Proteins containing these motifs may act alone as monomers, or they may form homo- or heterodimers that interact with DNA.

The helix-turn-helix motif consists of two  $\alpha$  helices connected at a fixed angle by a short chain of amino acids. One of the helices binds to the major groove. Helix-turn-helix motifs are  
15 exemplified by the homeobox motif which is present in homeodomain proteins. These proteins are critical for specifying the anterior-posterior body axis during development and are conserved throughout the animal kingdom. The Antennapedia and Ultrabithorax proteins of Drosophila melanogaster are prototypical homeodomain proteins (Pabo, C.O. and R.T. Sauer (1992) Annu. Rev. Biochem. 61:1053-1095).

20 The zinc finger motif, which binds zinc ions, generally contains tandem repeats of about 30 amino acids consisting of periodically spaced cysteine and histidine residues. Examples of this sequence pattern, designated C2H2 and C3HC4 ("RING" finger), have been described (Lewin, supra). Zinc finger proteins each contain an  $\alpha$  helix and an antiparallel  $\beta$  sheet whose proximity and conformation are maintained by the zinc ion. Contact with DNA is made by the arginine preceding  
25 the  $\alpha$  helix and by the second, third, and sixth residues of the  $\alpha$  helix. Variants of the zinc finger motif include poorly defined cysteine-rich motifs which bind zinc or other metal ions. These motifs may not contain histidine residues and are generally nonrepetitive.

The leucine zipper motif comprises a stretch of amino acids rich in leucine which can form an amphipathic  $\alpha$  helix. This structure provides the basis for dimerization of two leucine zipper  
30 proteins. The region adjacent to the leucine zipper is usually basic, and upon protein dimerization, is optimally positioned for binding to the major groove. Proteins containing such motifs are generally referred to as bZIP transcription factors.

The helix-loop-helix motif (HLH) consists of a short  $\alpha$  helix connected by a loop to a longer  $\alpha$  helix. The loop is flexible and allows the two helices to fold back against each other and to bind to  
35 DNA. The transcription factor Myc contains a prototypical HLH motif.

Most transcription factors contain characteristic DNA binding motifs, and variations on the above motifs and new motifs have been and are currently being characterized (Faisst, S. and S. Meyer (1992) *Nucleic Acids Res.* 20:3-26).

Many neoplastic disorders in humans can be attributed to inappropriate gene expression.

- 5 Malignant cell growth may result from either excessive expression of tumor promoting genes or insufficient expression of tumor suppressor genes (Cleary, M.L. (1992) *Cancer Surv.* 15:89-104). Chromosomal translocations may also produce chimeric loci which fuse the coding sequence of one gene with the regulatory regions of a second unrelated gene. Such an arrangement likely results in inappropriate gene transcription, potentially contributing to malignancy.

- 10 In addition, the immune system responds to infection or trauma by activating a cascade of events that coordinate the progressive selection, amplification, and mobilization of cellular defense mechanisms. A complex and balanced program of gene activation and repression is involved in this process. However, hyperactivity of the immune system as a result of improper or insufficient regulation of gene expression may result in considerable tissue or organ damage. This damage is  
15 well documented in immunological responses associated with arthritis, allergens, heart attack, stroke, and infections (Isselbacher, K.J. et al. (1996) Harrison's Principles of Internal Medicine, 13/e, McGraw Hill, Inc. and Teton Data Systems Software).

- Furthermore, the generation of multicellular organisms is based upon the induction and coordination of cell differentiation at the appropriate stages of development. Central to this process  
20 is differential gene expression, which confers the distinct identities of cells and tissues throughout the body. Failure to regulate gene expression during development can result in developmental disorders. Human developmental disorders caused by mutations in zinc finger-type transcriptional regulators include: urogenital developmental abnormalities associated with WT1; Greig cephalopolysyndactyly, Pallister-Hall syndrome, and postaxial polydactyly type A (GLI3); and  
25 Townes-Brooks syndrome, characterized by anal, renal, limb, and ear abnormalities (SALL1) (Engelkamp, D. and V. van Heyningen (1996) *Curr. Opin. Genet. Dev.* 6:334-342; Kohlhase, J. et al. (1999) *Am. J. Hum. Genet.* 64:435-445).

### Cell Membrane Molecules

- 30 Eukaryotic cells are surrounded by plasma membranes which enclose the cell and maintain an environment inside the cell that is distinct from its surroundings. In addition, eukaryotic organisms are distinct from prokaryotes in possessing many intracellular organelle and vesicle structures. Many of the metabolic reactions which distinguish eukaryotic biochemistry from prokaryotic biochemistry take place within these structures. The plasma membrane and the  
35 membranes surrounding organelles and vesicles are composed of phosphoglycerides, fatty acids, cholesterol, phospholipids, glycolipids, proteoglycans, and proteins. These components confer

identity and functionality to the membranes with which they associate.

#### Integral Membrane Proteins

The majority of known integral membrane proteins are transmembrane proteins (TM) which are characterized by an extracellular, a transmembrane, and an intracellular domain. TM domains are typically comprised of 15 to 25 hydrophobic amino acids which are predicted to adopt an  $\alpha$ -helical conformation. TM proteins are classified as bitopic (Types I and II) and polytopic (Types III and IV) (Singer, S.J. (1990) *Annu. Rev. Cell Biol.* 6:247-296). Bitopic proteins span the membrane once while polytopic proteins contain multiple membrane-spanning segments. TM proteins function as cell-surface receptors, receptor-interacting proteins, transporters of ions or metabolites, ion channels, cell anchoring proteins, and cell type-specific surface antigens.

Many membrane proteins (MPs) contain amino acid sequence motifs that target these proteins to specific subcellular sites. Examples of these motifs include PDZ domains, KDEL, RGD, NGR, and GSL sequence motifs, von Willebrand factor A (vWFA) domains, and EGF-like domains. RGD, NGR, and GSL motif-containing peptides have been used as drug delivery agents in targeted cancer treatment of tumor vasculature (Arap, W. et al. (1998) *Science* 279:377-380). Furthermore, MPs may also contain amino acid sequence motifs, such as the carbohydrate recognition domain (CRD), that mediate interactions with extracellular or intracellular molecules.

#### G-Protein Coupled Receptors

G-protein coupled receptors (GPCR) are a superfamily of integral membrane proteins which transduce extracellular signals. GPCRs include receptors for biogenic amines, lipid mediators of inflammation, peptide hormones, and sensory signal mediators. The structure of these highly-conserved receptors consists of seven hydrophobic transmembrane regions, an extracellular N-terminus, and a cytoplasmic C-terminus. Three extracellular loops alternate with three intracellular loops to link the seven transmembrane regions. Cysteine disulfide bridges connect the second and third extracellular loops. The most conserved regions of GPCRs are the transmembrane regions and the first two cytoplasmic loops. A conserved, acidic-Arg-aromatic residue triplet present in the second cytoplasmic loop may interact with G proteins. A GPCR consensus pattern is characteristic of most proteins belonging to this superfamily (ExPASy PROSITE document PS00237; and Watson, S. and S. Arkinstall (1994) *The G-protein Linked Receptor Facts Book*, Academic Press, San Diego CA, pp. 2-6). Mutations and changes in transcriptional activation of GPCR-encoding genes have been associated with neurological disorders such as schizophrenia, Parkinson's disease, Alzheimer's disease, drug addiction, and feeding disorders.

#### Scavenger Receptors

Macrophage scavenger receptors with broad ligand specificity may participate in the binding of low density lipoproteins (LDL) and foreign antigens. Scavenger receptors types I and II are trimeric membrane proteins with each subunit containing a small N-terminal intracellular domain, a

transmembrane domain, a large extracellular domain, and a C-terminal cysteine-rich domain. The extracellular domain contains a short spacer region, an  $\alpha$ -helical coiled-coil region, and a triple helical collagen-like region. These receptors have been shown to bind a spectrum of ligands, including chemically modified lipoproteins and albumin, polyribonucleotides, polysaccharides, phospholipids, and asbestos (Matsumoto, A. et al. (1990) Proc. Natl. Acad. Sci. USA 87:9133-9137; and Elomaa, O. et al. (1995) Cell 80:603-609). The scavenger receptors are thought to play a key role in atherogenesis by mediating uptake of modified LDL in arterial walls, and in host defense by binding bacterial endotoxins, bacteria, and protozoa.

#### Tetraspan Family Proteins

The transmembrane 4 superfamily (TM4SF) or tetraspan family is a multigene family encoding type III integral membrane proteins (Wright, M.D. and M.G. Tomlinson (1994) Immunol. Today 15:588-594). The TM4SF is comprised of membrane proteins which traverse the cell membrane four times. Members of the TM4SF include platelet and endothelial cell membrane proteins, melanoma-associated antigens, leukocyte surface glycoproteins, colonic carcinoma antigens, tumor-associated antigens, and surface proteins of the schistosome parasites (Jankowski, S.A. (1994) Oncogene 9:1205-1211). Members of the TM4SF share about 25-30% amino acid sequence identity with one another.

A number of TM4SF members have been implicated in signal transduction, control of cell adhesion, regulation of cell growth and proliferation, including development and oncogenesis, and cell motility, including tumor cell metastasis. Expression of TM4SF proteins is associated with a variety of tumors and the level of expression may be altered when cells are growing or activated.

#### Tumor Antigens

Tumor antigens are cell surface molecules that are differentially expressed in tumor cells relative to normal cells. Tumor antigens distinguish tumor cells immunologically from normal cells and provide diagnostic and therapeutic targets for human cancers (Takagi, S. et al. (1995) Int. J. Cancer 61:706-715; Liu, E. et al. (1992) Oncogene 7:1027-1032).

#### Leukocyte Antigens

Other types of cell surface antigens include those identified on leukocytic cells of the immune system. These antigens have been identified using systematic, monoclonal antibody (mAb)-based "shot gun" techniques. These techniques have resulted in the production of hundreds of mAbs directed against unknown cell surface leukocytic antigens. These antigens have been grouped into "clusters of differentiation" based on common immunocytochemical localization patterns in various differentiated and undifferentiated leukocytic cell types. Antigens in a given cluster are presumed to identify a single cell surface protein and are assigned a "cluster of differentiation" or "CD" designation. Some of the genes encoding proteins identified by CD antigens have been cloned and verified by standard molecular biology techniques. CD antigens have been characterized as both

transmembrane proteins and cell surface proteins anchored to the plasma membrane via covalent attachment to fatty acid-containing glycolipids such as glycosylphosphatidylinositol (GPI).

(Reviewed in Barclay, A.N. et al. (1995) The Leucocyte Antigen Facts Book, Academic Press, San Diego CA, pp. 17-20.)

5 Ion Channels

Ion channels are found in the plasma membranes of virtually every cell in the body. For example, chloride channels mediate a variety of cellular functions including regulation of membrane potentials and absorption and secretion of ions across epithelial membranes. Chloride channels also regulate the pH of organelles such as the Golgi apparatus and endosomes (see, e.g., Greger, R. (1988) 10 *Annu. Rev. Physiol.* 50:111-122). Electrophysiological and pharmacological properties of chloride channels, including ion conductance, current-voltage relationships, and sensitivity to modulators, suggest that different chloride channels exist in muscles, neurons, fibroblasts, epithelial cells, and lymphocytes.

Many ion channels have sites for phosphorylation by one or more protein kinases including 15 protein kinase A, protein kinase C, tyrosine kinase, and casein kinase II, all of which regulate ion channel activity in cells. Inappropriate phosphorylation of proteins in cells has been linked to changes in cell cycle progression and cell differentiation. Changes in the cell cycle have been linked to induction of apoptosis or cancer. Changes in cell differentiation have been linked to diseases and disorders of the reproductive system, immune system, skeletal muscle, and other organ systems.

20 Proton Pumps

Proton ATPases comprise a large class of membrane proteins that use the energy of ATP hydrolysis to generate an electrochemical proton gradient across a membrane. The resultant gradient may be used to transport other ions across the membrane ( $\text{Na}^+$ ,  $\text{K}^+$ , or  $\text{Cl}^-$ ) or to maintain organelle pH. Proton ATPases are further subdivided into the mitochondrial F-ATPases, the plasma membrane 25 ATPases, and the vacuolar ATPases. The vacuolar ATPases establish and maintain an acidic pH within various organelles involved in the processes of endocytosis and exocytosis (Mellman, I. et al. (1986) *Annu. Rev. Biochem.* 55:663-700).

Proton-coupled, 12 membrane-spanning domain transporters such as PEPT 1 and PEPT 2 are responsible for gastrointestinal absorption and for renal reabsorption of peptides using an 30 electrochemical  $\text{H}^+$  gradient as the driving force. Another type of peptide transporter, the TAP transporter, is a heterodimer consisting of TAP 1 and TAP 2 and is associated with antigen processing. Peptide antigens are transported across the membrane of the endoplasmic reticulum by TAP so they can be expressed on the cell surface in association with MHC molecules. Each TAP protein consists of multiple hydrophobic membrane spanning segments and a highly conserved 35 ATP-binding cassette (Boll, M. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:284-289). Pathogenic microorganisms, such as herpes simplex virus, may encode inhibitors of TAP-mediated peptide

transport in order to evade immune surveillance (Marusina, K. and J.J Manaco (1996) Curr. Opin. Hematol. 3:19-26).

#### ABC Transporters

The ATP-binding cassette (ABC) transporters, also called the "traffic ATPases", comprise a  
5 superfamily of membrane proteins that mediate transport and channel functions in prokaryotes and  
eukaryotes (Higgins, C.F. (1992) Annu. Rev. Cell Biol. 8:67-113). ABC proteins share a similar  
overall structure and significant sequence homology. All ABC proteins contain a conserved domain  
of approximately two hundred amino acid residues which includes one or more nucleotide binding  
domains. Mutations in ABC transporter genes are associated with various disorders, such as  
10 hyperbilirubinemia II/Dubin-Johnson syndrome, recessive Stargardt's disease, X-linked  
adrenoleukodystrophy, multidrug resistance, celiac disease, and cystic fibrosis.

#### Peripheral and Anchored Membrane Proteins

Some membrane proteins are not membrane-spanning but are attached to the plasma  
membrane via membrane anchors or interactions with integral membrane proteins. Membrane  
15 anchors are covalently joined to a protein post-translationally and include such moieties as prenyl,  
myristyl, and glycosylphosphatidyl inositol groups. Membrane localization of peripheral and  
anchored proteins is important for their function in processes such as receptor-mediated signal  
transduction. For example, prenylation of Ras is required for its localization to the plasma membrane  
and for its normal and oncogenic functions in signal transduction.

#### Vesicle Coat Proteins

Intercellular communication is essential for the development and survival of multicellular  
organisms. Cells communicate with one another through the secretion and uptake of protein  
signaling molecules. The uptake of proteins into the cell is achieved by the endocytic pathway, in  
which the interaction of extracellular signaling molecules with plasma membrane receptors results in  
25 the formation of plasma membrane-derived vesicles that enclose and transport the molecules into the  
cytosol. These transport vesicles fuse with and mature into endosomal and lysosomal (digestive)  
compartments. The secretion of proteins from the cell is achieved by exocytosis, in which molecules  
inside of the cell proceed through the secretory pathway. In this pathway, molecules transit from the  
ER to the Golgi apparatus and finally to the plasma membrane, where they are secreted from the cell.

30 Several steps in the transit of material along the secretory and endocytic pathways require the  
formation of transport vesicles. Specifically, vesicles form at the transitional endoplasmic reticulum  
(tER), the rim of Golgi cisternae, the face of the Trans-Golgi Network (TGN), the plasma membrane  
(PM), and tubular extensions of the endosomes. Vesicle formation occurs when a region of  
membrane buds off from the donor organelle. The membrane-bound vesicle contains proteins to be  
35 transported and is surrounded by a proteinaceous coat, the components of which are recruited from  
the cytosol. Two different classes of coat protein have been identified. Clathrin coats form on



vesicles derived from the TGN and PM, whereas coatomer (COP) coats form on vesicles derived from the ER and Golgi. COP coats can be further classified as COPI, involved in retrograde traffic through the Golgi and from the Golgi to the ER, and COPII, involved in anterograde traffic from the ER to the Golgi (Mellman, *supra*).

5 In clathrin-based vesicle formation, adapter proteins bring vesicle cargo and coat proteins together at the surface of the budding membrane. Adapter protein-1 and -2 select cargo from the TGN and plasma membrane, respectively, based on molecular information encoded on the cytoplasmic tail of integral membrane cargo proteins. Adapter proteins also recruit clathrin to the bud site. Clathrin is a protein complex consisting of three large and three small polypeptide chains  
10 arranged in a three-legged structure called a triskelion. Multiple triskelions and other coat proteins appear to self-assemble on the membrane to form a coated pit. This assembly process may serve to deform the membrane into a budding vesicle. GTP-bound ADP-ribosylation factor (Arf) is also incorporated into the coated assembly. Another small G-protein, dynamin, forms a ring complex around the neck of the forming vesicle and may provide the mechanochemical force to seal the bud,  
15 thereby releasing the vesicle. The coated vesicle complex is then transported through the cytosol. During the transport process, Arf-bound GTP is hydrolyzed to GDP, and the coat dissociates from the transport vesicle (West, M.A. et al. (1997) J. Cell Biol. 138:1239-1254).

Vesicles which bud from the ER and the Golgi are covered with a protein coat similar to the clathrin coat of endocytic and TGN vesicles. The coat protein (COP) is assembled from cytosolic  
20 precursor molecules at specific budding regions on the organelle. The COP coat consists of two major components, a G-protein (Arf or Sar) and coat protomer (coatomer). Coatomer is an equimolar complex of seven proteins, termed alpha-, beta-, beta'-, gamma-, delta-, epsilon- and zeta-COP. The coatomer complex binds to dilysine motifs contained on the cytoplasmic tails of integral membrane proteins. These include the KKXX retrieval motif of membrane proteins of the ER and  
25 dibasic/diphenylamine motifs of members of the p24 family. The p24 family of type I membrane proteins represent the major membrane proteins of COPI vesicles (Harter, C. and F.T. Wieland (1998) Proc. Natl. Acad. Sci. USA 95:11649-11654).

#### Organelle Associated Molecules

30 Eukaryotic cells are organized into various cellular organelles which has the effect of separating specific molecules and their functions from one another and from the cytosol. Within the cell, various membrane structures surround and define these organelles while allowing them to interact with one another and the cell environment through both active and passive transport processes. Important cell organelles include the nucleus, the Golgi apparatus, the endoplasmic  
35 reticulum, mitochondria, peroxisomes, lysosomes, endosomes, and secretory vesicles.

#### Nucleus

The cell nucleus contains all of the genetic information of the cell in the form of DNA, and the components and machinery necessary for replication of DNA and for transcription of DNA into RNA. (See Alberts, B. et al. (1994) Molecular Biology of the Cell, Garland Publishing Inc., New York NY, pp. 335-399.) DNA is organized into compact structures in the nucleus by interactions  
5 with various DNA-binding proteins such as histones and non-histone chromosomal proteins. DNA-specific nucleases, DNases, partially degrade these compacted structures prior to DNA replication or transcription. DNA replication takes place with the aid of DNA helicases which unwind the double-stranded DNA helix, and DNA polymerases that duplicate the separated DNA strands.

10 Transcriptional regulatory proteins are essential for the control of gene expression. Some of these proteins function as transcription factors that initiate, activate, repress, or terminate gene transcription. Transcription factors generally bind to the promoter, enhancer, and upstream regulatory regions of a gene in a sequence-specific manner, although some factors bind regulatory elements within or downstream of a gene's coding region. Transcription factors may bind to a  
15 specific region of DNA singly or as a complex with other accessory factors. (Reviewed in Lewin, B. (1990) Genes IV, Oxford University Press, New York NY, and Cell Press, Cambridge MA, pp. 554-570.) Many transcription factors incorporate DNA-binding structural motifs which comprise either  $\alpha$  helices or  $\beta$  sheets that bind to the major groove of DNA. Four well-characterized structural motifs are helix-turn-helix, zinc finger, leucine zipper, and helix-loop-helix. Proteins containing  
20 these motifs may act alone as monomers, or they may form homo- or heterodimers that interact with DNA.

Many neoplastic disorders in humans can be attributed to inappropriate gene expression. Malignant cell growth may result from either excessive expression of tumor promoting genes or insufficient expression of tumor suppressor genes (Cleary, M.L. (1992) *Cancer Surv.* 15:89-104).  
25 Chromosomal translocations may also produce chimeric loci which fuse the coding sequence of one gene with the regulatory regions of a second unrelated gene. Such an arrangement likely results in inappropriate gene transcription, potentially contributing to malignancy.

In addition, the immune system responds to infection or trauma by activating a cascade of events that coordinate the progressive selection, amplification, and mobilization of cellular defense  
30 mechanisms. A complex and balanced program of gene activation and repression is involved in this process. However, hyperactivity of the immune system as a result of improper or insufficient regulation of gene expression may result in considerable tissue or organ damage. This damage is well documented in immunological responses associated with arthritis, allergens, heart attack, stroke, and infections (Isselbacher, K.J. et al. (1996) Harrison's Principles of Internal Medicine, 13/e,  
35 McGraw Hill, Inc. and Teton Data Systems Software).

Transcription of DNA into RNA also takes place in the nucleus catalyzed by RNA

polymerases. Three types of RNA polymerase exist. RNA polymerase I makes large ribosomal RNAs, while RNA polymerase III makes a variety of small, stable RNAs including 5S ribosomal RNA and the transfer RNAs (tRNA). RNA polymerase II transcribes genes that will be translated into proteins. The primary transcript of RNA polymerase II is called heterogenous nuclear RNA  
5 (hnRNA), and must be further processed by splicing to remove non-coding sequences called introns. RNA splicing is mediated by small nuclear ribonucleoprotein complexes, or snRNPs, producing mature messenger RNA (mRNA) which is then transported out of the nucleus for translation into proteins.

#### Nucleolus

10 The nucleolus is a highly organized subcompartment in the nucleus that contains high concentrations of RNA and proteins and functions mainly in ribosomal RNA synthesis and assembly (Alberts, et al. *supra*, pp. 379-382). Ribosomal RNA (rRNA) is a structural RNA that is complexed with proteins to form ribonucleoprotein structures called ribosomes. Ribosomes provide the platform on which protein synthesis takes place.

15 Ribosomes are assembled in the nucleolus initially from a large, 45S rRNA combined with a variety of proteins imported from the cytoplasm, as well as smaller, 5S rRNAs. Later processing of the immature ribosome results in formation of smaller ribosomal subunits which are transported from the nucleolus to the cytoplasm where they are assembled into functional ribosomes.

#### Endoplasmic Reticulum

20 In eukaryotes, proteins are synthesized within the endoplasmic reticulum (ER), delivered from the ER to the Golgi apparatus for post-translational processing and sorting, and transported from the Golgi to specific intracellular and extracellular destinations. Synthesis of integral membrane proteins, secreted proteins, and proteins destined for the lumen of a particular organelle occurs on the rough endoplasmic reticulum (ER). The rough ER is so named because of the rough appearance in  
25 electron micrographs imparted by the attached ribosomes on which protein synthesis proceeds. Synthesis of proteins destined for the ER actually begins in the cytosol with the synthesis of a specific signal peptide which directs the growing polypeptide and its attached ribosome to the ER membrane where the signal peptide is removed and protein synthesis is completed. Soluble proteins destined for the ER lumen, for secretion, or for transport to the lumen of other organelles pass  
30 completely into the ER lumen. Transmembrane proteins destined for the ER or for other cell membranes are translocated across the ER membrane but remain anchored in the lipid bilayer of the membrane by one or more membrane-spanning  $\alpha$ -helical regions.

Translocated polypeptide chains destined for other organelles or for secretion also fold and assemble in the ER lumen with the aid of certain "resident" ER proteins. Protein folding in the ER is  
35 aided by two principal types of protein isomerases, protein disulfide isomerase (PDI), and peptidyl-prolyl isomerase (PPI). PDI catalyzes the oxidation of free sulfhydryl groups in cysteine residues to

form intramolecular disulfide bonds in proteins. PPI, an enzyme that catalyzes the isomerization of certain proline imide bonds in oligopeptides and proteins, is considered to govern one of the rate limiting steps in the folding of many proteins to their final functional conformation. The cyclophilins represent a major class of PPI that was originally identified as the major receptor for the

5 immunosuppressive drug cyclosporin A (Handschumacher, R.E. et al. (1984) Science 226:544-547). Molecular "chaperones" such as BiP (binding protein) in the ER recognize incorrectly folded proteins as well as proteins not yet folded into their final form and bind to them, both to prevent improper aggregation between them, and to promote proper folding.

The "N-linked" glycosylation of most soluble secreted and membrane-bound proteins by

10 oligosacchrides linked to asparagine residues in proteins is also performed in the ER. This reaction is catalyzed by a membrane-bound enzyme, oligosaccharyl transferase.

#### Golgi Apparatus

The Golgi apparatus is a complex structure that lies adjacent to the ER in eukaryotic cells and serves primarily as a sorting and dispatching station for products of the ER (Alberts, et al. *supra*, pp.

15 600-610). Additional posttranslational processing, principally additional glycosylation, also occurs in the Golgi. Indeed, the Golgi is a major site of carbohydrate synthesis, including most of the glycosaminoglycans of the extracellular matrix. N-linked oligosaccharides, added to proteins in the ER, are also further modified in the Golgi by the addition of more sugar residues to form complex N-linked oligosaccharides. "O-linked" glycosylation of proteins also occurs in the Golgi by the addition

20 of N-acetylgalactosamine to the hydroxyl group of a serine or threonine residue followed by the sequential addition of other sugar residues to the first. This process is catalyzed by a series of glycosyltransferases each specific for a particular donor sugar nucleotide and acceptor molecule (Lodish, H. et al. (1995) Molecular Cell Biology, W.H. Freeman and Co., New York NY, pp.700-708). In many cases, both N- and O-linked oligosaccharides appear to be required for the secretion of

25 proteins or the movement of plasma membrane glycoproteins to the cell surface.

The terminal compartment of the Golgi is the Trans-Golgi Network (TGN), where both membrane and luminal proteins are sorted for their final destination. Transport (or secretory) vesicles destined for intracellular compartments, such as lysosomes, bud off of the TGN. Other transport vesicles bud off containing proteins destined for the plasma membrane, such as receptors,

30 adhesion molecules, and ion channels, and secretory proteins, such as hormones, neurotransmitters, and digestive enzymes.

#### Vacuoles

The vacuole system is a collection of membrane bound compartments in eukaryotic cells that functions in the processes of endocytosis and exocytosis. They include phagosomes, lysosomes,

35 endosomes, and secretory vesicles. Endocytosis is the process in cells of internalizing nutrients, solutes or small particles (pinocytosis) or large particles such as internalized receptors, viruses,

bacteria, or bacterial toxins (phagocytosis). Exocytosis is the process of transporting molecules to the cell surface. It facilitates placement or localization of membrane-bound receptors or other membrane proteins and secretion of hormones, neurotransmitters, digestive enzymes, wastes, etc.

A common property of all of these vacuoles is an acidic pH environment ranging from  
5 approximately pH 4.5-5.0. This acidity is maintained by the presence of a proton ATPase that uses the energy of ATP hydrolysis to generate an electrochemical proton gradient across a membrane (Mellman, I. et al. (1986) *Annu. Rev. Biochem.* 55:663-700). Eukaryotic vacuolar proton ATPase (vp-ATPase) is a multimeric enzyme composed of 3-10 different subunits. One of these subunits is a highly hydrophobic polypeptide of approximately 16 kDa that is similar to the proteolipid component  
10 of vp-ATPases from eubacteria, fungi, and plant vacuoles (Mandel, M. et al. (1988) *Proc. Natl. Acad. Sci. USA* 85:5521-5524). The 16 kDa proteolipid component is the major subunit of the membrane portion of vp-ATPase and functions in the transport of protons across the membrane.

#### Lysosomes

Lysosomes are membranous vesicles containing various hydrolytic enzymes used for the  
15 controlled intracellular digestion of macromolecules. Lysosomes contain some 40 types of enzymes including proteases, nucleases, glycosidases, lipases, phospholipases, phosphatases, and sulfatases, all of which are acid hydrolases that function at a pH of about 5. Lysosomes are surrounded by a unique membrane containing transport proteins that allow the final products of macromolecule degradation, such as sugars, amino acids, and nucleotides, to be transported to the cytosol where they may be  
20 either excreted or reutilized by the cell. A vp-ATPase, such as that described above, maintains the acidic environment necessary for hydrolytic activity (Alberts, supra, pp. 610-611).

#### Endosomes

Endosomes are another type of acidic vacuole that is used to transport substances from the cell surface to the interior of the cell in the process of endocytosis. Like lysosomes, endosomes have  
25 an acidic environment provided by a vp-ATPase (Alberts et al. supra, pp. 610-618). Two types of endosomes are apparent based on tracer uptake studies that distinguish their time of formation in the cell and their cellular location. Early endosomes are found near the plasma membrane and appear to function primarily in the recycling of internalized receptors back to the cell surface. Late endosomes appear later in the endocytic process close to the Golgi apparatus and the nucleus, and appear to be  
30 associated with delivery of endocytosed material to lysosomes or to the TGN where they may be recycled. Specific proteins are associated with particular transport vesicles and their target compartments that may provide selectivity in targeting vesicles to their proper compartments. A cytosolic prenylated GTP-binding protein, Rab, is one such protein. Rabs 4, 5, and 11 are associated with the early endosome, whereas Rabs 7 and 9 associate with the late endosome.

#### Mitochondria

Mitochondria are oval-shaped organelles comprising an outer membrane, a tightly folded

inner membrane, an intermembrane space between the outer and inner membranes, and a matrix inside the inner membrane. The outer membrane contains many porin molecules that allow ions and charged molecules to enter the intermembrane space, while the inner membrane contains a variety of transport proteins that transfer only selected molecules. Mitochondria are the primary sites of energy production in cells.

Energy is produced by the oxidation of glucose and fatty acids. Glucose is initially converted to pyruvate in the cytoplasm. Fatty acids and pyruvate are transported to the mitochondria for complete oxidation to CO<sub>2</sub> coupled by enzymes to the transport of electrons from NADH and FADH<sub>2</sub> to oxygen and to the synthesis of ATP (oxidative phosphorylation) from ADP and P<sub>i</sub>.

Pyruvate is transported into the mitochondria and converted to acetyl-CoA for oxidation via the citric acid cycle, involving pyruvate dehydrogenase components, dihydrolipoyl transacetylase, and dihydrolipoyl dehydrogenase. Enzymes involved in the citric acid cycle include: citrate synthetase, aconitases, isocitrate dehydrogenase, alpha-ketoglutarate dehydrogenase complex including transsuccinylases, succinyl CoA synthetase, succinate dehydrogenase, fumarases, and malate dehydrogenase. Acetyl CoA is oxidized to CO<sub>2</sub> with concomitant formation of NADH, FADH<sub>2</sub>, and GTP. In oxidative phosphorylation, the transfer of electrons from NADH and FADH<sub>2</sub> to oxygen by dehydrogenases is coupled to the synthesis of ATP from ADP and P<sub>i</sub> by the F<sub>0</sub>F<sub>1</sub> ATPase complex in the mitochondrial inner membrane. Enzyme complexes responsible for electron transport and ATP synthesis include the F<sub>0</sub>F<sub>1</sub> ATPase complex, ubiquinone(CoQ)-cytochrome c reductase, ubiquinone reductase, cytochrome b, cytochrome c<sub>1</sub>, FeS protein, and cytochrome c oxidase.

#### Peroxisomes

Peroxisomes, like mitochondria, are a major site of oxygen utilization. They contain one or more enzymes, such as catalase and urate oxidase, that use molecular oxygen to remove hydrogen atoms from specific organic substrates in an oxidative reaction that produces hydrogen peroxide (Alberts, *supra*, pp. 574-577). Catalase oxidizes a variety of substrates including phenols, formic acid, formaldehyde, and alcohol and is important in peroxisomes of liver and kidney cells for detoxifying various toxic molecules that enter the bloodstream. Another major function of oxidative reactions in peroxisomes is the breakdown of fatty acids in a process called  $\beta$  oxidation.  $\beta$  oxidation results in shortening of the alkyl chain of fatty acids by blocks of two carbon atoms that are converted to acetyl CoA and exported to the cytosol for reuse in biosynthetic reactions.

Also like mitochondria, peroxisomes import their proteins from the cytosol using a specific signal sequence located near the C-terminus of the protein. The importance of this import process is evident in the inherited human disease Zellweger syndrome, in which a defect in importing proteins into peroxisomes leads to a peroxisomal deficiency resulting in severe abnormalities in the brain, liver, and kidneys, and death soon after birth. One form of this disease has been shown to be due to a mutation in the gene encoding a peroxisomal integral membrane protein called peroxisome assembly

factor-1.

The discovery of new human molecules satisfies a need in the art by providing new compositions which are useful in the diagnosis, study, prevention, and treatment of diseases associated with, as well as effects of exogenous compounds on, the expression of human molecules.

5

### SUMMARY OF THE INVENTION

The present invention relates to nucleic acid sequences comprising human diagnostic and therapeutic polynucleotides (dithp) as presented in the Sequence Listing. The dithp uniquely identify genes encoding human structural, functional, and regulatory molecules.

- 10 The invention provides an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the
- 15 polynucleotide of b); and e) an RNA equivalent of a) through d). In one alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670. In another alternative, the polynucleotide comprises at least 30 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; b) a
- 20 polynucleotide comprising a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In another alternative, the polynucleotide comprises at least 60 contiguous nucleotides of a
- 25 polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; b) a polynucleotide comprising a naturally occurring polynucleotide comprising a polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the
- 30 polynucleotide of b); and e) an RNA equivalent of a) through d). The invention further provides a composition for the detection of expression of human diagnostic and therapeutic polynucleotides comprising at least one isolated polynucleotide comprising a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; b) a polynucleotide comprising a naturally occurring polynucleotide
- 35 sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; c) a polynucleotide complementary to the polynucleotide of a); d) a

polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d); and a detectable label.

The invention also provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a polynucleotide sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of SEQ ID NO:1-670; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.

The invention also provides a method for detecting a target polynucleotide in a sample, said target polynucleotide having a polynucleotide sequence of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide, and b) detecting the presence or absence of said hybridization complex, and, optionally, if present, the amount thereof. In one alternative, the invention provides a composition comprising a target polynucleotide of the method, wherein said probe comprises at least 30 contiguous nucleotides. In one alternative, the invention provides a composition comprising a target polynucleotide of the method, wherein said probe comprises at least 60 contiguous nucleotides.

The invention further provides a recombinant polynucleotide comprising a promoter sequence operably linked to an isolated polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). In one alternative, the invention provides a cell transformed with the recombinant polynucleotide. In another alternative, the



invention provides a transgenic organism comprising the recombinant polynucleotide.

The invention also provides a method for producing a human diagnostic and therapeutic polypeptide, the method comprising a) culturing a cell under conditions suitable for expression of the human diagnostic and therapeutic polypeptide, wherein said cell is transformed with a recombinant polynucleotide, said recombinant polynucleotide comprising an isolated polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv), and b) recovering the human diagnostic and therapeutic polypeptide so expressed. The invention additionally provides a method wherein the polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347.

The invention also provides an isolated human diagnostic and therapeutic polypeptide (DITHP) encoded by at least one polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670. The invention further provides a method of screening for a test compound that specifically binds to the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347. The method comprises a) combining the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347 with at least one test compound under suitable conditions, and b) detecting binding of the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347 to the test compound, thereby identifying a compound that specifically binds to the polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347.

The invention further provides a microarray wherein at least one element of the microarray is an isolated polynucleotide comprising at least 30 contiguous nucleotides of a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The invention also provides a method for generating a transcript image of a sample which contains polynucleotides. The method comprises a) labeling the polynucleotides of the sample, b) contacting the elements of the microarray with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and c) quantifying the expression of the polynucleotides in the sample.

Additionally, the invention provides a method for screening a compound for effectiveness in

altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide selected from the group consisting of a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence  
5 selected from the group consisting of SEQ ID NO:1-670; c) a polynucleotide complementary to the polynucleotide of a); d) a polynucleotide complementary to the polynucleotide of b); and e) an RNA equivalent of a) through d). The method comprises a) exposing a sample comprising the target polynucleotide to a compound, b) detecting altered expression of the target polynucleotide, and c) comparing the expression of the target polynucleotide in the presence of varying amounts of the  
10 compound and in the absence of the compound.

The invention further provides a method for assessing toxicity of a test compound, said method comprising a) treating a biological sample containing nucleic acids with the test compound; b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide selected from the group consisting of i) a polynucleotide  
15 comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv). Hybridization occurs under  
20 conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide selected from the group consisting of i) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; ii) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a  
25 polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670; iii) a polynucleotide complementary to the polynucleotide of i); iv) a polynucleotide complementary to the polynucleotide of ii); and v) an RNA equivalent of i) through iv), and alternatively, the target polynucleotide comprises a polynucleotide sequence of a fragment of a polynucleotide selected from the group consisting of i-v above; c) quantifying the amount of hybridization complex; and d)  
30 comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

The invention further provides an isolated polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID  
35 NO:671-1347, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, c) a

biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347. In one alternative, the invention provides an isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347.

The invention further provides an isolated polynucleotide encoding a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347. In one alternative, the polynucleotide encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347. In another alternative, the polynucleotide comprises a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670.

Additionally, the invention provides an isolated antibody which specifically binds to a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347.

The invention further provides a composition comprising a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, and a pharmaceutically acceptable excipient. In one embodiment, the composition comprises a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347. The invention additionally provides a method of treating a disease or condition associated with decreased expression of functional DITHP, comprising administering to a patient in need of such treatment the composition.

The invention also provides a method for screening a compound for effectiveness as an agonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting agonist activity in the sample. In one alternative, the invention provides a composition comprising an agonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with decreased expression of functional DITHP, comprising administering to a patient in need of such treatment the composition.

Additionally, the invention provides a method for screening a compound for effectiveness as an antagonist of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347. The method comprises a) exposing a sample comprising the polypeptide to a compound, and b) detecting antagonist activity in the sample. In one alternative, the invention provides a composition comprising an antagonist compound identified by the method and a pharmaceutically acceptable excipient. In another alternative, the invention provides a method of treating a disease or condition associated with overexpression of functional DITHP, comprising administering to a patient in need of such treatment the composition.

The invention further provides a method of screening for a compound that modulates the activity of a polypeptide selected from the group consisting of a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, and d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347. The method comprises a) combining the polypeptide with at least one test compound under conditions permissive for the activity of the polypeptide, b) assessing the activity of the polypeptide in the presence of the test compound, and c)

comparing the activity of the polypeptide in the presence of the test compound with the activity of the polypeptide in the absence of the test compound, wherein a change in the activity of the polypeptide in the presence of the test compound is indicative of a compound that modulates the activity of the polypeptide.

5

### DESCRIPTION OF THE TABLES

Table 1 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with the sequence identification numbers (SEQ ID NO:s) and open reading frame identification numbers (ORF IDs) corresponding to polypeptides encoded by the template ID.

10

Table 2 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with their GenBank hits (GI Numbers), probability scores, and functional annotations corresponding to the GenBank hits.

15

Table 3 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with polynucleotide segments of each template sequence as defined by the indicated "start" and "stop" nucleotide positions. The reading frames of the polynucleotide segments and the Pfam hits, Pfam descriptions, and E-values corresponding to the polypeptide domains encoded by the polynucleotide segments are indicated.

20

Table 4 shows the sequence identification numbers (SEQ ID NO:s) and template identification numbers (template IDs) corresponding to the polynucleotides of the present invention, along with polynucleotide segments of each template sequence as defined by the indicated "start" and "stop" nucleotide positions. The reading frames of the polynucleotide segments are shown, and the polypeptides encoded by the polynucleotide segments constitute either signal peptide (SP) or transmembrane (TM) domains, as indicated. For TM domains, the membrane topology of the encoded polypeptide sequence is indicated as being transmembrane or on the cytosolic or non-cytosolic side of the cell membrane or organelle.

25

Table 5 shows the sequence identification numbers and template identification numbers (/template IDs) corresponding to the polynucleotides of the present invention, along with component sequence identification spans corresponding to each template. The component sequences, which were used to assemble the template sequences, are defined by the spans indicating the nucleotide positions along each template.

30

Table 6 shows the tissue distribution profiles for the templates of the invention.

35

Table 7 shows the sequence identification numbers (SEQ ID NO:s) corresponding to the polypeptides of the present invention, along with the reading frames used to obtain the polypeptide

segments, the lengths of the polypeptide segments, the "start" and "stop" nucleotide positions of the polynucleotide sequences used to define the encoded polypeptide segments, the GenBank hits (GI Numbers), probability scores, and functional annotations corresponding to the GenBank hits.

Table 8 summarizes the bioinformatics tools which are useful for analysis of the  
 5 polynucleotides of the present invention. The first column of Table 8 lists analytical tools, programs, and algorithms, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the  
 10 homology between two sequences).

## DETAILED DESCRIPTION OF THE INVENTION

Before the nucleic acid sequences and methods are presented, it is to be understood that this invention is not limited to the particular machines, methods, and materials described. Although  
 15 particular embodiments are described, machines, methods, and materials similar or equivalent to these embodiments may be used to practice the invention. The preferred machines, methods, and materials set forth are not intended to limit the scope of the invention which is limited only by the appended claims.

The singular forms "a", "an", and "the" include plural reference unless the context clearly  
 20 dictates otherwise. All technical and scientific terms have the meanings commonly understood by one of ordinary skill in the art. All publications are incorporated by reference for the purpose of describing and disclosing the cell lines, vectors, and methodologies which are presented and which might be used in connection with the invention. Nothing in the specification is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

25

### Definitions

As used herein, the lower case "dithp" refers to a nucleic acid sequence, while the upper case "DITHP" refers to an amino acid sequence encoded by dithp. A "full-length" dithp refers to a nucleic acid sequence containing the entire coding region of a gene endogenously expressed in human tissue.

30 "Adjuvants" are materials such as Freund's adjuvant, mineral gels (aluminum hydroxide), and surface active substances (lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol) which may be administered to increase a host's immunological response.

"Allele" refers to an alternative form of a nucleic acid sequence. Alleles result from a  
 35 "mutation," a change or an alternative reading of the genetic code. Any given gene may have none, one, or many allelic forms. Mutations which give rise to alleles include deletions, additions, or

substitutions of nucleotides. Each of these changes may occur alone, or in combination with the others, one or more times in a given nucleic acid sequence. The present invention encompasses allelic dithp.

An "allelic variant" is an alternative form of the gene encoding DITHP. Allelic variants may  
5 result from at least one mutation in the nucleic acid sequence and may result in altered mRNAs or in polypeptides whose structure or function may or may not be altered. A gene may have none, one, or many allelic variants of its naturally occurring form. Common mutational changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone, or in combination with the others, one or more times  
10 in a given sequence.

"Altered" nucleic acid sequences encoding DITHP include those sequences with deletions, insertions, or substitutions of different nucleotides, resulting in a polypeptide the same as DITHP or a polypeptide with at least one functional characteristic of DITHP. Included within this definition are polymorphisms which may or may not be readily detectable using a particular oligonucleotide probe  
15 of the polynucleotide encoding DITHP, and improper or unexpected hybridization to allelic variants, with a locus other than the normal chromosomal locus for the polynucleotide sequence encoding DITHP. The encoded protein may also be "altered," and may contain deletions, insertions, or substitutions of amino acid residues which produce a silent change and result in a functionally equivalent DITHP. Deliberate amino acid substitutions may be made on the basis of similarity in  
20 polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues, as long as the biological or immunological activity of DITHP is retained. For example, negatively charged amino acids may include aspartic acid and glutamic acid, and positively charged amino acids may include lysine and arginine. Amino acids with uncharged polar side chains having similar hydrophilicity values may include: asparagine and glutamine; and serine and threonine.  
25 Amino acids with uncharged side chains having similar hydrophilicity values may include: leucine, isoleucine, and valine; glycine and alanine; and phenylalanine and tyrosine.

"Amino acid sequence" refers to a peptide, a polypeptide, or a protein of either natural or synthetic origin. The amino acid sequence is not limited to the complete, endogenous amino acid sequence and may be a fragment, epitope, variant, or derivative of a protein expressed by a nucleic  
30 acid sequence.

"Amplification" refers to the production of additional copies of a sequence and is carried out using polymerase chain reaction (PCR) technologies well known in the art.

"Antibody" refers to intact molecules as well as to fragments thereof, such as Fab, F(ab')<sub>2</sub>, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind  
35 DITHP polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or peptide used to immunize an

animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

5           The term "aptamer" refers to a nucleic acid or oligonucleotide molecule that binds to a specific molecular target. Aptamers are derived from an *in vitro* evolutionary process (e.g., SELEX (Systematic Evolution of Ligands by EXponential Enrichment), described in U.S. Patent No. 5,270,163), which selects for target-specific aptamer sequences from large combinatorial libraries. Aptamer compositions may be double-stranded or single-stranded, and may include  
10   deoxyribonucleotides, ribonucleotides, nucleotide derivatives, or other nucleotide-like molecules. The nucleotide components of an aptamer may have modified sugar groups (e.g., the 2'-OH group of a ribonucleotide may be replaced by 2'-F or 2'-NH<sub>2</sub>), which may improve a desired property, e.g., resistance to nucleases or longer lifetime in blood. Aptamers may be conjugated to other molecules, e.g., a high molecular weight carrier to slow clearance of the aptamer from the circulatory system.  
15   Aptamers may be specifically cross-linked to their cognate ligands, e.g., by photo-activation of a cross-linker. (See, e.g., Brody, E.N. and L. Gold (2000) J. Biotechnol. 74:5-13.)

          The term "intramer" refers to an aptamer which is expressed *in vivo*. For example, a vaccinia virus-based RNA expression system has been used to express specific RNA aptamers at high levels in the cytoplasm of leukocytes (Blind, M. et al. (1999) Proc. Natl Acad. Sci. USA 96:3606-3610).

20           The term "spiegelmer" refers to an aptamer which includes L-DNA, L-RNA, or other left-handed nucleotide derivatives or nucleotide-like molecules. Aptamers containing left-handed nucleotides are resistant to degradation by naturally occurring enzymes, which normally act on substrates containing right-handed nucleotides.

          "Antisense sequence" refers to a sequence capable of specifically hybridizing to a target  
25   sequence. The antisense sequence may include DNA, RNA, or any nucleic acid mimic or analog such as peptide nucleic acid (PNA); oligonucleotides having modified backbone linkages such as phosphorothioates, methylphosphonates, or benzylphosphonates; oligonucleotides having modified sugar groups such as 2'-methoxyethyl sugars or 2'-methoxyethoxy sugars; or oligonucleotides having modified bases such as 5-methyl cytosine, 2'-deoxyuracil, or 7-deaza-2'-deoxyguanosine.

30           "Antisense technology" refers to any technology which relies on the specific hybridization of an antisense sequence to a target sequence.

          A "bin" is a portion of computer memory space used by a computer program for storage of data, and bounded in such a manner that data stored in a bin may be retrieved by the program.

          "Biologically active" refers to an amino acid sequence having a structural, regulatory, or  
35   biochemical function of a naturally occurring amino acid sequence.

          "Clone joining" is a process for combining gene bins based upon the bins' containing



sequence information from the same clone. The sequences may assemble into a primary gene transcript as well as one or more splice variants.

"Complementary" describes the relationship between two single-stranded nucleic acid sequences that anneal by base-pairing (5'-A-G-T-3' pairs with its complement 3'-T-C-A-5').

5 A "component sequence" is a nucleic acid sequence selected by a computer program such as PHRED and used to assemble a consensus or template sequence from one or more component sequences.

A "consensus sequence" or "template sequence" is a nucleic acid sequence which has been assembled from overlapping sequences, using a computer program for fragment assembly such as the  
10 GELVIEW fragment assembly system (Genetics Computer Group (GCG), Madison WI) or using a relational database management system (RDMS).

"Conservative amino acid substitutions" are those substitutions that, when made, least interfere with the properties of the original protein, i.e., the structure and especially the function of the protein is conserved and not significantly changed by such substitutions. The table below shows  
15 amino acids which may be substituted for an original amino acid in a protein and which are regarded as conservative substitutions.

	Original Residue	Conservative Substitution
	Ala	Gly, Ser
20	Arg	His, Lys
	Asn	Asp, Gln, His
	Asp	Asn, Glu
	Cys	Ala, Ser
	Gln	Asn, Glu, His
25	Glu	Asp, Gln, His
	Gly	Ala
	His	Asn, Arg, Gln, Glu
	Ile	Leu, Val
	Leu	Ile, Val
30	Lys	Arg, Gln, Glu
	Met	Leu, Ile
	Phe	His, Met, Leu, Trp, Tyr
	Ser	Cys, Thr
	Thr	Ser, Val
35	Trp	Phe, Tyr
	Tyr	His, Phe, Trp
	Val	Ile, Leu, Thr

40 Conservative substitutions generally maintain (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a beta sheet or alpha helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain.

"Deletion" refers to a change in either a nucleic acid sequence in which at least one nucleotide or amino acid residue, respectively, is absent.

"Derivative" refers to the chemical modification of a nucleic acid sequence, such as by replacement of hydrogen by an alkyl, acyl, amino, hydroxyl, or other group.

5 "Differential expression" refers to increased or upregulated; or decreased, downregulated, or absent gene or protein expression, determined by comparing at least two different samples. Such comparisons may be carried out between, for example, a treated and an untreated sample, or a diseased and a normal sample.

10 The terms "element" and "array element" refer to a polynucleotide, polypeptide, or other chemical compound having a unique and defined position on a microarray.

The term "modulate" refers to a change in the activity of ABBR. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of ABBR.

15 "E-value" refers to the statistical probability that a match between two sequences occurred by chance.

"Exon shuffling" refers to the recombination of different coding regions (exons). Since an exon may represent a structural or functional domain of the encoded protein, new proteins may be assembled through the novel reassortment of stable substructures, thus allowing acceleration of the evolution of new protein functions.

20 A "fragment" is a unique portion of dithp or DITHP which is identical in sequence to but shorter in length than the parent sequence. A fragment may comprise up to the entire length of the defined sequence, minus one nucleotide/amino acid residue. For example, a fragment may comprise from 10 to 1000 contiguous amino acid residues or nucleotides. A fragment used as a probe, primer, antigen, therapeutic molecule, or for other purposes, may be at least 5, 10, 15, 16, 20, 25, 30, 40, 50, 25 60, 75, 100, 150, 250 or at least 500 contiguous amino acid residues or nucleotides in length.

Fragments may be preferentially selected from certain regions of a molecule. For example, a polypeptide fragment may comprise a certain length of contiguous amino acids selected from the first 250 or 500 amino acids (or first 25% or 50%) of a polypeptide as shown in a certain defined sequence. Clearly these lengths are exemplary, and any length that is supported by the specification, 30 including the Sequence Listing and the figures, may be encompassed by the present embodiments.

A fragment of dithp comprises a region of unique polynucleotide sequence that specifically identifies dithp, for example, as distinct from any other sequence in the same genome. A fragment of dithp is useful, for example, in hybridization and amplification technologies and in analogous methods that distinguish dithp from related polynucleotide sequences. The precise length of a 35 fragment of dithp and the region of dithp to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A fragment of DITHP is encoded by a fragment of dithp. A fragment of DITHP comprises a region of unique amino acid sequence that specifically identifies DITHP. For example, a fragment of DITHP is useful as an immunogenic peptide for the development of antibodies that specifically recognize DITHP. The precise length of a fragment of DITHP and the region of DITHP to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment.

A "full length" nucleotide sequence is one containing at least a start site for translation to a protein sequence, followed by an open reading frame and a stop site, and encoding a "full length" polypeptide.

"Hit" refers to a sequence whose annotation will be used to describe a given template. Criteria for selecting the top hit are as follows: if the template has one or more exact nucleic acid matches, the top hit is the exact match with highest percent identity. If the template has no exact matches but has significant protein hits, the top hit is the protein hit with the lowest E-value. If the template has no significant protein hits, but does have significant non-exact nucleotide hits, the top hit is the nucleotide hit with the lowest E-value.

"Homology" refers to sequence similarity either between a reference nucleic acid sequence and at least a fragment of a dithp or between a reference amino acid sequence and a fragment of a DITHP.

"Hybridization" refers to the process by which a strand of nucleotides anneals with a complementary strand through base pairing. Specific hybridization is an indication that two nucleic acid sequences share a high degree of identity. Specific hybridization complexes form under defined annealing conditions, and remain hybridized after the "washing" step. The defined hybridization conditions include the annealing conditions and the washing step(s), the latter of which is particularly important in determining the stringency of the hybridization process, with more stringent conditions allowing less non-specific binding, i.e., binding between pairs of nucleic acid probes that are not perfectly matched. Permissive conditions for annealing of nucleic acid sequences are routinely determinable and may be consistent among hybridization experiments, whereas wash conditions may be varied among experiments to achieve the desired stringency.

Generally, stringency of hybridization is expressed with reference to the temperature under which the wash step is carried out. Generally, such wash temperatures are selected to be about 5°C to 20°C lower than the thermal melting point ( $T_m$ ) for the specific sequence at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength and pH) at which 50% of the target sequence hybridizes to a perfectly matched probe. An equation for calculating  $T_m$  and conditions for nucleic acid hybridization is well known and can be found in Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; specifically see volume 2, chapter 9.

High stringency conditions for hybridization between polynucleotides of the present invention include wash conditions of 68°C in the presence of about 0.2 x SSC and about 0.1% SDS, for 1 hour. Alternatively, temperatures of about 65°C, 60°C, or 55°C may be used. SSC concentration may be varied from about 0.2 to 2 x SSC, with SDS being present at about 0.1%.

5 Typically, blocking reagents are used to block non-specific hybridization. Such blocking reagents include, for instance, denatured salmon sperm DNA at about 100-200 µg/ml. Useful variations on these conditions will be readily apparent to those skilled in the art. Hybridization, particularly under high stringency conditions, may be suggestive of evolutionary similarity between the nucleotides. Such similarity is strongly indicative of a similar role for the nucleotides and their resultant proteins.

10 Other parameters, such as temperature, salt concentration, and detergent concentration may be varied to achieve the desired stringency. Denaturants, such as formamide at a concentration of about 35-50% v/v, may also be used under particular circumstances, such as RNA:DNA hybridizations. Appropriate hybridization conditions are routinely determinable by one of ordinary skill in the art.

15 "Immunologically active" or "immunogenic" describes the potential for a natural, recombinant, or synthetic peptide, epitope, polypeptide, or protein to induce antibody production in appropriate animals, cells, or cell lines.

"Immune response" can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression  
20 of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

An "immunogenic fragment" is a polypeptide or oligopeptide fragment of ABBR which is capable of eliciting an immune response when introduced into a living organism, for example, a mammal. The term "immunogenic fragment" also includes any polypeptide or oligopeptide fragment  
25 of ABBR which is useful in any of the antibody production methods disclosed herein or known in the art.

"Insertion" or "addition" refers to a change in either a nucleic or amino acid sequence in which at least one nucleotide or residue, respectively, is added to the sequence.

"Labeling" refers to the covalent or noncovalent joining of a polynucleotide, polypeptide, or  
30 antibody with a reporter molecule capable of producing a detectable or measurable signal.

"Microarray" is any arrangement of nucleic acids, amino acids, antibodies, etc., on a substrate. The substrate may be a solid support such as beads, glass, paper, nitrocellulose, nylon, or an appropriate membrane.

"Linkers" are short stretches of nucleotide sequence which may be added to a vector or a  
35 dithp to create restriction endonuclease sites to facilitate cloning. "Polylinkers" are engineered to incorporate multiple restriction enzyme sites and to provide for the use of enzymes which leave 5' or

3' overhangs (e.g., BamHI, EcoRI, and HindIII) and those which provide blunt ends (e.g., EcoRV, SnaBI, and StuI).

"Naturally occurring" refers to an endogenous polynucleotide or polypeptide that may be isolated from viruses or prokaryotic or eukaryotic cells.

5 "Nucleic acid sequence" refers to the specific order of nucleotides joined by phosphodiester bonds in a linear, polymeric arrangement. Depending on the number of nucleotides, the nucleic acid sequence can be considered an oligomer, oligonucleotide, or polynucleotide. The nucleic acid can be DNA, RNA, or any nucleic acid analog, such as PNA, may be of genomic or synthetic origin, may be either double-stranded or single-stranded, and can represent either the sense or antisense  
10 (complementary) strand.

"Oligomer" refers to a nucleic acid sequence of at least about 6 nucleotides and as many as about 60 nucleotides, preferably about 15 to 40 nucleotides, and most preferably between about 20 and 30 nucleotides, that may be used in hybridization or amplification technologies. Oligomers may be used as, e.g., primers for PCR, and are usually chemically synthesized.

15 "Operably linked" refers to the situation in which a first nucleic acid sequence is placed in a functional relationship with the second nucleic acid sequence. For instance, a promoter is operably linked to a coding sequence if the promoter affects the transcription or expression of the coding sequence. Generally, operably linked DNA sequences may be in close proximity or contiguous and, where necessary to join two protein coding regions, in the same reading frame.

20 "Peptide nucleic acid" (PNA) refers to a DNA mimic in which nucleotide bases are attached to a pseudopeptide backbone to increase stability. PNAs, also designated antigene agents, can prevent gene expression by targeting complementary messenger RNA.

The phrases "percent identity" and "% identity", as applied to polynucleotide sequences, refer to the percentage of residue matches between at least two polynucleotide sequences aligned  
25 using a standardized algorithm. Such an algorithm may insert, in a standardized and reproducible way, gaps in the sequences being compared in order to optimize alignment between two sequences, and therefore achieve a more meaningful comparison of the two sequences.

Percent identity between polynucleotide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e  
30 sequence alignment program. This program is part of the LASERGENE software package, a suite of molecular biological analysis programs (DNASTAR, Madison WI). CLUSTAL V is described in Higgins, D.G. and Sharp, P.M. (1989) CABIOS 5:151-153 and in Higgins, D.G. et al. (1992) CABIOS 8:189-191. For pairwise alignments of polynucleotide sequences, the default parameters are set as follows: Ktuple=2, gap penalty=5, window=4, and "diagonals saved"=4. The "weighted"  
35 residue weight table is selected as the default. Percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polynucleotide sequence pairs.

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at

5 <http://www.ncbi.nlm.nih.gov/BLAST/>. The BLAST software suite includes various sequence analysis programs including "BLASTN," that is used to determine alignment between a known polynucleotide sequence and other sequences on a variety of databases. Also available is a tool called "BLAST 2 Sequences" that is used for direct pairwise comparison of two nucleotide sequences. "BLAST 2 Sequences" can be accessed and used interactively at

10 <http://www.ncbi.nlm.nih.gov/gorf/bl2/>. The "BLAST 2 Sequences" tool can be used for both BLASTN and BLASTP (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use BLASTN with the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) set at default parameters. Such default parameters may be, for example:

15       *Matrix: BLOSUM62*  
           *Reward for match: 1*  
           *Penalty for mismatch: -2*  
           *Open Gap: 5 and Extension Gap: 2 penalties*  
           *Gap x drop-off: 50*  
 20       *Expect: 10*  
           *Word Size: 11*  
           *Filter: on*

Percent identity may be measured over the length of an entire defined sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example,

25 over the length of a fragment taken from a larger, defined sequence, for instance, a fragment of at least 20, at least 30, at least 40, at least 50, at least 70, at least 100, or at least 200 contiguous nucleotides. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

30 Nucleic acid sequences that do not show a high degree of identity may nevertheless encode similar amino acid sequences due to the degeneracy of the genetic code. It is understood that changes in nucleic acid sequence can be made using this degeneracy to produce multiple nucleic acid sequences that all encode substantially the same protein.

The phrases "percent identity" and "% identity", as applied to polypeptide sequences, refer to

35 the percentage of residue matches between at least two polypeptide sequences aligned using a standardized algorithm. Methods of polypeptide sequence alignment are well-known. Some

alignment methods take into account conservative amino acid substitutions. Such conservative substitutions, explained in more detail above, generally preserve the hydrophobicity and acidity of the substituted residue, thus preserving the structure (and therefore function) of the folded polypeptide.

Percent identity between polypeptide sequences may be determined using the default parameters of the CLUSTAL V algorithm as incorporated into the MEGALIGN version 3.12e sequence alignment program (described and referenced above). For pairwise alignments of polypeptide sequences using CLUSTAL V, the default parameters are set as follows: Ktuple=1, gap penalty=3, window=5, and "diagonals saved"=5. The PAM250 matrix is selected as the default residue weight table. As with polynucleotide alignments, the percent identity is reported by CLUSTAL V as the "percent similarity" between aligned polypeptide sequence pairs.

Alternatively the NCBI BLAST software suite may be used. For example, for a pairwise comparison of two polypeptide sequences, one may use the "BLAST 2 Sequences" tool Version 2.0.9 (May-07-1999) with BLASTP set at default parameters. Such default parameters may be, for example:

15        *Matrix: BLOSUM62*  
           *Open Gap: 11 and Extension Gap: 1 penalty*  
           *Gap x drop-off: 50*  
           *Expect: 10*  
           *Word Size: 3*  
 20        *Filter: on*

Percent identity may be measured over the length of an entire defined polypeptide sequence, for example, as defined by a particular SEQ ID number, or may be measured over a shorter length, for example, over the length of a fragment taken from a larger, defined polypeptide sequence, for instance, a fragment of at least 15, at least 20, at least 30, at least 40, at least 50, at least 70 or at least 150 contiguous residues. Such lengths are exemplary only, and it is understood that any fragment length supported by the sequences shown herein, in figures or Sequence Listings, may be used to describe a length over which percentage identity may be measured.

"Post-translational modification" of a DITHP may involve lipidation, glycosylation, phosphorylation, acetylation, racemization, proteolytic cleavage, and other modifications known in the art. These processes may occur synthetically or biochemically. Biochemical modifications will vary by cell type depending on the enzymatic milieu and the DITHP.

"Probe" refers to dithp or fragments thereof, which are used to detect identical, allelic or related nucleic acid sequences. Probes are isolated oligonucleotides or polynucleotides attached to a detectable label or reporter molecule. Typical labels include radioactive isotopes, ligands, chemiluminescent agents, and enzymes. "Primers" are short nucleic acids, usually DNA oligonucleotides, which may be annealed to a target polynucleotide by complementary base-pairing.

The primer may then be extended along the target DNA strand by a DNA polymerase enzyme. Primer pairs can be used for amplification (and identification) of a nucleic acid sequence, e.g., by the polymerase chain reaction (PCR).

Probes and primers as used in the present invention typically comprise at least 15 contiguous  
5 nucleotides of a known sequence. In order to enhance specificity, longer probes and primers may also be employed, such as probes and primers that comprise at least 20, 30, 40, 50, 60, 70, 80, 90, 100, or at least 150 consecutive nucleotides of the disclosed nucleic acid sequences. Probes and primers may be considerably longer than these examples, and it is understood that any length supported by the specification, including the figures and Sequence Listing, may be used.

10 Methods for preparing and using probes and primers are described in the references, for example Sambrook et al., 1989, Molecular Cloning: A Laboratory Manual, 2<sup>nd</sup> ed., vol. 1-3, Cold Spring Harbor Press, Plainview NY; Ausubel et al., 1987, Current Protocols in Molecular Biology, Greene Publ. Assoc. & Wiley-Intersciences, New York NY; Innis et al., 1990, PCR Protocols, A Guide to Methods and Applications, Academic Press, San Diego CA. PCR primer pairs can be  
15 derived from a known sequence, for example, by using computer programs intended for that purpose such as Primer (Version 0.5, 1991, Whitehead Institute for Biomedical Research, Cambridge MA).

Oligonucleotides for use as primers are selected using software known in the art for such purpose. For example, OLIGO 4.06 software is useful for the selection of PCR primer pairs of up to 100 nucleotides each, and for the analysis of oligonucleotides and larger polynucleotides of up to  
20 5,000 nucleotides from an input polynucleotide sequence of up to 32 kilobases. Similar primer selection programs have incorporated additional features for expanded capabilities. For example, the PrimOU primer selection program (available to the public from the Genome Center at University of Texas South West Medical Center, Dallas TX) is capable of choosing specific primers from megabase sequences and is thus useful for designing primers on a genome-wide scope. The Primer3  
25 primer selection program (available to the public from the Whitehead Institute/MIT Center for Genome Research, Cambridge MA) allows the user to input a "mispriming library," in which sequences to avoid as primer binding sites are user-specified. Primer3 is useful, in particular, for the selection of oligonucleotides for microarrays. (The source code for the latter two primer selection programs may also be obtained from their respective sources and modified to meet the user's specific  
30 needs.) The PrimeGen program (available to the public from the UK Human Genome Mapping Project Resource Centre, Cambridge UK) designs primers based on multiple sequence alignments, thereby allowing selection of primers that hybridize to either the most conserved or least conserved regions of aligned nucleic acid sequences. Hence, this program is useful for identification of both unique and conserved oligonucleotides and polynucleotide fragments. The oligonucleotides and  
35 polynucleotide fragments identified by any of the above selection methods are useful in hybridization technologies, for example, as PCR or sequencing primers, microarray elements, or specific probes to



identify fully or partially complementary polynucleotides in a sample of nucleic acids. Methods of oligonucleotide selection are not limited to those described above.

“Purified” refers to molecules, either polynucleotides or polypeptides that are isolated or separated from their natural environment and are at least 60% free, preferably at least 75% free, and  
5 most preferably at least 90% free from other compounds with which they are naturally associated.

A “recombinant nucleic acid” is a sequence that is not naturally occurring or has a sequence that is made by an artificial combination of two or more otherwise separated segments of sequence. This artificial combination is often accomplished by chemical synthesis or, more commonly, by the artificial manipulation of isolated segments of nucleic acids, e.g., by genetic engineering techniques  
10 such as those described in Sambrook, supra. The term recombinant includes nucleic acids that have been altered solely by addition, substitution, or deletion of a portion of the nucleic acid. Frequently, a recombinant nucleic acid may include a nucleic acid sequence operably linked to a promoter sequence. Such a recombinant nucleic acid may be part of a vector that is used, for example, to transform a cell.

15 Alternatively, such recombinant nucleic acids may be part of a viral vector, e.g., based on a vaccinia virus, that could be used to vaccinate a mammal wherein the recombinant nucleic acid is expressed, inducing a protective immunological response in the mammal.

“Regulatory element” refers to a nucleic acid sequence from nontranslated regions of a gene, and includes enhancers, promoters, introns, and 3’ untranslated regions, which interact with host  
20 proteins to carry out or regulate transcription or translation.

“Reporter” molecules are chemical or biochemical moieties used for labeling a nucleic acid, an amino acid, or an antibody. They include radionuclides; enzymes; fluorescent, chemiluminescent, or chromogenic agents; substrates; cofactors; inhibitors; magnetic particles; and other moieties known in the art.

25 An “RNA equivalent,” in reference to a DNA sequence, is composed of the same linear sequence of nucleotides as the reference DNA sequence with the exception that all occurrences of the nitrogenous base thymine are replaced with uracil, and the sugar backbone is composed of ribose instead of deoxyribose.

“Sample” is used in its broadest sense. Samples may contain nucleic or amino acids, antibodies, or other materials, and may be derived from any source (e.g., bodily fluids including, but  
30 not limited to, saliva, blood, and urine; chromosome(s), organelles, or membranes isolated from a cell; genomic DNA, RNA, or cDNA in solution or bound to a substrate; and cleared cells or tissues or blots or imprints from such cells or tissues).

“Specific binding” or “specifically binding” refers to the interaction between a protein or  
35 peptide and its agonist, antibody, antagonist, or other binding partner. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope,

recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

5 "Substitution" refers to the replacement of at least one nucleotide or amino acid by a different nucleotide or amino acid.

"Substrate" refers to any suitable rigid or semi-rigid support including, e.g., membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles or capillaries. The substrate can have a variety of surface forms, such as wells,  
10 trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

A "transcript image" or "expression profile" refers to the collective pattern of gene expression by a particular cell type or tissue under given conditions at a given time.

"Transformation" refers to a process by which exogenous DNA enters a recipient cell. Transformation may occur under natural or artificial conditions using various methods well known in  
15 the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed.

"Transformants" include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well  
20 as cells which transiently express inserted DNA or RNA.

A "transgenic organism," as used herein, is any organism, including but not limited to animals and plants, in which one or more of the cells of the organism contains heterologous nucleic acid introduced by way of human intervention, such as by transgenic techniques well known in the art. The nucleic acid is introduced into the cell, directly or indirectly by introduction into a precursor of  
25 the cell, by way of deliberate genetic manipulation, such as by microinjection or by infection with a recombinant virus. The term genetic manipulation does not include classical cross-breeding, or in vitro fertilization, but rather is directed to the introduction of a recombinant DNA molecule. The transgenic organisms contemplated in accordance with the present invention include bacteria, cyanobacteria, fungi, and plants and animals. The isolated DNA of the present invention can be  
30 introduced into the host by methods known in the art, for example infection, transfection, transformation or transconjugation. Techniques for transferring the DNA of the present invention into such organisms are widely known and provided in references such as Sambrook et al. (1989), supra.

A "variant" of a particular nucleic acid sequence is defined as a nucleic acid sequence having  
35 at least 25% sequence identity to the particular nucleic acid sequence over a certain length of one of the nucleic acid sequences using BLASTN with the "BLAST 2 Sequences" tool Version 2.0.9 (May-

07-1999) set at default parameters. Such a pair of nucleic acids may show, for example, at least 30%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater sequence identity over a certain defined length. The variant may result in "conservative" amino acid changes which do not affect structural and/or chemical properties. A variant may be described as, for example, an "allelic" (as defined above), "splice," "species," or "polymorphic" variant. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The corresponding polypeptide may possess additional functional domains or lack domains that are present in the reference molecule. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

In an alternative, variants of the polynucleotides of the present invention may be generated through recombinant methods. One possible method is a DNA shuffling technique such as MOLECULARBREEDING (Maxygen Inc., Santa Clara CA; described in U.S. Patent Number 5,837,458; Chang, C.-C. et al. (1999) Nat. Biotechnol. 17:793-797; Christians, F.C. et al. (1999) Nat. Biotechnol. 17:259-264; and Crameri, A. et al. (1996) Nat. Biotechnol. 14:315-319) to alter or improve the biological properties of DITHP, such as its biological or enzymatic activity or its ability to bind to other molecules or compounds. DNA shuffling is a process by which a library of gene variants is produced using PCR-mediated recombination of gene fragments. The library is then subjected to selection or screening procedures that identify those gene variants with the desired properties. These preferred variants may then be pooled and further subjected to recursive rounds of DNA shuffling and selection/screening. Thus, genetic diversity is created through "artificial" breeding and rapid molecular evolution. For example, fragments of a single gene containing random point mutations may be recombined, screened, and then reshuffled until the desired properties are optimized. Alternatively, fragments of a given gene may be recombined with fragments of homologous genes in the same gene family, either from the same or different species, thereby maximizing the genetic diversity of multiple naturally occurring genes in a directed and controllable manner.

A "variant" of a particular polypeptide sequence is defined as a polypeptide sequence having at least 40% sequence identity to the particular polypeptide sequence over a certain length of one of the polypeptide sequences using BLASTP with the "BLAST 2 Sequences" tool Version 2.0.9 (May-

07-1999) set at default parameters. Such a pair of polypeptides may show, for example, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% or greater identity over a certain defined length of one of the polypeptides.

5

## THE INVENTION

In a particular embodiment, cDNA sequences derived from human tissues and cell lines were aligned based on nucleotide sequence identity and assembled into "consensus" or "template" sequences which are designated by the template identification numbers (template IDs) in column 2 of Table 2. The sequence identification numbers (SEQ ID NO:s) corresponding to the template IDs are shown in column 1. The template sequences have similarity to GenBank sequences, or "hits," as designated by the GI Numbers in column 3. The statistical probability of each GenBank hit is indicated by a probability score in column 4, and the functional annotation corresponding to each GenBank hit is listed in column 5.

The invention incorporates the nucleic acid sequences of these templates as disclosed in the Sequence Listing and the use of these sequences in the diagnosis and treatment of disease states characterized by defects in human molecules. The invention further utilizes these sequences in hybridization and amplification technologies, and in particular, in technologies which assess gene expression patterns correlated with specific cells or tissues and their responses *in vivo* or *in vitro* to pharmaceutical agents, toxins, and other treatments. In this manner, the sequences of the present invention are used to develop a transcript image for a particular cell or tissue.

### Derivation of Nucleic Acid Sequences

cDNA was isolated from libraries constructed using RNA derived from normal and diseased human tissues and cell lines. The human tissues and cell lines used for cDNA library construction were selected from a broad range of sources to provide a diverse population of cDNAs representative of gene transcription throughout the human body. Descriptions of the human tissues and cell lines used for cDNA library construction are provided in the LIFESEQ database (Incyte Genomics, Inc. (Incyte), Palo Alto CA). Human tissues were broadly selected from, for example, cardiovascular, dermatologic, endocrine, gastrointestinal, hematopoietic/immune system, musculoskeletal, neural, reproductive, and urologic sources.

Cell lines used for cDNA library construction were derived from, for example, leukemic cells, teratocarcinomas, neuroepitheliomas, cervical carcinoma, lung fibroblasts, and endothelial cells. Such cell lines include, for example, THP-1, Jurkat, HUVEC, hNT2, WI38, HeLa, and other cell lines commonly used and available from public depositories (American Type Culture Collection, Manassas VA). Prior to mRNA isolation, cell lines were untreated, treated with a pharmaceutical

agent such as 5'-aza-2'-deoxycytidine, treated with an activating agent such as lipopolysaccharide in the case of leukocytic cell lines, or, in the case of endothelial cell lines, subjected to shear stress.

#### Sequencing of the cDNAs

5           Methods for DNA sequencing are well known in the art. Conventional enzymatic methods employ the Klenow fragment of DNA polymerase I, SEQUENASE DNA polymerase (U.S. Biochemical Corporation, Cleveland OH), Taq polymerase (Applied Biosystems, Foster City CA), thermostable T7 polymerase (Amersham Pharmacia Biotech, Inc. (Amersham Pharmacia Biotech), Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found  
10 in the ELONGASE amplification system (Life Technologies Inc. (Life Technologies), Gaithersburg MD), to extend the nucleic acid sequence from an oligonucleotide primer annealed to the DNA template of interest. Methods have been developed for the use of both single-stranded and double-stranded templates. Chain termination reaction products may be electrophoresed on urea-polyacrylamide gels and detected either by autoradiography (for radioisotope-labeled nucleotides) or  
15 by fluorescence (for fluorophore-labeled nucleotides). Automated methods for mechanized reaction preparation, sequencing, and analysis using fluorescence detection methods have been developed. Machines used to prepare cDNAs for sequencing can include the MICROLAB 2200 liquid transfer system (Hamilton Company (Hamilton), Reno NV), Peltier thermal cycler (PTC200; MJ Research, Inc. (MJ Research), Watertown MA), and ABI CATALYST 800 thermal cycler (Applied  
20 Biosystems). Sequencing can be carried out using, for example, the ABI 373 or 377 (Applied Biosystems) or MEGABACE 1000 (Molecular Dynamics, Inc. (Molecular Dynamics), Sunnyvale CA) DNA sequencing systems, or other automated and manual sequencing systems well known in the art.

          The nucleotide sequences of the Sequence Listing have been prepared by current, state-of-  
25 the-art, automated methods and, as such, may contain occasional sequencing errors or unidentified nucleotides. Such unidentified nucleotides are designated by an N. These infrequent unidentified bases do not represent a hindrance to practicing the invention for those skilled in the art. Several methods employing standard recombinant techniques may be used to correct errors and complete the missing sequence information. (See, e.g., those described in Ausubel, F.M. et al. (1997) Short  
30 Protocols in Molecular Biology, John Wiley & Sons, New York NY; and Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY.)

#### Assembly of cDNA Sequences

          Human polynucleotide sequences may be assembled using programs or algorithms well  
35 known in the art. Sequences to be assembled are related, wholly or in part, and may be derived from a single or many different transcripts. Assembly of the sequences can be performed using such

programs as PHRAP (Phils Revised Assembly Program) and the GELVIEW fragment assembly system (GCG), or other methods known in the art.

Alternatively, cDNA sequences are used as "component" sequences that are assembled into "template" or "consensus" sequences as follows. Sequence chromatograms are processed, verified, and quality scores are obtained using PHRED. Raw sequences are edited using an editing pathway known as Block 1 (See, e.g., the LIFESEQ Assembled User Guide, Incyte Genomics, Palo Alto, CA). A series of BLAST comparisons is performed and low-information segments and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) are replaced by "n's", or masked, to prevent spurious matches. Mitochondrial and ribosomal RNA sequences are also removed. The processed sequences are then loaded into a relational database management system (RDMS) which assigns edited sequences to existing templates, if available. When additional sequences are added into the RDMS, a process is initiated which modifies existing templates or creates new templates from works in progress (i.e., nonfinal assembled sequences) containing queued sequences or the sequences themselves. After the new sequences have been assigned to templates, the templates can be merged into bins. If multiple templates exist in one bin, the bin can be split and the templates reannotated.

Once gene bins have been generated based upon sequence alignments, bins are "clone joined" based upon clone information. Clone joining occurs when the 5' sequence of one clone is present in one bin and the 3' sequence from the same clone is present in a different bin, indicating that the two bins should be merged into a single bin. Only bins which share at least two different clones are merged.

A resultant template sequence may contain either a partial or a full length open reading frame, or all or part of a genetic regulatory element. This variation is due in part to the fact that the full length cDNAs of many genes are several hundred, and sometimes several thousand, bases in length. With current technology, cDNAs comprising the coding regions of large genes cannot be cloned because of vector limitations, incomplete reverse transcription of the mRNA, or incomplete "second strand" synthesis. Template sequences may be extended to include additional contiguous sequences derived from the parent RNA transcript using a variety of methods known to those of skill in the art. Extension may thus be used to achieve the full length coding sequence of a gene.

### 30 Analysis of the cDNA Sequences

The cDNA sequences are analyzed using a variety of programs and algorithms which are well known in the art. (See, e.g., Ausubel, 1997, supra, Chapter 7.7; Meyers, R.A. (Ed.) (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853; and Table 8.) These analyses comprise both reading frame determinations, e.g., based on triplet codon periodicity for particular organisms (Fickett, J.W. (1982) Nucleic Acids Res. 10:5303-5318); analyses of potential start and stop codons; and homology searches.

Computer programs known to those of skill in the art for performing computer-assisted searches for amino acid and nucleic acid sequence similarity, include, for example, Basic Local Alignment Search Tool (BLAST; Altschul, S.F. (1993) J. Mol. Evol. 36:290-300; Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410). BLAST is especially useful in determining exact matches and  
5 comparing two sequence fragments of arbitrary but equal lengths, whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user (Karlin, S. et al. (1988) Proc. Natl. Acad. Sci. USA 85:841-845). Using an appropriate search tool (e.g., BLAST or HMM), GenBank, SwissProt, BLOCKS, PFAM and other databases may be searched for sequences containing regions of homology to a query dithp or DITHP of the present  
10 invention.

Other approaches to the identification, assembly, storage, and display of nucleotide and polypeptide sequences are provided in "Relational Database for Storing Biomolecule Information," U.S.S.N. 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S. Patent Number 5,953,727; and "Relational Database and System for Storing  
15 Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein in their entirety.

Protein hierarchies can be assigned to the putative encoded polypeptide based on, e.g., motif, BLAST, or biological analysis. Methods for assigning these hierarchies are described, for example, in "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence  
20 Data," U.S. Patent Number 6,023,659, incorporated herein by reference.

#### Identification of Human Diagnostic and Therapeutic Molecules Encoded by dithp

The identities of the DITHP encoded by the dithp of the present invention were obtained by analysis of the assembled cDNA sequences.

25 SEQ ID NO:671, SEQ ID NO:672, SEQ ID NO:673, SEQ ID NO:674, SEQ ID NO:675, SEQ ID NO:676, SEQ ID NO:677, SEQ ID NO:678, SEQ ID NO:679, SEQ ID NO:680, SEQ ID NO:681, SEQ ID NO:682, SEQ ID NO:683, SEQ ID NO:684, SEQ ID NO:685, SEQ ID NO:686, SEQ ID NO:687, SEQ ID NO:688, SEQ ID NO:689, SEQ ID NO:690, SEQ ID NO:691, SEQ ID NO:692, SEQ ID NO:693, SEQ ID NO:694, SEQ ID NO:695, SEQ ID NO:696, SEQ ID NO:697, SEQ ID  
30 NO:698, SEQ ID NO:699, SEQ ID NO:700, SEQ ID NO:701, SEQ ID NO:702, SEQ ID NO:703, SEQ ID NO:704, SEQ ID NO:705, SEQ ID NO:706, SEQ ID NO:707, SEQ ID NO:708, SEQ ID NO:709, SEQ ID NO:710, SEQ ID NO:711, SEQ ID NO:712, SEQ ID NO:713, SEQ ID NO:714, SEQ ID NO:715, SEQ ID NO:716, SEQ ID NO:717, SEQ ID NO:718 and SEQ ID NO:719, encoded by SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ  
35 ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID

NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, respectively, are, for example, human enzyme molecules.

SEQ ID NO:720, SEQ ID NO:721, SEQ ID NO:722, SEQ ID NO:723, SEQ ID NO:724, SEQ ID NO:725, SEQ ID NO:726, SEQ ID NO:727, SEQ ID NO:728, SEQ ID NO:729, SEQ ID NO:730, SEQ ID NO:731, SEQ ID NO:732, SEQ ID NO:733, SEQ ID NO:734, SEQ ID NO:735, SEQ ID NO:736, SEQ ID NO:737, SEQ ID NO:738, SEQ ID NO:739, SEQ ID NO:740, SEQ ID NO:741, SEQ ID NO:742, SEQ ID NO:743, SEQ ID NO:744 and SEQ ID NO:745, encoded by SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:73 and SEQ ID NO:74, respectively, are, for example, extracellular information transmission molecules.

SEQ ID NO:746, SEQ ID NO:747, SEQ ID NO:748, SEQ ID NO:749, SEQ ID NO:750, SEQ ID NO:751, SEQ ID NO:752, SEQ ID NO:753, SEQ ID NO:754, SEQ ID NO:755, SEQ ID NO:756, SEQ ID NO:757, SEQ ID NO:758, SEQ ID NO:759, SEQ ID NO:760, SEQ ID NO:761, SEQ ID NO:762, SEQ ID NO:763, SEQ ID NO:764, SEQ ID NO:765, SEQ ID NO:766, SEQ ID NO:767, SEQ ID NO:768, SEQ ID NO:769, SEQ ID NO:770, SEQ ID NO:771, SEQ ID NO:772, SEQ ID NO:773, SEQ ID NO:774, SEQ ID NO:775, SEQ ID NO:776, SEQ ID NO:777, SEQ ID NO:778, SEQ ID NO:779, SEQ ID NO:780, SEQ ID NO:781, SEQ ID NO:782, SEQ ID NO:783, SEQ ID NO:784, SEQ ID NO:785, SEQ ID NO:786, SEQ ID NO:787, SEQ ID NO:788 and SEQ ID NO:789, encoded by SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116 and SEQ ID NO:117, respectively, are, for example, receptor molecules.

SEQ ID NO:790, SEQ ID NO:791, SEQ ID NO:792, SEQ ID NO:793, SEQ ID NO:794, SEQ ID NO:795, SEQ ID NO:796, SEQ ID NO:797, SEQ ID NO:798, SEQ ID NO:799, SEQ ID NO:800,



SEQ ID NO:801, SEQ ID NO:802, SEQ ID NO:803, SEQ ID NO:804, SEQ ID NO:805, SEQ ID NO:806, SEQ ID NO:807, SEQ ID NO:808, SEQ ID NO:809, SEQ ID NO:810, SEQ ID NO:811, SEQ ID NO:812, SEQ ID NO:813, SEQ ID NO:814, SEQ ID NO:815, SEQ ID NO:816, SEQ ID NO:817, SEQ ID NO:818, SEQ ID NO:819, SEQ ID NO:820, SEQ ID NO:821, SEQ ID NO:822, SEQ ID NO:823, SEQ ID NO:824, SEQ ID NO:825, SEQ ID NO:826, SEQ ID NO:827, SEQ ID NO:828, SEQ ID NO:829, SEQ ID NO:830, SEQ ID NO:831, SEQ ID NO:832, SEQ ID NO:833, SEQ ID NO:834, SEQ ID NO:835, SEQ ID NO:836, SEQ ID NO:837, SEQ ID NO:838, SEQ ID NO:839, SEQ ID NO:840, SEQ ID NO:841, SEQ ID NO:842, SEQ ID NO:843, SEQ ID NO:844, SEQ ID NO:845, SEQ ID NO:846, SEQ ID NO:847, SEQ ID NO:848, SEQ ID NO:849, SEQ ID NO:850, SEQ ID NO:851, SEQ ID NO:852, SEQ ID NO:853, SEQ ID NO:854, SEQ ID NO:855, SEQ ID NO:856, SEQ ID NO:857, SEQ ID NO:858, SEQ ID NO:859, SEQ ID NO:860, SEQ ID NO:861, SEQ ID NO:862, SEQ ID NO:863, SEQ ID NO:864, SEQ ID NO:865, SEQ ID NO:866, SEQ ID NO:867 and SEQ ID NO:868, encoded by SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193 and SEQ ID NO:194, respectively, are, for example, intracellular signaling molecules.

SEQ ID NO:869, SEQ ID NO:870, SEQ ID NO:871, SEQ ID NO:872, SEQ ID NO:873, SEQ ID NO:874, SEQ ID NO:875, SEQ ID NO:876, SEQ ID NO:877, SEQ ID NO:878, SEQ ID NO:879, SEQ ID NO:880, SEQ ID NO:881, SEQ ID NO:882, SEQ ID NO:883, SEQ ID NO:884, SEQ ID NO:885, SEQ ID NO:886, SEQ ID NO:887, SEQ ID NO:888, SEQ ID NO:889, SEQ ID NO:890, SEQ ID NO:891, SEQ ID NO:892, SEQ ID NO:893, SEQ ID NO:894, SEQ ID NO:895, SEQ ID NO:896, SEQ ID NO:897, SEQ ID NO:898, SEQ ID NO:899, SEQ ID NO:900, SEQ ID NO:901, SEQ ID NO:902, SEQ ID NO:903 and SEQ ID NO:904, encoded by SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,

SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, 5 SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229 and SEQ ID NO:230, respectively, are, for example, transcription factor molecules.

SEQ ID NO:905, SEQ ID NO:906, SEQ ID NO:907, SEQ ID NO:908, SEQ ID NO:909, SEQ ID NO:910, SEQ ID NO:911, SEQ ID NO:912, SEQ ID NO:913, SEQ ID NO:914, SEQ ID NO:915, SEQ ID NO:916, SEQ ID NO:917, SEQ ID NO:918, SEQ ID NO:919, SEQ ID NO:920, SEQ ID 10 NO:921, SEQ ID NO:922, SEQ ID NO:923, SEQ ID NO:924, SEQ ID NO:925, SEQ ID NO:926, SEQ ID NO:927, SEQ ID NO:928, SEQ ID NO:929, SEQ ID NO:930, SEQ ID NO:931, SEQ ID NO:932, SEQ ID NO:933, SEQ ID NO:934, SEQ ID NO:935, SEQ ID NO:936, SEQ ID NO:937, SEQ ID NO:938, SEQ ID NO:939, SEQ ID NO:940, SEQ ID NO:941, SEQ ID NO:942, SEQ ID NO:943, SEQ ID NO:944, SEQ ID NO:945, SEQ ID NO:946, SEQ ID NO:947, SEQ ID NO:948, 15 SEQ ID NO:949, SEQ ID NO:950, SEQ ID NO:951, SEQ ID NO:952, SEQ ID NO:953, SEQ ID NO:954, SEQ ID NO:955, SEQ ID NO:956, SEQ ID NO:957, SEQ ID NO:958, SEQ ID NO:959, SEQ ID NO:960, SEQ ID NO:961, SEQ ID NO:962, SEQ ID NO:963, SEQ ID NO:964, SEQ ID NO:965, SEQ ID NO:966, SEQ ID NO:967, SEQ ID NO:968, SEQ ID NO:969, SEQ ID NO:970, SEQ ID NO:971, SEQ ID NO:972, SEQ ID NO:973, SEQ ID NO:974, SEQ ID NO:975, SEQ ID 20 NO:976, SEQ ID NO:977, SEQ ID NO:978, SEQ ID NO:979, SEQ ID NO:980, SEQ ID NO:981, SEQ ID NO:982, SEQ ID NO:983, SEQ ID NO:984, SEQ ID NO:985, SEQ ID NO:986, SEQ ID NO:987, SEQ ID NO:988, SEQ ID NO:989, SEQ ID NO:990, SEQ ID NO:991, SEQ ID NO:992, SEQ ID NO:993, SEQ ID NO:994, SEQ ID NO:995, SEQ ID NO:996, SEQ ID NO:997, SEQ ID NO:998, SEQ ID NO:999, SEQ ID NO:1000, SEQ ID NO:1001, SEQ ID NO:1002, SEQ ID 25 NO:1003, SEQ ID NO:1004, SEQ ID NO:1005, SEQ ID NO:1006, SEQ ID NO:1007, SEQ ID NO:1008, SEQ ID NO:1009, SEQ ID NO:1010, SEQ ID NO:1011, SEQ ID NO:1012, SEQ ID NO:1013, SEQ ID NO:1014, SEQ ID NO:1015, SEQ ID NO:1016, SEQ ID NO:1017 and SEQ ID NO:1018, encoded by SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, 30 SEQ ID NO:241, SEQ ID NO:242, SEQ ID NO:243, SEQ ID NO:244, SEQ ID NO:245, SEQ ID NO:246, SEQ ID NO:247, SEQ ID NO:248, SEQ ID NO:249, SEQ ID NO:250, SEQ ID NO:251, SEQ ID NO:252, SEQ ID NO:253, SEQ ID NO:254, SEQ ID NO:255, SEQ ID NO:256, SEQ ID NO:257, SEQ ID NO:258, SEQ ID NO:259, SEQ ID NO:260, SEQ ID NO:261, SEQ ID NO:262, SEQ ID NO:263, SEQ ID NO:264, SEQ ID NO:265, SEQ ID NO:266, SEQ ID NO:267, SEQ ID 35 NO:268, SEQ ID NO:269, SEQ ID NO:270, SEQ ID NO:271, SEQ ID NO:271, SEQ ID NO:272, SEQ ID NO:273, SEQ ID NO:274, SEQ ID NO:275, SEQ ID NO:276, SEQ ID NO:277, SEQ ID

NO:278, SEQ ID NO:279, SEQ ID NO:280, SEQ ID NO:281, SEQ ID NO:282, SEQ ID NO:283, SEQ ID NO:284, SEQ ID NO:285, SEQ ID NO:286, SEQ ID NO:287, SEQ ID NO:288, SEQ ID NO:289, SEQ ID NO:290, SEQ ID NO:291, SEQ ID NO:292, SEQ ID NO:293, SEQ ID NO:294, SEQ ID NO:295, SEQ ID NO:296, SEQ ID NO:297, SEQ ID NO:298, SEQ ID NO:299, SEQ ID NO:300, SEQ ID NO:301, SEQ ID NO:302, SEQ ID NO:303, SEQ ID NO:304, SEQ ID NO:305, SEQ ID NO:306, SEQ ID NO:307, SEQ ID NO:308, SEQ ID NO:309, SEQ ID NO:310, SEQ ID NO:311, SEQ ID NO:312, SEQ ID NO:313, SEQ ID NO:314, SEQ ID NO:315, SEQ ID NO:316, SEQ ID NO:317, SEQ ID NO:317, SEQ ID NO:318, SEQ ID NO:319, SEQ ID NO:320, SEQ ID NO:321, SEQ ID NO:322, SEQ ID NO:323, SEQ ID NO:324, SEQ ID NO:325, SEQ ID NO:326, SEQ ID NO:327, SEQ ID NO:328, SEQ ID NO:329, SEQ ID NO:330, SEQ ID NO:331, SEQ ID NO:332, SEQ ID NO:333, SEQ ID NO:334, SEQ ID NO:335, SEQ ID NO:336, SEQ ID NO:337, SEQ ID NO:338, SEQ ID NO:339, SEQ ID NO:340, SEQ ID NO:341 and SEQ ID NO:342, respectively, are, for example, zinc finger-type transcriptional regulators.

SEQ ID NO:1019, SEQ ID NO:1020, SEQ ID NO:1021, SEQ ID NO:1022, SEQ ID NO:1023, SEQ ID NO:1024, SEQ ID NO:1025, SEQ ID NO:1026, SEQ ID NO:1027, SEQ ID NO:1028, SEQ ID NO:1029, SEQ ID NO:1030, SEQ ID NO:1031, SEQ ID NO:1032, SEQ ID NO:1033, SEQ ID NO:1034, SEQ ID NO:1035, SEQ ID NO:1036, SEQ ID NO:1037, SEQ ID NO:1038, SEQ ID NO:1039, SEQ ID NO:1040, SEQ ID NO:1041, SEQ ID NO:1042 and SEQ ID NO:1043, encoded by SEQ ID NO:343, SEQ ID NO:344, SEQ ID NO:345, SEQ ID NO:346, SEQ ID NO:347, SEQ ID NO:348, SEQ ID NO:349, SEQ ID NO:350, SEQ ID NO:351, SEQ ID NO:352, SEQ ID NO:353, SEQ ID NO:354, SEQ ID NO:355, SEQ ID NO:356, SEQ ID NO:357, SEQ ID NO:358, SEQ ID NO:359, SEQ ID NO:360, SEQ ID NO:361, SEQ ID NO:362, SEQ ID NO:363, SEQ ID NO:364, SEQ ID NO:365, SEQ ID NO:366 and SEQ ID NO:367, respectively, are, for example, membrane transport molecules.

SEQ ID NO:1044, SEQ ID NO:1045, SEQ ID NO:1046, SEQ ID NO:1047, SEQ ID NO:1048, SEQ ID NO:1049, SEQ ID NO:1050, SEQ ID NO:1051, SEQ ID NO:1052, SEQ ID NO:1053, SEQ ID NO:1054, SEQ ID NO:1055, SEQ ID NO:1056, SEQ ID NO:1057, SEQ ID NO:1058, SEQ ID NO:1059, SEQ ID NO:1060, SEQ ID NO:1061, SEQ ID NO:1062, SEQ ID NO:1063, SEQ ID NO:1064, SEQ ID NO:1065, SEQ ID NO:1066, SEQ ID NO:1067, SEQ ID NO:1068, SEQ ID NO:1069, SEQ ID NO:1070, SEQ ID NO:1071, SEQ ID NO:1072, SEQ ID NO:1073, SEQ ID NO:1074, SEQ ID NO:1075, SEQ ID NO:1076, SEQ ID NO:1077 and SEQ ID NO:1078, encoded by SEQ ID NO:368, SEQ ID NO:369, SEQ ID NO:370, SEQ ID NO:371, SEQ ID NO:372, SEQ ID NO:373, SEQ ID NO:374, SEQ ID NO:375, SEQ ID NO:376, SEQ ID NO:377, SEQ ID NO:378, SEQ ID NO:379, SEQ ID NO:380, SEQ ID NO:381, SEQ ID NO:382, SEQ ID NO:383, SEQ ID NO:384, SEQ ID NO:385, SEQ ID NO:386, SEQ ID NO:387, SEQ ID NO:388, SEQ ID NO:389, SEQ ID NO:390, SEQ ID NO:391, SEQ ID NO:392, SEQ ID NO:393, SEQ ID

NO:394, SEQ ID NO:395, SEQ ID NO:396, SEQ ID NO:397, SEQ ID NO:398, SEQ ID NO:399, SEQ ID NO:400, SEQ ID NO:401 and SEQ ID NO:402, respectively, are, for example, protein modification and maintenance molecules.

5 SEQ ID NO:1079, SEQ ID NO:1080, SEQ ID NO:1081, SEQ ID NO:1082, SEQ ID NO:1083, SEQ ID NO:1084, SEQ ID NO:1085, SEQ ID NO:1086, SEQ ID NO:1087, SEQ ID NO:1088, SEQ ID NO:1089, SEQ ID NO:1090, SEQ ID NO:1091, SEQ ID NO:1092, SEQ ID NO:1093, SEQ ID NO:1094, SEQ ID NO:1095 and SEQ ID NO:1096, encoded by SEQ ID NO:403, SEQ ID NO:404, SEQ ID NO:405, SEQ ID NO:406, SEQ ID NO:407, SEQ ID NO:408, SEQ ID NO:409, SEQ ID NO:410, SEQ ID NO:411, SEQ ID NO:412, SEQ ID NO:413, SEQ ID NO:414, 10 SEQ ID NO:415, SEQ ID NO:416, SEQ ID NO:417, SEQ ID NO:418, SEQ ID NO:419 and SEQ ID NO:420, respectively, are, for example, nucleic acid synthesis and modification molecules.

SEQ ID NO:1097, SEQ ID NO:1098, SEQ ID NO:1099, SEQ ID NO:1100, SEQ ID NO:1101, SEQ ID NO:1102, SEQ ID NO:1103 and SEQ ID NO:1104, encoded by SEQ ID NO:421, SEQ ID NO:422, SEQ ID NO:423, SEQ ID NO:424, SEQ ID NO:425, SEQ ID NO:426, SEQ ID 15 NO:427 and SEQ ID NO:428, respectively, are, for example, adhesion molecules.

SEQ ID NO:1105, SEQ ID NO:1106, SEQ ID NO:1107, SEQ ID NO:1108, SEQ ID NO:1109, SEQ ID NO:1110, SEQ ID NO:1111, SEQ ID NO:1112, SEQ ID NO:1113, SEQ ID NO:1114, SEQ ID NO:1115, SEQ ID NO:1116, SEQ ID NO:1117, SEQ ID NO:1118, SEQ ID NO:1119, SEQ ID NO:1120, SEQ ID NO:1121, SEQ ID NO:1122, SEQ ID NO:1123, SEQ ID 20 NO:1124, SEQ ID NO:1125, SEQ ID NO:1126, SEQ ID NO:1127, SEQ ID NO:1128, SEQ ID NO:1129, SEQ ID NO:1130, SEQ ID NO:1131, SEQ ID NO:1132, SEQ ID NO:1133, SEQ ID NO:1134, SEQ ID NO:1135 and SEQ ID NO:1136, encoded by SEQ ID NO:429, SEQ ID NO:430, SEQ ID NO:431, SEQ ID NO:432, SEQ ID NO:433, SEQ ID NO:434, SEQ ID NO:435, SEQ ID NO:436, SEQ ID NO:437, SEQ ID NO:438, SEQ ID NO:439, SEQ ID NO:440, SEQ ID NO:441, 25 SEQ ID NO:442, SEQ ID NO:443, SEQ ID NO:444, SEQ ID NO:445, SEQ ID NO:446, SEQ ID NO:447, SEQ ID NO:448, SEQ ID NO:449, SEQ ID NO:450, SEQ ID NO:451, SEQ ID NO:452, SEQ ID NO:453, SEQ ID NO:454, SEQ ID NO:455, SEQ ID NO:456, SEQ ID NO:457, SEQ ID NO:458, SEQ ID NO:459 and SEQ ID NO:460, respectively, are, for example, antigen recognition molecules.

30 SEQ ID NO:1137, SEQ ID NO:1138, SEQ ID NO:1139, SEQ ID NO:1140, SEQ ID NO:1141, SEQ ID NO:1142, SEQ ID NO:1143, SEQ ID NO:1144 and SEQ ID NO:1145, encoded by SEQ ID NO:461, SEQ ID NO:462, SEQ ID NO:463, SEQ ID NO:464, SEQ ID NO:465, SEQ ID NO:466, SEQ ID NO:467, SEQ ID NO:468 and SEQ ID NO:469, respectively, are, for example, electron transfer associated molecules.

35 SEQ ID NO:1146, SEQ ID NO:1147, SEQ ID NO:1148, SEQ ID NO:1149, SEQ ID NO:1150, SEQ ID NO:1151, SEQ ID NO:1152, SEQ ID NO:1153, SEQ ID NO:1154, SEQ ID

NO:1155, SEQ ID NO:1156, SEQ ID NO:1157, SEQ ID NO:1158, SEQ ID NO:1159, SEQ ID NO:1160, SEQ ID NO:1161, SEQ ID NO:1162, SEQ ID NO:1163, SEQ ID NO:1164, SEQ ID NO:1165 and SEQ ID NO:1166, encoded by SEQ ID NO:470, SEQ ID NO:470, SEQ ID NO:471, SEQ ID NO:472, SEQ ID NO:473, SEQ ID NO:474, SEQ ID NO:475, SEQ ID NO:476, SEQ ID NO:477, SEQ ID NO:478, SEQ ID NO:479, SEQ ID NO:480, SEQ ID NO:481, SEQ ID NO:482, SEQ ID NO:483, SEQ ID NO:484, SEQ ID NO:485, SEQ ID NO:486, SEQ ID NO:487, SEQ ID NO:488 and SEQ ID NO:489, respectively, are, for example, secreted/extracellular matrix molecules.

SEQ ID NO:1167, SEQ ID NO:1168, SEQ ID NO:1169, SEQ ID NO:1170, SEQ ID NO:1171, SEQ ID NO:1172, SEQ ID NO:1173, SEQ ID NO:1174, SEQ ID NO:1175, SEQ ID NO:1176, SEQ ID NO:1177, SEQ ID NO:1178, SEQ ID NO:1179, SEQ ID NO:1180, SEQ ID NO:1181, SEQ ID NO:1182, SEQ ID NO:1183, SEQ ID NO:1184, SEQ ID NO:1185, SEQ ID NO:1186, SEQ ID NO:1187, SEQ ID NO:1188, SEQ ID NO:1189, SEQ ID NO:1190, SEQ ID NO:1191, SEQ ID NO:1192, SEQ ID NO:1193 and SEQ ID NO:1194, encoded by SEQ ID NO:490, SEQ ID NO:491, SEQ ID NO:492, SEQ ID NO:493, SEQ ID NO:494, SEQ ID NO:495, SEQ ID NO:496, SEQ ID NO:497, SEQ ID NO:498, SEQ ID NO:499, SEQ ID NO:500, SEQ ID NO:501, SEQ ID NO:502, SEQ ID NO:503, SEQ ID NO:504, SEQ ID NO:505, SEQ ID NO:506, SEQ ID NO:507, SEQ ID NO:508, SEQ ID NO:509, SEQ ID NO:510, SEQ ID NO:511, SEQ ID NO:512, SEQ ID NO:513, SEQ ID NO:514, SEQ ID NO:515, SEQ ID NO:516 and SEQ ID NO:517, respectively, are, for example, cytoskeletal molecules.

SEQ ID NO:1195, SEQ ID NO:1196, SEQ ID NO:1197, SEQ ID NO:1198, SEQ ID NO:1199, SEQ ID NO:1200, SEQ ID NO:1201, SEQ ID NO:1202, SEQ ID NO:1203, SEQ ID NO:1204, SEQ ID NO:1205, SEQ ID NO:1206, SEQ ID NO:1207, SEQ ID NO:1208, SEQ ID NO:1209, SEQ ID NO:1210, SEQ ID NO:1211, SEQ ID NO:1212 and SEQ ID NO:1213, encoded by SEQ ID NO:518, SEQ ID NO:519, SEQ ID NO:520, SEQ ID NO:521, SEQ ID NO:522, SEQ ID NO:523, SEQ ID NO:524, SEQ ID NO:525, SEQ ID NO:526, SEQ ID NO:527, SEQ ID NO:528, SEQ ID NO:529, SEQ ID NO:530, SEQ ID NO:531, SEQ ID NO:532, SEQ ID NO:533, SEQ ID NO:534, SEQ ID NO:535 and SEQ ID NO:536, respectively, are, for example, cell membrane molecules.

SEQ ID NO:1214, SEQ ID NO:1215, SEQ ID NO:1216, SEQ ID NO:1217, SEQ ID NO:1218, SEQ ID NO:1219, SEQ ID NO:1220, SEQ ID NO:1221, SEQ ID NO:1222, SEQ ID NO:1223, SEQ ID NO:1224, SEQ ID NO:1225, SEQ ID NO:1226, SEQ ID NO:1227, SEQ ID NO:1228, SEQ ID NO:1229, SEQ ID NO:1230, SEQ ID NO:1231, SEQ ID NO:1232, SEQ ID NO:1233, SEQ ID NO:1234, SEQ ID NO:1235, SEQ ID NO:1236, SEQ ID NO:1237, SEQ ID NO:1238, SEQ ID NO:1239, SEQ ID NO:1240, SEQ ID NO:1241, SEQ ID NO:1242 and SEQ ID NO:1243, encoded by SEQ ID NO:537, SEQ ID NO:538, SEQ ID NO:539, SEQ ID NO:540, SEQ ID NO:541, SEQ ID NO:542, SEQ ID NO:543, SEQ ID NO:544, SEQ ID NO:545, SEQ ID NO:546,

SEQ ID NO:547, SEQ ID NO:548, SEQ ID NO:549, SEQ ID NO:550, SEQ ID NO:551, SEQ ID NO:552, SEQ ID NO:553, SEQ ID NO:554, SEQ ID NO:555, SEQ ID NO:556, SEQ ID NO:557, SEQ ID NO:558, SEQ ID NO:559, SEQ ID NO:560, SEQ ID NO:561, SEQ ID NO:562, SEQ ID NO:563, SEQ ID NO:564, SEQ ID NO:565 and SEQ ID NO:566, respectively, are, for example, 5 ribosomal molecules.

SEQ ID NO:1244 and SEQ ID NO:1245, encoded by SEQ ID NO:567 and SEQ ID NO:568, respectively, are, for example, chromatin molecules.

SEQ ID NO:1246, SEQ ID NO:1247, SEQ ID NO:1248, SEQ ID NO:1249, SEQ ID NO:1250, SEQ ID NO:1251, SEQ ID NO:1252, SEQ ID NO:1253, SEQ ID NO:1254, SEQ ID NO:1255, SEQ ID NO:1256, SEQ ID NO:1257, SEQ ID NO:1258, SEQ ID NO:1259, SEQ ID NO:1260, SEQ ID NO:1261, SEQ ID NO:1262, SEQ ID NO:1263, SEQ ID NO:1264, SEQ ID NO:1265, SEQ ID NO:1266, SEQ ID NO:1267, SEQ ID NO:1268, SEQ ID NO:1269, SEQ ID NO:1270, SEQ ID NO:1271, SEQ ID NO:1272, SEQ ID NO:1273, SEQ ID NO:1274, SEQ ID NO:1275, SEQ ID NO:1276 and SEQ ID NO:1277, encoded by SEQ ID NO:569, SEQ ID NO:570; 15 SEQ ID NO:571, SEQ ID NO:572, SEQ ID NO:573, SEQ ID NO:574, SEQ ID NO:575, SEQ ID NO:576, SEQ ID NO:577, SEQ ID NO:578, SEQ ID NO:579, SEQ ID NO:580, SEQ ID NO:581, SEQ ID NO:582, SEQ ID NO:583, SEQ ID NO:584, SEQ ID NO:585, SEQ ID NO:586, SEQ ID NO:587, SEQ ID NO:588, SEQ ID NO:589, SEQ ID NO:590, SEQ ID NO:591, SEQ ID NO:592, SEQ ID NO:593, SEQ ID NO:594, SEQ ID NO:595, SEQ ID NO:596, SEQ ID NO:597, SEQ ID NO:598, SEQ ID NO:599 and SEQ ID NO:600, respectively, are, for example, organelle associated 20 molecules.

SEQ ID NO:1278, SEQ ID NO:1279, SEQ ID NO:1280, SEQ ID NO:1281, SEQ ID NO:1282, SEQ ID NO:1283, SEQ ID NO:1284, SEQ ID NO:1285, SEQ ID NO:1286, SEQ ID NO:1287, SEQ ID NO:1288, SEQ ID NO:1289, SEQ ID NO:1290, SEQ ID NO:1291, SEQ ID NO:1292, SEQ ID NO:1293, SEQ ID NO:1294, SEQ ID NO:1295, SEQ ID NO:1296, SEQ ID NO:1297, SEQ ID NO:1298, SEQ ID NO:1299, SEQ ID NO:1300, SEQ ID NO:1301, SEQ ID NO:1302, SEQ ID NO:1303, SEQ ID NO:1304, SEQ ID NO:1305, SEQ ID NO:1306 and SEQ ID NO:1307, encoded by SEQ ID NO:601, SEQ ID NO:602, SEQ ID NO:603, SEQ ID NO:604, SEQ ID NO:605, SEQ ID NO:606, SEQ ID NO:607, SEQ ID NO:608, SEQ ID NO:609, SEQ ID NO:610, 30 SEQ ID NO:611, SEQ ID NO:612, SEQ ID NO:613, SEQ ID NO:614, SEQ ID NO:615, SEQ ID NO:616, SEQ ID NO:617, SEQ ID NO:618, SEQ ID NO:619, SEQ ID NO:620, SEQ ID NO:621, SEQ ID NO:622, SEQ ID NO:623, SEQ ID NO:624, SEQ ID NO:625, SEQ ID NO:626, SEQ ID NO:627, SEQ ID NO:628, SEQ ID NO:629 and SEQ ID NO:630, respectively, are, for example, biochemical pathway molecules.

SEQ ID NO:1308, SEQ ID NO:1309, SEQ ID NO:1310, SEQ ID NO:1311, SEQ ID NO:1312, SEQ ID NO:1313, SEQ ID NO:1314, SEQ ID NO:1315, SEQ ID NO:1316, SEQ ID

NO:1317, SEQ ID NO:1318, SEQ ID NO:1319, SEQ ID NO:1320, SEQ ID NO:1321, SEQ ID NO:1322, SEQ ID NO:1323, SEQ ID NO:1324, SEQ ID NO:1325, SEQ ID NO:1326, SEQ ID NO:1327, SEQ ID NO:1328, SEQ ID NO:1329, SEQ ID NO:1330, SEQ ID NO:1331, SEQ ID NO:1332, SEQ ID NO:1333, SEQ ID NO:1334, SEQ ID NO:1335, SEQ ID NO:1336, SEQ ID NO:1337, SEQ ID NO:1338, SEQ ID NO:1339, SEQ ID NO:1340, SEQ ID NO:1341, SEQ ID NO:1342, SEQ ID NO:1343, SEQ ID NO:1344, SEQ ID NO:1345, SEQ ID NO:1346 and SEQ ID NO:1347, encoded by SEQ ID NO:631, SEQ ID NO:632, SEQ ID NO:633, SEQ ID NO:634, SEQ ID NO:635, SEQ ID NO:636, SEQ ID NO:637, SEQ ID NO:638, SEQ ID NO:639, SEQ ID NO:640, SEQ ID NO:641, SEQ ID NO:642, SEQ ID NO:643, SEQ ID NO:644, SEQ ID NO:645, SEQ ID NO:646, SEQ ID NO:647, SEQ ID NO:648, SEQ ID NO:649, SEQ ID NO:650, SEQ ID NO:651, SEQ ID NO:652, SEQ ID NO:653, SEQ ID NO:654, SEQ ID NO:655, SEQ ID NO:656, SEQ ID NO:657, SEQ ID NO:658, SEQ ID NO:659, SEQ ID NO:660, SEQ ID NO:661, SEQ ID NO:662, SEQ ID NO:663, SEQ ID NO:664, SEQ ID NO:665, SEQ ID NO:666, SEQ ID NO:667, SEQ ID NO:668, SEQ ID NO:669 and SEQ ID NO:670, respectively, are, for example, molecules associated with growth and development.

#### Sequences of Human Diagnostic and Therapeutic Molecules

The dithp of the present invention may be used for a variety of diagnostic and therapeutic purposes. For example, a dithp may be used to diagnose a particular condition, disease, or disorder associated with human molecules. Such conditions, diseases, and disorders include, but are not limited to, a cell proliferative disorder, such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, a cancer of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; an autoimmune/inflammatory disorder, such as inflammation, actinic keratosis, acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, arteriosclerosis, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, bronchitis, bursitis, cholecystitis, cirrhosis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, paroxysmal nocturnal hemoglobinuria, hepatitis, hypereosinophilia, irritable bowel syndrome, episodic lymphopenia with lymphocytotoxins, mixed connective tissue disease (MCTD), multiple sclerosis, myasthenia gravis,

myocardial or pericardial inflammation, myelofibrosis, osteoarthritis, osteoporosis, pancreatitis, polycythemia vera, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, primary thrombocythemia, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome,

5 complications of cancer, hemodialysis, and extracorporeal circulation, trauma, and hematopoietic cancer including lymphoma, leukemia, and myeloma; an infection caused by a viral agent classified as adenovirus, arenavirus, bunyavirus, calicivirus, coronavirus, filovirus, hepadnavirus, herpesvirus, flavivirus, orthomyxovirus, parvovirus, papovavirus, paramyxovirus, picornavirus, poxvirus, reovirus, retrovirus, rhabdovirus, or togavirus; an infection caused by a bacterial agent classified as

10 pneumococcus, staphylococcus, streptococcus, bacillus, corynebacterium, clostridium, meningococcus, gonococcus, listeria, moraxella, kingella, haemophilus, legionella, bordetella, gram-negative enterobacterium including shigella, salmonella, or campylobacter, pseudomonas, vibrio, brucella, francisella, yersinia, bartonella, norcardium, actinomyces, mycobacterium, spirochaetale, rickettsia, chlamydia, or mycoplasma; an infection caused by a fungal agent classified as aspergillus,

15 blastomyces, dermatophytes, cryptococcus, coccidioides, malassezia, histoplasma, or other mycosis-causing fungal agent; and an infection caused by a parasite classified as plasmodium or malaria-causing, parasitic entamoeba, leishmania, trypanosoma, toxoplasma, pneumocystis carinii, intestinal protozoa such as giardia, trichomonas, tissue nematode such as trichinella, intestinal nematode such as ascaris, lymphatic filarial nematode, trematode such as schistosoma, and cestode such as

20 tapeworm; a developmental disorder such as renal tubular acidosis, anemia, Cushing's syndrome, achondroplastic dwarfism, Duchenne and Becker muscular dystrophy, epilepsy, gonadal dysgenesis, WAGR syndrome (Wilms' tumor, aniridia, genitourinary abnormalities, and mental retardation), Smith-Magenis syndrome, myelodysplastic syndrome, hereditary mucoepithelial dysplasia, hereditary keratodermas, hereditary neuropathies such as Charcot-Marie-Tooth disease and

25 neurofibromatosis, hypothyroidism, hydrocephalus, seizure disorders such as Sydenham's chorea and cerebral palsy, spina bifida, anencephaly, craniorachischisis, congenital glaucoma, cataract, and sensorineural hearing loss; an endocrine disorder such as a disorder of the hypothalamus and/or pituitary resulting from lesions such as a primary brain tumor, adenoma, infarction associated with pregnancy, hypophysectomy, aneurysm, vascular malformation, thrombosis, infection, immunological

30 disorder, and complication due to head trauma; a disorder associated with hypopituitarism including hypogonadism, Sheehan syndrome, diabetes insipidus, Kallman's disease, Hand-Schuller-Christian disease, Letterer-Siwe disease, sarcoidosis, empty sella syndrome, and dwarfism; a disorder associated with hyperpituitarism including acromegaly, gigantism, and syndrome of inappropriate antidiuretic hormone (ADH) secretion (SIADH) often caused by benign adenoma; a disorder

35 associated with hypothyroidism including goiter, myxedema, acute thyroiditis associated with bacterial infection, subacute thyroiditis associated with viral infection, autoimmune thyroiditis



(Hashimoto's disease), and cretinism; a disorder associated with hyperthyroidism including thyrotoxicosis and its various forms, Grave's disease, pretibial myxedema, toxic multinodular goiter, thyroid carcinoma, and Plummer's disease; a disorder associated with hyperparathyroidism including Conn disease (chronic hypercalcemia); a pancreatic disorder such as Type I or Type II diabetes mellitus and associated complications; a disorder associated with the adrenals such as hyperplasia, carcinoma, or adenoma of the adrenal cortex, hypertension associated with alkalosis, amyloidosis, hypokalemia, Cushing's disease, Liddle's syndrome, and Arnold-Healy-Gordon syndrome, pheochromocytoma tumors, and Addison's disease; a disorder associated with gonadal steroid hormones such as: in women, abnormal prolactin production, infertility, endometriosis, perturbation of the menstrual cycle, polycystic ovarian disease, hyperprolactinemia, isolated gonadotropin deficiency, amenorrhea, galactorrhea, hermaphroditism, hirsutism and virilization, breast cancer, and, in post-menopausal women, osteoporosis; and, in men, Leydig cell deficiency, male climacteric phase, and germinal cell aplasia, a hypergonadal disorder associated with Leydig cell tumors, androgen resistance associated with absence of androgen receptors, syndrome of 5  $\alpha$ -reductase, and gynecomastia; a metabolic disorder such as Addison's disease, cerebrotendinous xanthomatosis, congenital adrenal hyperplasia, coumarin resistance, cystic fibrosis, diabetes, fatty hepatocirrhosis, fructose-1,6-diphosphatase deficiency, galactosemia, goiter, glucagonoma, glycogen storage diseases, hereditary fructose intolerance, hyperadrenalism, hypoadrenalism, hyperparathyroidism, hypoparathyroidism, hypercholesterolemia, hyperthyroidism, hypoglycemia, hypothyroidism, hyperlipidemia, hyperlipemia, lipid myopathies, lipodystrophies, lysosomal storage diseases, mannosidosis, neuraminidase deficiency, obesity, pentosuria phenylketonuria, pseudovitamin D-deficiency rickets; disorders of carbohydrate metabolism such as congenital type II dyserythropoietic anemia, diabetes, insulin-dependent diabetes mellitus, non-insulin-dependent diabetes mellitus, fructose-1,6-diphosphatase deficiency, galactosemia, glucagonoma, hereditary fructose intolerance, hypoglycemia, mannosidosis, neuraminidase deficiency, obesity, galactose epimerase deficiency, glycogen storage diseases, lysosomal storage diseases, fructosuria, pentosuria, and inherited abnormalities of pyruvate metabolism; disorders of lipid metabolism such as fatty liver, cholestasis, primary biliary cirrhosis, carnitine deficiency, carnitine palmitoyltransferase deficiency, myoadenylate deaminase deficiency, hypertriglyceridemia, lipid storage disorders such as Fabry's disease, Gaucher's disease, Niemann-Pick's disease, metachromatic leukodystrophy, adrenoleukodystrophy, GM<sub>2</sub> gangliosidosis, and ceroid lipofuscinosis, abetalipoproteinemia, Tangier disease, hyperlipoproteinemia, diabetes mellitus, lipodystrophy, lipomatosis, acute panniculitis, disseminated fat necrosis, adiposis dolorosa, lipid adrenal hyperplasia, minimal change disease, lipomas, atherosclerosis, hypercholesterolemia, hypercholesterolemia with hypertriglyceridemia, primary hypoalphalipoproteinemia, hypothyroidism, renal disease, liver disease, lecithin:cholesterol acyltransferase deficiency, cerebrotendinous xanthomatosis, sitosterolemia, hypocholesterolemia,

Tay-Sachs disease, Sandhoff's disease, hyperlipidemia, hyperlipemia, lipid myopathies, and obesity; and disorders of copper metabolism such as Menke's disease, Wilson's disease, and Ehlers-Danlos syndrome type IX; a neurological disorder such as epilepsy, ischemic cerebrovascular disease, stroke, cerebral neoplasms, Alzheimer's disease, Pick's disease, Huntington's disease, dementia, Parkinson's disease and other extrapyramidal disorders, amyotrophic lateral sclerosis and other motor neuron disorders, progressive neural muscular atrophy, retinitis pigmentosa, hereditary ataxias, multiple sclerosis and other demyelinating diseases, bacterial and viral meningitis, brain abscess, subdural empyema, epidural abscess, suppurative intracranial thrombophlebitis, myelitis and radiculitis, viral central nervous system disease, prion diseases including kuru, Creutzfeldt-Jakob disease, and

10 Gerstmann-Straussler-Scheinker syndrome, fatal familial insomnia, nutritional and metabolic diseases of the nervous system, neurofibromatosis, tuberous sclerosis, cerebelloretinal hemangioblastomatosis, encephalotrigeminal syndrome, mental retardation and other developmental disorder of the central nervous system, cerebral palsy, a neuroskeletal disorder, an autonomic nervous system disorder, a cranial nerve disorder, a spinal cord disease, muscular dystrophy and other neuromuscular disorder, a

15 peripheral nervous system disorder, dermatomyositis and polymyositis, inherited, metabolic, endocrine, and toxic myopathy, myasthenia gravis, periodic paralysis, a mental disorder including mood, anxiety, and schizophrenic disorders, seasonal affective disorder (SAD), akathisia, amnesia, catatonia, diabetic neuropathy, tardive dyskinesia, dystonias, paranoid psychoses, postherpetic neuralgia, and Tourette's disorder; a gastrointestinal disorder including ulcerative colitis, gastric and

20 duodenal ulcers, cystinuria, dibasicaminoaciduria, hypercystinuria, lysinuria, hartnup disease, tryptophan malabsorption, methionine malabsorption, histidinuria, iminoglycinuria, dicarboxylicaminoaciduria, cystinosis, renal glycosuria, hypouricemia, familial hypophosphatemic rickets, congenital chloridorrhea, distal renal tubular acidosis, Menkes' disease, Wilson's disease, lethal diarrhea, juvenile pernicious anemia, folate malabsorption, adrenoleukodystrophy, hereditary

25 myoglobinuria, and Zellweger syndrome; a transport disorder such as akinesia, amyotrophic lateral sclerosis, ataxia telangiectasia, cystic fibrosis, Becker's muscular dystrophy, Bell's palsy, Charcot-Marie Tooth disease, diabetes mellitus, diabetes insipidus, diabetic neuropathy, Duchenne muscular dystrophy, hyperkalemic periodic paralysis, normokalemic periodic paralysis, Parkinson's disease, malignant hyperthermia, multidrug resistance, myasthenia gravis, myotonic dystrophy, catatonia,

30 tardive dyskinesia, dystonias, peripheral neuropathy, cerebral neoplasms, prostate cancer, cardiac disorders associated with transport, e.g., angina, bradyarrhythmia, tachyarrhythmia, hypertension, Long QT syndrome, myocarditis, cardiomyopathy, nemaline myopathy, centronuclear myopathy, lipid myopathy, mitochondrial myopathy, thyrotoxic myopathy, ethanol myopathy, dermatomyositis, inclusion body myositis, infectious myositis, and polymyositis, neurological disorders associated

35 with transport, e.g., Alzheimer's disease, amnesia, bipolar disorder, dementia, depression, epilepsy, Tourette's disorder, paranoid psychoses, and schizophrenia, and other disorders associated with

transport, e.g., neurofibromatosis, postherpetic neuralgia, trigeminal neuropathy, sarcoidosis, sickle cell anemia, cataracts, infertility, pulmonary artery stenosis, sensorineural autosomal deafness, hyperglycemia, hypoglycemia, Grave's disease, goiter, glucose-galactose malabsorption syndrome, hypercholesterolemia, Cushing's disease, and Addison's disease; and a connective tissue disorder

5 such as osteogenesis imperfecta, Ehlers-Danlos syndrome, chondrodysplasias, Marfan syndrome, Alport syndrome, familial aortic aneurysm, achondroplasia, mucopolysaccharidoses, osteoporosis, osteopetrosis, Paget's disease, rickets, osteomalacia, hyperparathyroidism, renal osteodystrophy, osteonecrosis, osteomyelitis, osteoma, osteoid osteoma, osteoblastoma, osteosarcoma, osteochondroma, chondroma, chondroblastoma, chondromyxoid fibroma, chondrosarcoma, fibrous

10 cortical defect, nonossifying fibroma, fibrous dysplasia, fibrosarcoma, malignant fibrous histiocytoma, Ewing's sarcoma, primitive neuroectodermal tumor, giant cell tumor, osteoarthritis, rheumatoid arthritis, ankylosing spondyloarthritis, Reiter's syndrome, psoriatic arthritis, enteropathic arthritis, infectious arthritis, gout, gouty arthritis, calcium pyrophosphate crystal deposition disease, ganglion, synovial cyst, villonodular synovitis, systemic sclerosis, Dupuytren's contracture, hepatic

15 fibrosis, lupus erythematosus, mixed connective tissue disease, epidermolysis bullosa simplex, bullous congenital ichthyosiform erythroderma (epidermolytic hyperkeratosis), non-epidermolytic and epidermolytic palmoplantar keratoderma, ichthyosis bullosa of Siemens, pachyonychia congenita, and white sponge nevus. The dithp can be used to detect the presence of, or to quantify the amount of, a dithp-related polynucleotide in a sample. This information is then compared to information

20 obtained from appropriate reference samples, and a diagnosis is established. Alternatively, a polynucleotide complementary to a given dithp can inhibit or inactivate a therapeutically relevant gene related to the dithp.

#### Analysis of dithp Expression Patterns

25 The expression of dithp may be routinely assessed by hybridization-based methods to determine, for example, the tissue-specificity, disease-specificity, or developmental stage-specificity of dithp expression. For example, the level of expression of dithp may be compared among different cell types or tissues, among diseased and normal cell types or tissues, among cell types or tissues at different developmental stages, or among cell types or tissues undergoing various treatments. This

30 type of analysis is useful, for example, to assess the relative levels of dithp expression in fully or partially differentiated cells or tissues, to determine if changes in dithp expression levels are correlated with the development or progression of specific disease states, and to assess the response of a cell or tissue to a specific therapy, for example, in pharmacological or toxicological studies. Methods for the analysis of dithp expression are based on hybridization and amplification

35 technologies and include membrane-based procedures such as northern blot analysis, high-throughput procedures that utilize, for example, microarrays, and PCR-based procedures.

Hybridization and Genetic Analysis

The dithp, their fragments, or complementary sequences, may be used to identify the presence of and/or to determine the degree of similarity between two (or more) nucleic acid sequences. The dithp may be hybridized to naturally occurring or recombinant nucleic acid sequences under  
5 appropriately selected temperatures and salt concentrations. Hybridization with a probe based on the nucleic acid sequence of at least one of the dithp allows for the detection of nucleic acid sequences, including genomic sequences, which are identical or related to the dithp of the Sequence Listing. Probes may be selected from non-conserved or unique regions of at least one of the polynucleotides of SEQ ID NO:1-670 and tested for their ability to identify or amplify the target nucleic acid  
10 sequence using standard protocols.

Polynucleotide sequences that are capable of hybridizing, in particular, to those shown in SEQ ID NO:1-670 and fragments thereof, can be identified using various conditions of stringency. (See, e.g., Wahl, G.M. and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) Hybridization conditions are discussed in "Definitions."

15 A probe for use in Southern or northern hybridization may be derived from a fragment of a dithp sequence, or its complement, that is up to several hundred nucleotides in length and is either single-stranded or double-stranded. Such probes may be hybridized in solution to biological materials such as plasmids, bacterial, yeast, or human artificial chromosomes, cleared or sectioned tissues, or to artificial substrates containing dithp. Microarrays are particularly suitable for identifying the  
20 presence of and detecting the level of expression for multiple genes of interest by examining gene expression correlated with, e.g., various stages of development, treatment with a drug or compound, or disease progression. An array analogous to a dot or slot blot may be used to arrange and link polynucleotides to the surface of a substrate using one or more of the following: mechanical (vacuum), chemical, thermal, or UV bonding procedures. Such an array may contain any number of  
25 dithp and may be produced by hand or by using available devices, materials, and machines.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) *Proc. Natl. Acad. Sci. USA* 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) *Proc. Natl. Acad. Sci. USA* 94:2150-  
30 2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)

Probes may be labeled by either PCR or enzymatic techniques using a variety of commercially available reporter molecules. For example, commercial kits are available for radioactive and chemiluminescent labeling (Amersham Pharmacia Biotech) and for alkaline phosphatase labeling (Life Technologies). Alternatively, dithp may be cloned into commercially  
35 available vectors for the production of RNA probes. Such probes may be transcribed in the presence of at least one labeled nucleotide (e.g., <sup>32</sup>P-ATP, Amersham Pharmacia Biotech).

Additionally the polynucleotides of SEQ ID NO:1-670 or suitable fragments thereof can be used to isolate full length cDNA sequences utilizing hybridization and/or amplification procedures well known in the art, e.g., cDNA library screening, PCR amplification, etc. The molecular cloning of such full length cDNA sequences may employ the method of cDNA library screening with probes  
5 using the hybridization, stringency, washing, and probing strategies described above and in Ausubel, supra, Chapters 3, 5, and 6. These procedures may also be employed with genomic libraries to isolate genomic sequences of dithp in order to analyze, e.g., regulatory elements. Genetic Mapping

Gene identification and mapping are important in the investigation and treatment of almost all conditions, diseases, and disorders. Cancer, cardiovascular disease, Alzheimer's disease, arthritis,  
10 diabetes, and mental illnesses are of particular interest. Each of these conditions is more complex than the single gene defects of sickle cell anemia or cystic fibrosis, with select groups of genes being predictive of predisposition for a particular condition, disease, or disorder. For example, cardiovascular disease may result from malfunctioning receptor molecules that fail to clear cholesterol from the bloodstream, and diabetes may result when a particular individual's immune  
15 system is activated by an infection and attacks the insulin-producing cells of the pancreas. In some studies, Alzheimer's disease has been linked to a gene on chromosome 21; other studies predict a different gene and location. Mapping of disease genes is a complex and reiterative process and generally proceeds from genetic linkage analysis to physical mapping.

As a condition is noted among members of a family, a genetic linkage map traces parts of  
20 chromosomes that are inherited in the same pattern as the condition. Statistics link the inheritance of particular conditions to particular regions of chromosomes, as defined by RFLP or other markers. (See, for example, Lander, E. S. and Botstein, D. (1986) Proc. Natl. Acad. Sci. USA 83:7353-7357.) Occasionally, genetic markers and their locations are known from previous studies. More often, however, the markers are simply stretches of DNA that differ among individuals. Examples of  
25 genetic linkage maps can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) World Wide Web site.

In another embodiment of the invention, dithp sequences may be used to generate hybridization probes useful in chromosomal mapping of naturally occurring genomic sequences. Either coding or noncoding sequences of dithp may be used, and in some instances, noncoding  
30 sequences may be preferable over coding sequences. For example, conservation of a dithp coding sequence among members of a multi-gene family may potentially cause undesired cross hybridization during chromosomal mapping. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes  
35 (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355; Price, C.M. (1993) Blood Rev. 7:127-134; and Trask, B.J.

(1991) Trends Genet. 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data. (See, e.g., Meyers, supra, pp. 965-968.) Correlation between the location of dithp on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The dithp sequences may also be used to detect polymorphisms that are genetically linked to the inheritance of a particular condition, disease, or disorder.

In situ hybridization of chromosomal preparations and genetic mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending existing genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of the corresponding human chromosome is not known. These new marker sequences can be mapped to human chromosomes and may provide valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once a disease or syndrome has been crudely correlated by genetic linkage with a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequences of the subject invention may also be used to detect differences in chromosomal architecture due to translocation, inversion, etc., among normal, carrier, or affected individuals.

Once a disease-associated gene is mapped to a chromosomal region, the gene must be cloned in order to identify mutations or other alterations (e.g., translocations or inversions) that may be correlated with disease. This process requires a physical map of the chromosomal region containing the disease-gene of interest along with associated markers. A physical map is necessary for determining the nucleotide sequence of and order of marker genes on a particular chromosomal region. Physical mapping techniques are well known in the art and require the generation of overlapping sets of cloned DNA fragments from a particular organelle, chromosome, or genome. These clones are analyzed to reconstruct and catalog their order. Once the position of a marker is determined, the DNA from that region is obtained by consulting the catalog and selecting clones from that region. The gene of interest is located through positional cloning techniques using hybridization or similar methods.

#### Diagnostic Uses

The dithp of the present invention may be used to design probes useful in diagnostic assays. Such assays, well known to those skilled in the art, may be used to detect or confirm conditions, disorders, or diseases associated with abnormal levels of dithp expression. Labeled probes developed from dithp sequences are added to a sample under hybridizing conditions of desired stringency. In

some instances, dithp, or fragments or oligonucleotides derived from dithp, may be used as primers in amplification steps prior to hybridization. The amount of hybridization complex formed is quantified and compared with standards for that cell or tissue. If dithp expression varies significantly from the standard, the assay indicates the presence of the condition, disorder, or disease. Qualitative or  
5 quantitative diagnostic methods may include northern, dot blot, or other membrane or dip-stick based technologies or multiple-sample format technologies such as PCR, enzyme-linked immunosorbent assay (ELISA)-like, pin, or chip-based assays.

The probes described above may also be used to monitor the progress of conditions, disorders, or diseases associated with abnormal levels of dithp expression, or to evaluate the efficacy  
10 of a particular therapeutic treatment. The candidate probe may be identified from the dithp that are specific to a given human tissue and have not been observed in GenBank or other genome databases. Such a probe may be used in animal studies, preclinical tests, clinical trials, or in monitoring the treatment of an individual patient. In a typical process, standard expression is established by methods well known in the art for use as a basis of comparison, samples from patients affected by the disorder  
15 or disease are combined with the probe to evaluate any deviation from the standard profile, and a therapeutic agent is administered and effects are monitored to generate a treatment profile. Efficacy is evaluated by determining whether the expression progresses toward or returns to the standard normal pattern. Treatment profiles may be generated over a period of several days or several months. Statistical methods well known to those skilled in the art may be use to determine the significance of  
20 such therapeutic agents.

The polynucleotides are also useful for identifying individuals from minute biological samples, for example, by matching the RFLP pattern of a sample's DNA to that of an individual's DNA. The polynucleotides of the present invention can also be used to determine the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be  
25 used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, an individual can be identified through a unique set of DNA sequences. Once a unique ID database is established for an individual, positive identification of that individual can be made from extremely small tissue samples.

In a particular aspect, oligonucleotide primers derived from the dithp of the invention may be  
30 used to detect single nucleotide polymorphisms (SNPs). SNPs are substitutions, insertions and deletions that are a frequent cause of inherited or acquired genetic disease in humans. Methods of SNP detection include, but are not limited to, single-stranded conformation polymorphism (SSCP) and fluorescent SSCP (fSSCP) methods. In SSCP, oligonucleotide primers derived from dithp are used to amplify DNA using the polymerase chain reaction (PCR). The DNA may be derived, for  
35 example, from diseased or normal tissue, biopsy samples, bodily fluids, and the like. SNPs in the DNA cause differences in the secondary and tertiary structures of PCR products in single-stranded

form, and these differences are detectable using gel electrophoresis in non-denaturing gels. In fSCCP, the oligonucleotide primers are fluorescently labeled, which allows detection of the amplimers in high-throughput equipment such as DNA sequencing machines. Additionally, sequence database analysis methods, termed in silico SNP (isSNP), are capable of identifying polymorphisms by comparing the sequences of individual overlapping DNA fragments which assemble into a common consensus sequence. These computer-based methods filter out sequence variations due to laboratory preparation of DNA and sequencing errors using statistical models and automated analyses of DNA sequence chromatograms. In the alternative, SNPs may be detected and characterized by mass spectrometry using, for example, the high throughput MASSARRAY system (Sequenom, Inc., San Diego CA).

DNA-based identification techniques are critical in forensic technology. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using, e.g., PCR, to identify individuals. (See, e.g., Erlich, H. (1992) PCR Technology, Freeman and Co., New York, NY). Similarly, polynucleotides of the present invention can be used as polymorphic markers.

There is also a need for reagents capable of identifying the source of a particular tissue. Appropriate reagents can comprise, for example, DNA probes or primers prepared from the sequences of the present invention that are specific for particular tissues. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

The polynucleotides of the present invention can also be used as molecular weight markers on nucleic acid gels or Southern blots, as diagnostic probes for the presence of a specific mRNA in a particular cell type, in the creation of subtracted cDNA libraries which aid in the discovery of novel polynucleotides, in selection and synthesis of oligomers for attachment to an array or other support, and as an antigen to elicit an immune response.

#### Disease Model Systems Using dithp

The dithp of the invention or their mammalian homologs may be "knocked out" in an animal model system using homologous recombination in embryonic stem (ES) cells. Such techniques are well known in the art and are useful for the generation of animal models of human disease. (See, e.g., U.S. Patent Number 5,175,383 and U.S. Patent Number 5,767,337.) For example, mouse ES cells, such as the mouse 129/SvJ cell line, are derived from the early mouse embryo and grown in culture. The ES cells are transformed with a vector containing the gene of interest disrupted by a marker gene, e.g., the neomycin phosphotransferase gene (neo; Capecchi, M.R. (1989) *Science* 244:1288-1292). The vector integrates into the corresponding region of the host genome by homologous recombination. Alternatively, homologous recombination takes place using the Cre-loxP system to



knockout a gene of interest in a tissue- or developmental stage-specific manner (Marth, J.D. (1996) Clin. Invest. 97:1999-2002; Wagner, K.U. et al. (1997) Nucleic Acids Res. 25:4323-4330).

Transformed ES cells are identified and microinjected into mouse cell blastocysts such as those from the C57BL/6 mouse strain. The blastocysts are surgically transferred to pseudopregnant dams, and the resulting chimeric progeny are genotyped and bred to produce heterozygous or homozygous strains. Transgenic animals thus generated may be tested with potential therapeutic or toxic agents.

The dithp of the invention may also be manipulated in vitro in ES cells derived from human blastocysts. Human ES cells have the potential to differentiate into at least eight separate cell lineages including endoderm, mesoderm, and ectodermal cell types. These cell lineages differentiate into, for example, neural cells, hematopoietic lineages, and cardiomyocytes (Thomson, J.A. et al. (1998) Science 282:1145-1147).

The dithp of the invention can also be used to create "knockin" humanized animals (pigs) or transgenic animals (mice or rats) to model human disease. With knockin technology, a region of dithp is injected into animal ES cells, and the injected sequence integrates into the animal cell genome. Transformed cells are injected into blastulae, and the blastulae are implanted as described above. Transgenic progeny or inbred lines are studied and treated with potential pharmaceutical agents to obtain information on treatment of a human disease. Alternatively, a mammal inbred to overexpress dithp, resulting, e.g., in the secretion of DITHP in its milk, may also serve as a convenient source of that protein (Janne, J. et al. (1998) Biotechnol. Annu. Rev. 4:55-74).

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#### Screening Assays

DITHP encoded by polynucleotides of the present invention may be used to screen for molecules that bind to or are bound by the encoded polypeptides. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the bound molecule. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a ligand or fragment thereof, a natural substrate, or a structural or functional mimetic. (See, Coligan et al., (1991) Current Protocols in Immunology 1(2): Chapter 5.) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or to at least a fragment of the receptor, e.g., the active site. In either case, the molecule can be rationally designed using known techniques. Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell membrane. Preferred cells include cells from mammals, yeast, Drosophila, or E. coli. Cells expressing the polypeptide or cell membrane fractions which contain the expressed polypeptide are then contacted with a test compound and binding, stimulation, or inhibition of activity of either the polypeptide or the molecule is analyzed.

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An assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a fluorophore, radioisotope, enzyme conjugate, or other detectable label. Alternatively, the assay may assess binding in the presence of a labeled competitor.

5 Additionally, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

10 Preferably, an ELISA assay using, e.g., a monoclonal or polyclonal antibody, can measure polypeptide level in a sample. The antibody can measure polypeptide level by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of the above assays can be used in a diagnostic or prognostic context. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the  
15 assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

#### Transcript Imaging and Toxicological Testing

Another embodiment relates to the use of dithp to develop a transcript image of a tissue or  
20 cell type. A transcript image represents the global pattern of gene expression by a particular tissue or cell type. Global gene expression patterns are analyzed by quantifying the number of expressed genes and their relative abundance under given conditions and at a given time. (See Seilhamer et al., "Comparative Gene Transcript Analysis," U.S. Patent Number 5,840,484, expressly incorporated by reference herein.) Thus a transcript image may be generated by hybridizing the polynucleotides of  
25 the present invention or their complements to the totality of transcripts or reverse transcripts of a particular tissue or cell type. In one embodiment, the hybridization takes place in high-throughput format, wherein the polynucleotides of the present invention or their complements comprise a subset of a plurality of elements on a microarray. The resultant transcript image would provide a profile of gene activity pertaining to human molecules for diagnostics and therapeutics.

30 Transcript images which profile dithp expression may be generated using transcripts isolated from tissues, cell lines, biopsies, or other biological samples. The transcript image may thus reflect dithp expression in vivo, as in the case of a tissue or biopsy sample, or in vitro, as in the case of a cell line.

Transcript images which profile dithp expression may also be used in conjunction with in  
35 vitro model systems and preclinical evaluation of pharmaceuticals, as well as toxicological testing of industrial and naturally-occurring environmental compounds. All compounds induce characteristic

gene expression patterns, frequently termed molecular fingerprints or toxicant signatures, which are indicative of mechanisms of action and toxicity (Nuwaysir, E. F. et al. (1999) Mol. Carcinog. 24:153-159; Steiner, S. and Anderson, N.L. (2000) Toxicol. Lett. 112-113:467-71, expressly incorporated by reference herein). If a test compound has a signature similar to that of a compound with known toxicity, it is likely to share those toxic properties. These fingerprints or signatures are most useful and refined when they contain expression information from a large number of genes and gene families. Ideally, a genome-wide measurement of expression provides the highest quality signature. Even genes whose expression is not altered by any tested compounds are important as well, as the levels of expression of these genes are used to normalize the rest of the expression data. The normalization procedure is useful for comparison of expression data after treatment with different compounds. While the assignment of gene function to elements of a toxicant signature aids in interpretation of toxicity mechanisms, knowledge of gene function is not necessary for the statistical matching of signatures which leads to prediction of toxicity. (See, for example, Press Release 00-02 from the National Institute of Environmental Health Sciences, released February 29, 2000, available at <http://www.niehs.nih.gov/oc/news/toxchip.htm>.) Therefore, it is important and desirable in toxicological screening using toxicant signatures to include all expressed gene sequences.

In one embodiment, the toxicity of a test compound is assessed by treating a biological sample containing nucleic acids with the test compound. Nucleic acids that are expressed in the treated biological sample are hybridized with one or more probes specific to the polynucleotides of the present invention, so that transcript levels corresponding to the polynucleotides of the present invention may be quantified. The transcript levels in the treated biological sample are compared with levels in an untreated biological sample. Differences in the transcript levels between the two samples are indicative of a toxic response caused by the test compound in the treated sample.

Another particular embodiment relates to the use of DITHP encoded by polynucleotides of the present invention to analyze the proteome of a tissue or cell type. The term proteome refers to the global pattern of protein expression in a particular tissue or cell type. Each protein component of a proteome can be subjected individually to further analysis. Proteome expression patterns, or profiles, are analyzed by quantifying the number of expressed proteins and their relative abundance under given conditions and at a given time. A profile of a cell's proteome may thus be generated by separating and analyzing the polypeptides of a particular tissue or cell type. In one embodiment, the separation is achieved using two-dimensional gel electrophoresis, in which proteins from a sample are separated by isoelectric focusing in the first dimension, and then according to molecular weight by sodium dodecyl sulfate slab gel electrophoresis in the second dimension (Steiner and Anderson, *supra*). The proteins are visualized in the gel as discrete and uniquely positioned spots, typically by staining the gel with an agent such as Coomassie Blue or silver or fluorescent stains. The optical density of each protein spot is generally proportional to the level of the protein in the sample. The

optical densities of equivalently positioned protein spots from different samples, for example, from biological samples either treated or untreated with a test compound or therapeutic agent, are compared to identify any changes in protein spot density related to the treatment. The proteins in the spots are partially sequenced using, for example, standard methods employing chemical or enzymatic cleavage followed by mass spectrometry. The identity of the protein in a spot may be determined by comparing its partial sequence, preferably of at least 5 contiguous amino acid residues, to the polypeptide sequences of the present invention. In some cases, further sequence data may be obtained for definitive protein identification.

A proteomic profile may also be generated using antibodies specific for DITHP to quantify the levels of DITHP expression. In one embodiment, the antibodies are used as elements on a microarray, and protein expression levels are quantified by exposing the microarray to the sample and detecting the levels of protein bound to each array element (Lueking, A. et al. (1999) *Anal. Biochem.* 270:103-11; Mendoz, L.G. et al. (1999) *Biotechniques* 27:778-88). Detection may be performed by a variety of methods known in the art, for example, by reacting the proteins in the sample with a thiol- or amino-reactive fluorescent compound and detecting the amount of fluorescence bound at each array element.

Toxicant signatures at the proteome level are also useful for toxicological screening, and should be analyzed in parallel with toxicant signatures at the transcript level. There is a poor correlation between transcript and protein abundances for some proteins in some tissues (Anderson, N.L. and Seilhamer, J. (1997) *Electrophoresis* 18:533-537), so proteome toxicant signatures may be useful in the analysis of compounds which do not significantly affect the transcript image, but which alter the proteomic profile. In addition, the analysis of transcripts in body fluids is difficult, due to rapid degradation of mRNA, so proteomic profiling may be more reliable and informative in such cases.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins that are expressed in the treated biological sample are separated so that the amount of each protein can be quantified. The amount of each protein is compared to the amount of the corresponding protein in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample. Individual proteins are identified by sequencing the amino acid residues of the individual proteins and comparing these partial sequences to the DITHP encoded by polynucleotides of the present invention.

In another embodiment, the toxicity of a test compound is assessed by treating a biological sample containing proteins with the test compound. Proteins from the biological sample are incubated with antibodies specific to the DITHP encoded by polynucleotides of the present invention. The amount of protein recognized by the antibodies is quantified. The amount of protein in the

treated biological sample is compared with the amount in an untreated biological sample. A difference in the amount of protein between the two samples is indicative of a toxic response to the test compound in the treated sample.

Transcript images may be used to profile dithp expression in distinct tissue types. This process can be used to determine human molecule activity in a particular tissue type relative to this activity in a different tissue type. Transcript images may be used to generate a profile of dithp expression characteristic of diseased tissue. Transcript images of tissues before and after treatment may be used for diagnostic purposes, to monitor the progression of disease, and to monitor the efficacy of drug treatments for diseases which affect the activity of human molecules.

Transcript images of cell lines can be used to assess human molecule activity and/or to identify cell lines that lack or misregulate this activity. Such cell lines may then be treated with pharmaceutical agents, and a transcript image following treatment may indicate the efficacy of these agents in restoring desired levels of this activity. A similar approach may be used to assess the toxicity of pharmaceutical agents as reflected by undesirable changes in human molecule activity.

Candidate pharmaceutical agents may be evaluated by comparing their associated transcript images with those of pharmaceutical agents of known effectiveness.

#### Antisense Molecules

The polynucleotides of the present invention are useful in antisense technology. Antisense technology or therapy relies on the modulation of expression of a target protein through the specific binding of an antisense sequence to a target sequence encoding the target protein or directing its expression. (See, e.g., Agrawal, S., ed. (1996) Antisense Therapeutics, Humana Press Inc., Totawa NJ; Alama, A. et al. (1997) *Pharmacol. Res.* 36(3):171-178; Crooke, S.T. (1997) *Adv. Pharmacol.* 40:1-49; Sharma, H.W. and R. Narayanan (1995) *Bioessays* 17(12):1055-1063; and Lavrosky, Y. et al. (1997) *Biochem. Mol. Med.* 62(1):11-22.) An antisense sequence is a polynucleotide sequence capable of specifically hybridizing to at least a portion of the target sequence. Antisense sequences bind to cellular mRNA and/or genomic DNA, affecting translation and/or transcription. Antisense sequences can be DNA, RNA, or nucleic acid mimics and analogs. (See, e.g., Rossi, J.J. et al. (1991) *Antisense Res. Dev.* 1(3):285-288; Lee, R. et al. (1998) *Biochemistry* 37(3):900-1010; Pardridge, W.M. et al. (1995) *Proc. Natl. Acad. Sci. USA* 92(12):5592-5596; and Nielsen, P. E. and Haaimea, G. (1997) *Chem. Soc. Rev.* 96:73-78.) Typically, the binding which results in modulation of expression occurs through hybridization or binding of complementary base pairs. Antisense sequences can also bind to DNA duplexes through specific interactions in the major groove of the double helix.

The polynucleotides of the present invention and fragments thereof can be used as antisense sequences to modify the expression of the polypeptide encoded by dithp. The antisense sequences can be produced ex vivo, such as by using any of the ABI nucleic acid synthesizer series (Applied

Biosystems) or other automated systems known in the art. Antisense sequences can also be produced biologically, such as by transforming an appropriate host cell with an expression vector containing the sequence of interest. (See, e.g., Agrawal, *supra*.)

In therapeutic use, any gene delivery system suitable for introduction of the antisense sequences into appropriate target cells can be used. Antisense sequences can be delivered intracellularly in the form of an expression plasmid which, upon transcription, produces a sequence complementary to at least a portion of the cellular sequence encoding the target protein. (See, e.g., Slater, J.E., et al. (1998) *J. Allergy Clin. Immunol.* 102(3):469-475; and Scanlon, K.J., et al. (1995) 9(13):1288-1296.) Antisense sequences can also be introduced intracellularly through the use of viral vectors, such as retrovirus and adeno-associated virus vectors. (See, e.g., Miller, A.D. (1990) *Blood* 76:271; Ausubel, F.M. et al. (1995) *Current Protocols in Molecular Biology*, John Wiley & Sons, New York NY; Uckert, W. and W. Walther (1994) *Pharmacol. Ther.* 63(3):323-347.) Other gene delivery mechanisms include liposome-derived systems, artificial viral envelopes, and other systems known in the art. (See, e.g., Rossi, J.J. (1995) *Br. Med. Bull.* 51(1):217-225; Boado, R.J. et al. (1998) 15 *J. Pharm. Sci.* 87(11):1308-1315; and Morris, M.C. et al. (1997) *Nucleic Acids Res.* 25(14):2730-2736.)

### Expression

In order to express a biologically active DITHP, the nucleotide sequences encoding DITHP or fragments thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. Methods which are well known to those skilled in the art may be used to construct expression vectors containing sequences encoding DITHP and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. (See, e.g., Sambrook, *supra*, Chapters 4, 8, 16, and 17; and Ausubel, *supra*, Chapters 9, 10, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding DITHP. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal (mammalian) cell systems. (See, e.g., Sambrook, *supra*; Ausubel, 1995, *supra*, Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509; Bitter, G.A. et al. (1987) *Methods Enzymol.* 153:516-544; Scorer, C.A. et al. (1994) *Bio/Technology* 12:181-184; Engelhard, E.K. et al. (1994) 35 *Proc. Natl. Acad. Sci. USA* 91:3224-3227; Sandig, V. et al. (1996) *Hum. Gene Ther.* 7:1937-1945;

Takamatsu, N. (1987) EMBO J. 6:307-311; Coruzzi, G. et al. (1984) EMBO J. 3:1671-1680; Broglie, R. et al. (1984) Science 224:838-843; Winter, J. et al. (1991) Results Probl. Cell Differ. 17:85-105; The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196; Logan, J. and T. Shenk (1984) Proc. Natl. Acad. Sci. USA 81:3655-3659; and Harrington, J.J. et al. (1997) Nat. Genet. 15:345-355.) Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses, or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. (See, e.g., Di Nicola, M. et al. (1998) Cancer Gen. Ther. 5(6):350-356; Yu, M. et al., (1993) Proc. Natl. Acad. Sci. USA 90(13):6340-6344; Buller, R.M. et al. (1985) Nature 317(6040):813-815; McGregor, D.P. et al. (1994) Mol. Immunol. 31(3):219-226; and Verma, I.M. and N. Somia (1997) Nature 389:239-242.) The invention is not limited by the host cell employed.

For long term production of recombinant proteins in mammalian systems, stable expression of DITHP in cell lines is preferred. For example, sequences encoding DITHP can be transformed into cell lines using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Any number of selection systems may be used to recover transformed cell lines. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.; Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. USA 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14; Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. USA 85:8047-8051; Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

#### Therapeutic Uses of dithp

The dithp of the invention may be used for somatic or germline gene therapy. Gene therapy may be performed to (i) correct a genetic deficiency (e.g., in the cases of severe combined immunodeficiency (SCID)-X1 disease characterized by X-linked inheritance (Cavazzana-Calvo, M. et al. (2000) Science 288:669-672), severe combined immunodeficiency syndrome associated with an inherited adenosine deaminase (ADA) deficiency (Blaese, R.M. et al. (1995) Science 270:475-480; Bordignon, C. et al. (1995) Science 270:470-475), cystic fibrosis (Zabner, J. et al. (1993) Cell 75:207-216; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:643-666; Crystal, R.G. et al. (1995) Hum. Gene Therapy 6:667-703), thalassemias, familial hypercholesterolemia, and hemophilia resulting from Factor VIII or Factor IX deficiencies (Crystal, R.G. (1995) Science 270:404-410; Verma, I.M. and Somia, N. (1997) Nature 389:239-242)), (ii) express a conditionally lethal gene product (e.g., in the case of cancers which result from unregulated cell proliferation), or (iii) express a protein which affords protection against intracellular parasites (e.g., against human retroviruses, such as human immunodeficiency virus (HIV) (Baltimore, D. (1988) Nature 335:395-396; Poeschla, E. et al. (1996) Proc. Natl. Acad. Sci. USA. 93:11395-11399), hepatitis B or C virus (HBV, HCV); fungal parasites,

such as Candida albicans and Paracoccidioides brasiliensis; and protozoan parasites such as Plasmodium falciparum and Trypanosoma cruzi). In the case where a genetic deficiency in dithp expression or regulation causes disease, the expression of dithp from an appropriate population of transduced cells may alleviate the clinical manifestations caused by the genetic deficiency.

5 In a further embodiment of the invention, diseases or disorders caused by deficiencies in dithp are treated by constructing mammalian expression vectors comprising dithp and introducing these vectors by mechanical means into dithp-deficient cells. Mechanical transfer technologies for use with cells in vivo or ex vitro include (i) direct DNA microinjection into individual cells, (ii) ballistic gold particle delivery, (iii) liposome-mediated transfection, (iv) receptor-mediated gene transfer, and (v) the use of DNA transposons (Morgan, R.A. and Anderson, W.F. (1993) *Annu. Rev. Biochem.* 62:191-217; Ivics, Z. (1997) *Cell* 91:501-510; Boulay, J-L. and Récipon, H. (1998) *Curr. Opin. Biotechnol.* 9:445-450).

Expression vectors that may be effective for the expression of dithp include, but are not limited to, the PCDNA 3.1, EPITAG, PRCCMV2, PREP, PVAX vectors (Invitrogen, Carlsbad CA),  
 15 PCMV-SCRIPT, PCMV-TAG, PEGSH/PERV (Stratagene, La Jolla CA), and PTET-OFF, PTET-ON, PTRE2, PTRE2-LUC, PTK-HYG (Clontech, Palo Alto CA). The dithp of the invention may be expressed using (i) a constitutively active promoter, (e.g., from cytomegalovirus (CMV), Rous sarcoma virus (RSV), SV40 virus, thymidine kinase (TK), or  $\beta$ -actin genes), (ii) an inducible promoter (e.g., the tetracycline-regulated promoter (Gossen, M. and Bujard, H. (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89:5547-5551; Gossen, M. et al., (1995) *Science* 268:1766-1769; Rossi, F.M.V. and Blau, H.M. (1998) *Curr. Opin. Biotechnol.* 9:451-456), commercially available in the T-REX plasmid (Invitrogen); the ecdysone-inducible promoter (available in the plasmids PVGRXR and PIND; Invitrogen); the FK506/rapamycin inducible promoter; or the RU486/mifepristone inducible promoter (Rossi, F.M.V. and Blau, H.M. supra), or (iii) a tissue-specific promoter or the native  
 20 promoter of the endogenous gene encoding DITHP from a normal individual.

Commercially available liposome transformation kits (e.g., the PERFECT LIPID TRANSFECTION KIT, available from Invitrogen) allow one with ordinary skill in the art to deliver polynucleotides to target cells in culture and require minimal effort to optimize experimental parameters. In the alternative, transformation is performed using the calcium phosphate method  
 30 (Graham, F.L. and Eb, A.J. (1973) *Virology* 52:456-467), or by electroporation (Neumann, E. et al. (1982) *EMBO J.* 1:841-845). The introduction of DNA to primary cells requires modification of these standardized mammalian transfection protocols.

In another embodiment of the invention, diseases or disorders caused by genetic defects with respect to dithp expression are treated by constructing a retrovirus vector consisting of (i) dithp under  
 35 the control of an independent promoter or the retrovirus long terminal repeat (LTR) promoter, (ii) appropriate RNA packaging signals, and (iii) a Rev-responsive element (RRE) along with additional



retrovirus *cis*-acting RNA sequences and coding sequences required for efficient vector propagation. Retrovirus vectors (e.g., PFB and PFBNEO) are commercially available (Stratagene) and are based on published data (Riviere, I. et al. (1995) Proc. Natl. Acad. Sci. U.S.A. 92:6733-6737), incorporated by reference herein. The vector is propagated in an appropriate vector producing cell line (VPCL) that

5 expresses an envelope gene with a tropism for receptors on the target cells or a promiscuous envelope protein such as VSVg (Armentano, D. et al. (1987) J. Virol. 61:1647-1650; Bender, M.A. et al. (1987) J. Virol. 61:1639-1646; Adam, M.A. and Miller, A.D. (1988) J. Virol. 62:3802-3806; Dull, T. et al. (1998) J. Virol. 72:8463-8471; Zufferey, R. et al. (1998) J. Virol. 72:9873-9880). U.S. Patent Number 5,910,434 to Rigg ("Method for obtaining retrovirus packaging cell lines producing high

10 transducing efficiency retroviral supernatant") discloses a method for obtaining retrovirus packaging cell lines and is hereby incorporated by reference. Propagation of retrovirus vectors, transduction of a population of cells (e.g., CD4<sup>+</sup> T-cells), and the return of transduced cells to a patient are procedures well known to persons skilled in the art of gene therapy and have been well documented (Ranga, U. et al. (1997) J. Virol. 71:7020-7029; Bauer, G. et al. (1997) Blood 89:2259-2267;

15 Bonyhadi, M.L. (1997) J. Virol. 71:4707-4716; Ranga, U. et al. (1998) Proc. Natl. Acad. Sci. U.S.A. 95:1201-1206; Su, L. (1997) Blood 89:2283-2290).

In the alternative, an adenovirus-based gene therapy delivery system is used to deliver dithp to cells which have one or more genetic abnormalities with respect to the expression of dithp. The construction and packaging of adenovirus-based vectors are well known to those with ordinary skill

20 in the art. Replication defective adenovirus vectors have proven to be versatile for importing genes encoding immunoregulatory proteins into intact islets in the pancreas (Csete, M.E. et al. (1995) Transplantation 27:263-268). Potentially useful adenoviral vectors are described in U.S. Patent Number 5,707,618 to Armentano ("Adenovirus vectors for gene therapy"), hereby incorporated by reference. For adenoviral vectors, see also Antinozzi, P.A. et al. (1999) Annu. Rev. Nutr. 19:511-544

25 and Verma, I.M. and Somia, N. (1997) Nature 18:389:239-242, both incorporated by reference herein.

In another alternative, a herpes-based, gene therapy delivery system is used to deliver dithp to target cells which have one or more genetic abnormalities with respect to the expression of dithp. The use of herpes simplex virus (HSV)-based vectors may be especially valuable for introducing dithp to cells of the central nervous system, for which HSV has a tropism. The construction and

30 packaging of herpes-based vectors are well known to those with ordinary skill in the art. A replication-competent herpes simplex virus (HSV) type 1-based vector has been used to deliver a reporter gene to the eyes of primates (Liu, X. et al. (1999) Exp. Eye Res. 169:385-395). The construction of a HSV-1 virus vector has also been disclosed in detail in U.S. Patent Number 5,804,413 to DeLuca ("Herpes simplex virus strains for gene transfer"), which is hereby incorporated

35 by reference. U.S. Patent Number 5,804,413 teaches the use of recombinant HSV d92 which consists of a genome containing at least one exogenous gene to be transferred to a cell under the control of the

appropriate promoter for purposes including human gene therapy. Also taught by this patent are the construction and use of recombinant HSV strains deleted for ICP4, ICP27 and ICP22. For HSV vectors, see also Goins, W. F. et al. 1999 J. Virol. 73:519-532 and Xu, H. et al., (1994) Dev. Biol. 163:152-161, hereby incorporated by reference. The manipulation of cloned herpesvirus sequences, the generation of recombinant virus following the transfection of multiple plasmids containing different segments of the large herpesvirus genomes, the growth and propagation of herpesvirus, and the infection of cells with herpesvirus are techniques well known to those of ordinary skill in the art.

In another alternative, an alphavirus (positive, single-stranded RNA virus) vector is used to deliver dithp to target cells. The biology of the prototypic alphavirus, Semliki Forest Virus (SFV), has been studied extensively and gene transfer vectors have been based on the SFV genome (Garoff, H. and Li, K.-J. (1998) Curr. Opin. Biotech. 9:464-469). During alphavirus RNA replication, a subgenomic RNA is generated that normally encodes the viral capsid proteins. This subgenomic RNA replicates to higher levels than the full-length genomic RNA, resulting in the overproduction of capsid proteins relative to the viral proteins with enzymatic activity (e.g., protease and polymerase). Similarly, inserting dithp into the alphavirus genome in place of the capsid-coding region results in the production of a large number of dithp RNAs and the synthesis of high levels of DITHP in vector transduced cells. While alphavirus infection is typically associated with cell lysis within a few days, the ability to establish a persistent infection in hamster normal kidney cells (BHK-21) with a variant of Sindbis virus (SIN) indicates that the lytic replication of alphaviruses can be altered to suit the needs of the gene therapy application (Dryga, S.A. et al. (1997) Virology 228:74-83). The wide host range of alphaviruses will allow the introduction of dithp into a variety of cell types. The specific transduction of a subset of cells in a population may require the sorting of cells prior to transduction. The methods of manipulating infectious cDNA clones of alphaviruses, performing alphavirus cDNA and RNA transfections, and performing alphavirus infections, are well known to those with ordinary skill in the art.

#### Antibodies

Anti-DITHP antibodies may be used to analyze protein expression levels. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, and Fab fragments. For descriptions of and protocols of antibody technologies, see, e.g., Pound J.D. (1998)

Immunochemical Protocols, Humana Press, Totowa, NJ.

The amino acid sequence encoded by the dithp of the Sequence Listing may be analyzed by appropriate software (e.g., LASERGENE NAVIGATOR software, DNASTAR) to determine regions of high immunogenicity. The optimal sequences for immunization are selected from the C-terminus, the N-terminus, and those intervening, hydrophilic regions of the polypeptide which are likely to be exposed to the external environment when the polypeptide is in its natural conformation. Analysis

used to select appropriate epitopes is also described by Ausubel (1997, supra, Chapter 11.7).

Peptides used for antibody induction do not need to have biological activity; however, they must be antigenic. Peptides used to induce specific antibodies may have an amino acid sequence consisting of at least five amino acids, preferably at least 10 amino acids, and most preferably at least 15 amino acids. A peptide which mimics an antigenic fragment of the natural polypeptide may be fused with another protein such as keyhole limpet hemocyanin (KLH; Sigma, St. Louis MO) for antibody production. A peptide encompassing an antigenic region may be expressed from a dithp, synthesized as described above, or purified from human cells.

Procedures well known in the art may be used for the production of antibodies. Various hosts including mice, goats, and rabbits, may be immunized by injection with a peptide. Depending on the host species, various adjuvants may be used to increase immunological response.

In one procedure, peptides about 15 residues in length may be synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with M-maleimidobenzoyl-N-hydroxysuccinimide ester (Ausubel, 1995, supra). Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. The resulting antisera are tested for antipeptide activity by binding the peptide to plastic, blocking with 1% bovine serum albumin (BSA), reacting with rabbit antisera, washing, and reacting with radioiodinated goat anti-rabbit IgG. Antisera with antipeptide activity are tested for anti-DITHP activity using protocols well known in the art, including ELISA, radioimmunoassay (RIA), and immunoblotting.

In another procedure, isolated and purified peptide may be used to immunize mice (about 100  $\mu$ g of peptide) or rabbits (about 1 mg of peptide). Subsequently, the peptide is radioiodinated and used to screen the immunized animals' B-lymphocytes for production of antipeptide antibodies. Positive cells are then used to produce hybridomas using standard techniques. About 20 mg of peptide is sufficient for labeling and screening several thousand clones. Hybridomas of interest are detected by screening with radioiodinated peptide to identify those fusions producing peptide-specific monoclonal antibody. In a typical protocol, wells of a multi-well plate (FAST, Becton-Dickinson, Palo Alto, CA) are coated with affinity-purified, specific rabbit-anti-mouse (or suitable anti-species IgG) antibodies at 10 mg/ml. The coated wells are blocked with 1% BSA and washed and exposed to supernatants from hybridomas. After incubation, the wells are exposed to radiolabeled peptide at 1 mg/ml.

Clones producing antibodies bind a quantity of labeled peptide that is detectable above background. Such clones are expanded and subjected to 2 cycles of cloning. Cloned hybridomas are injected into pristane-treated mice to produce ascites, and monoclonal antibody is purified from the ascitic fluid by affinity chromatography on protein A (Amersham Pharmacia Biotech). Several procedures for the production of monoclonal antibodies, including in vitro production, are described in Pound (supra). Monoclonal antibodies with antipeptide activity are tested for anti-DITHP activity

using protocols well known in the art, including ELISA, RIA, and immunoblotting.

Antibody fragments containing specific binding sites for an epitope may also be generated. For example, such fragments include, but are not limited to, the F(ab')<sub>2</sub> fragments produced by pepsin digestion of the antibody molecule, and the Fab fragments generated by reducing the disulfide bridges of the F(ab')<sub>2</sub> fragments. Alternatively, construction of Fab expression libraries in filamentous bacteriophage allows rapid and easy identification of monoclonal fragments with desired specificity (Pound, *supra*, Chaps. 45-47). Antibodies generated against polypeptide encoded by dithp can be used to purify and characterize full-length DITHP protein and its activity, binding partners, etc.

#### 10 Assays Using Antibodies

Anti-DITHP antibodies may be used in assays to quantify the amount of DITHP found in a particular human cell. Such assays include methods utilizing the antibody and a label to detect expression level under normal or disease conditions. The peptides and antibodies of the invention may be used with or without modification or labeled by joining them, either covalently or noncovalently, with a reporter molecule.

Protocols for detecting and measuring protein expression using either polyclonal or monoclonal antibodies are well known in the art. Examples include ELISA, RIA, and fluorescent activated cell sorting (FACS). Such immunoassays typically involve the formation of complexes between the DITHP and its specific antibody and the measurement of such complexes. These and other assays are described in Pound (*supra*).

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, including U.S. Ser. No. 60/280,067, U.S. Ser. No. 60/279,619, U.S. Ser. No. 60/280,068, U.S. Ser. No. 60/291,280, U.S. Ser. No. 60/291,849, U.S. Ser. No. 60/291,829, U.S. Ser. No. 60/299,428, U.S. Ser. No. 60/300,001, and U.S. Ser. No. 60/299,776, are hereby expressly incorporated by reference.

### 30 **EXAMPLES**

#### **I. Construction of cDNA Libraries**

RNA was purchased from CLONTECH Laboratories, Inc. (Palo Alto CA) or isolated from various tissues. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was

precipitated with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In most cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega Corporation (Promega), Madison WI),  
5 OLIGOTEX latex particles (QIAGEN, Inc. (QIAGEN), Valencia CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Inc., Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP  
10 vector system (Stratagene Cloning Systems, Inc. (Stratagene), La Jolla CA) or SUPERScript plasmid system (Life Technologies), using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, supra, Chapters 5.1 through 6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or  
15 enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), PSPORT1 plasmid (Life Technologies), PCDNA2.1 plasmid (Invitrogen, Carlsbad CA), PBK-CMV  
20 plasmid (Stratagene), PCR2-TOPOTA plasmid (Invitrogen), PCMV-ICIS plasmid (Stratagene), pIGEN (Incyte Genomics, Palo Alto CA), pRARE (Incyte Genomics), or pINCY (Incyte Genomics), or derivatives thereof. Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 $\alpha$ , DH10B, or ElectroMAX DH10B from Life Technologies.

25

## II. Isolation of cDNA Clones

Plasmids were recovered from host cells by *in vivo* excision using the UNIZAP vector system (Stratagene) or by cell lysis. Plasmids were purified using at least one of the following: the Magic or WIZARD Minipreps DNA purification system (Promega); the AGTC Miniprep purification kit (Edge  
30 BioSystems, Gaithersburg MD); and the QIAWELL 8, QIAWELL 8 Plus, and QIAWELL 8 Ultra plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit (QIAGEN). Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a  
35 high-throughput format. (Rao, V.B. (1994) Anal. Biochem. 216:1-14.) Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in

384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Inc. (Molecular Probes), Eugene OR) and a FLUOROSKAN II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

5    **III.    Sequencing and Analysis**

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 thermal cycler (Applied Biosystems) or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific Corp., Sunnyvale CA) or the MICROLAB 2200 liquid transfer system (Hamilton). cDNA  
10    sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA  
15    sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing system (Applied Biosystems) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, *supra*, Chapter 7.7). Some of the cDNA sequences were selected for extension using the techniques disclosed in Example VIII.

20    **IV.    Assembly and Analysis of Sequences**

Component sequences from chromatograms were subject to PHRED analysis and assigned a quality score. The sequences having at least a required quality score were subject to various pre-processing editing pathways to eliminate, e.g., low quality 3' ends, vector and linker sequences, polyA tails, Alu repeats, mitochondrial and ribosomal sequences, bacterial contamination sequences, and  
25    sequences smaller than 50 base pairs. In particular, low-information sequences and repetitive elements (e.g., dinucleotide repeats, Alu repeats, etc.) were replaced by "n's", or masked, to prevent spurious matches.

Processed sequences were then subject to assembly procedures in which the sequences were assigned to gene bins (bins). Each sequence could only belong to one bin. Sequences in each gene  
30    bin were assembled to produce consensus sequences (templates). Subsequent new sequences were added to existing bins using BLASTN (v.1.4 WashU) and CROSSMATCH. Candidate pairs were identified as all BLAST hits having a quality score greater than or equal to 150. Alignments of at least 82% local identity were accepted into the bin. The component sequences from each bin were assembled using a version of PHRAP. Bins with several overlapping component sequences were  
35    assembled using DEEP PHRAP. The orientation (sense or antisense) of each assembled template was determined based on the number and orientation of its component sequences. Template sequences as

disclosed in the sequence listing correspond to sense strand sequences (the "forward" reading frames), to the best determination. The complementary (antisense) strands are inherently disclosed herein. The component sequences which were used to assemble each template consensus sequence are listed in Table 5 by their positions along the template nucleotide sequences.

5       Bins were compared against each other and those having local similarity of at least 82% were combined and reassembled. Reassembled bins having templates of insufficient overlap (less than 95% local identity) were re-split. Assembled templates were also subject to analysis by STITCHER/EXON MAPPER algorithms which analyze the probabilities of the presence of splice variants, alternatively spliced exons, splice junctions, differential expression of alternative spliced  
10 genes across tissue types or disease states, etc. These resulting bins were subject to several rounds of the above assembly procedures.

Once gene bins were generated based upon sequence alignments, bins were clone joined based upon clone information. If the 5' sequence of one clone was present in one bin and the 3' sequence from the same clone was present in a different bin, it was likely that the two bins actually  
15 belonged together in a single bin. The resulting combined bins underwent assembly procedures to regenerate the consensus sequences.

The final assembled templates were subsequently annotated using the following procedure. Template sequences were analyzed using BLASTN (v2.0, NCBI) versus gbpri (GenBank version 128). "Hits" were defined as an exact match having from 95% local identity over 200 base pairs  
20 through 100% local identity over 100 base pairs, or a homolog match having an E-value, i.e. a probability score, of  $\leq 1 \times 10^{-8}$ . The hits were subject to frameshift FASTx versus GENPEPT (GenBank version 128). (See Table 8). In this analysis, a homolog match was defined as having an E-value of  $\leq 1 \times 10^{-8}$ . The assembly method used above was described in "System and Methods for Analyzing Biomolecular Sequences," U.S.S.N. 09/276,534, filed March 25, 1999, and the LIFESEQ  
25 Gold user manual (Incyte) both incorporated by reference herein.

Following assembly, template sequences were subjected to motif, BLAST, and functional analyses, and categorized in protein hierarchies using methods described in, e.g., "Database System Employing Protein Function Hierarchies for Viewing Biomolecular Sequence Data," U.S. Patent Number 6,023,659; "Relational Database for Storing Biomolecule Information," U.S.S.N.  
30 08/947,845, filed October 9, 1997; "Project-Based Full-Length Biomolecular Sequence Database," U.S. Patent Number 5,953,727; and "Relational Database and System for Storing Information Relating to Biomolecular Sequences," U.S.S.N. 09/034,807, filed March 4, 1998, all of which are incorporated by reference herein.

The template sequences were further analyzed by translating each template in all three  
35 forward reading frames and searching each translation against the Pfam database of hidden Markov model-based protein families and domains using the HMMER software package (available to the

public from Washington University School of Medicine, St. Louis MO). Regions of templates which, when translated, contain similarity to Pfam consensus sequences are reported in Table 3, along with descriptions of Pfam protein domains and families. Only those Pfam hits with an E-value of  $\leq 1 \times 10^{-3}$  are reported. (See also World Wide Web site <http://pfam.wustl.edu/> for detailed descriptions of Pfam protein domains and families.)

Additionally, the template sequences were translated in all three forward reading frames, and each translation was searched against hidden Markov models for signal peptides using the HMMER software package. Construction of hidden Markov models and their usage in sequence analysis has been described. (See, for example, Eddy, S.R. (1996) *Curr. Opin. Str. Biol.* 6:361-365.) Only those signal peptide hits with a cutoff score of 11 bits or greater are reported. A cutoff score of 11 bits or greater corresponds to at least about 91-94% true-positives in signal peptide prediction. Template sequences were also translated in all three forward reading frames, and each translation was searched against TMHMMER, a program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation (Sonnhammer, E.L. et al. (1998) *Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol.*, Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.) Regions of templates which, when translated, contain similarity to signal peptide or transmembrane consensus sequences are reported in Table 4.

The results of HMMER analysis as reported in Tables 3 and 4 may support the results of BLAST analysis as reported in Table 2 or may suggest alternative or additional properties of template-encoded polypeptides not previously uncovered by BLAST or other analyses.

Template sequences are further analyzed using the bioinformatics tools listed in Table 8, or using sequence analysis software known in the art such as MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Template sequences may be further queried against public databases such as the GenBank rodent, mammalian, vertebrate, prokaryote, and eukaryote databases.

The template sequences were translated to derive the corresponding longest open reading frame as presented by the polypeptide sequences as reported in Table 7. Alternatively, a polypeptide of the invention may begin at any of the methionine residues within the full length translated polypeptide. Polypeptide sequences were subsequently analyzed by querying against the GenBank protein database (GENPEPT, (GenBank version 128)). Full length polynucleotide sequences are also analyzed using MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR). Polynucleotide and polypeptide sequence alignments are generated using default parameters specified by the CLUSTAL algorithm as incorporated into the MEGALIGN multisequence alignment program (DNASTAR), which also calculates the percent identity between aligned sequences.



Table 7 shows sequences with homology to the polypeptides of the invention as identified by BLAST analysis against the GenBank protein (GENPEPT) database. Column 1 shows the polypeptide sequence identification number (SEQ ID NO:) for the polypeptide segments of the invention. Column 2 shows the reading frame used in the translation of the polynucleotide sequences encoding the polypeptide segments. Column 3 shows the length of the translated polypeptide segments. Columns 4 and 5 show the start and stop nucleotide positions of the polynucleotide sequences encoding the polypeptide segments. Column 6 shows the GenBank identification number (GI Number) of the nearest GenBank homolog. Column 7 shows the probability score for the match between each polypeptide and its GenBank homolog. Column 8 shows the annotation of the GenBank homolog.

#### V. Analysis of Polynucleotide Expression

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, *supra*, ch. 7; Ausubel, 1995, *supra*, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in cDNA databases such as GenBank or LIFESEQ (Incyte Genomics). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\text{BLAST Score} \times \text{Percent Identity}}{5 \times \text{minimum} \{ \text{length}(\text{Seq. 1}), \text{length}(\text{Seq. 2}) \}}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. The product score is a normalized value between 0 and 100, and is calculated as follows: the BLAST score is multiplied by the percent nucleotide identity and the product is divided by (5 times the length of the shorter of the two sequences). The BLAST score is calculated by assigning a score of +5 for every base that matches in a high-scoring segment pair (HSP), and -4 for every mismatch. Two sequences may share more than one HSP (separated by gaps). If there is more than one HSP, then the pair with the highest BLAST score is used to calculate the product score. The product score represents a balance between fractional overlap and quality in a BLAST alignment. For example, a product score of 100 is produced only for 100% identity over the entire length of the shorter of the two sequences being compared. A product score of 70 is produced either by 100% identity and 70% overlap at one end, or by 88% identity and 100% overlap at the other. A product score of 50 is produced either by 100% identity and 50% overlap at one end, or

79% identity and 100% overlap.

#### VI. Tissue Distribution Profiling

A tissue distribution profile is determined for each template by compiling the cDNA library  
 5 tissue classifications of its component cDNA sequences. Each component sequence, is derived from  
 a cDNA library constructed from a human tissue. Each human tissue is classified into one of the  
 following categories: cardiovascular system; connective tissue; digestive system; embryonic  
 structures; endocrine system; exocrine glands; genitalia, female; genitalia, male; germ cells; hemic  
 and immune system; liver; musculoskeletal system; nervous system; pancreas; respiratory system;  
 10 sense organs; skin; stomatognathic system; unclassified/mixed; or urinary tract. Template sequences,  
 component sequences, and cDNA library/tissue information are found in the LIFESEQ GOLD  
 database (Incyte Genomics, Palo Alto CA).

Table 6 shows the tissue distribution profile for the templates of the invention. For each  
 template, the three most frequently observed tissue categories are shown in column 3, along with the  
 15 percentage of component sequences belonging to each category. Only tissue categories with  
 percentage values of  $\geq 10\%$  are shown. A tissue distribution of "widely distributed" in column 3  
 indicates percentage values of  $<10\%$  in all tissue categories.

#### VII. Transcript Image Analysis

20 Transcript images are generated as described in Seilhamer et al., "Comparative Gene  
 Transcript Analysis," U.S. Patent Number 5,840,484, incorporated herein by reference.

#### VIII. Extension of Polynucleotide Sequences and Isolation of a Full-length cDNA

Oligonucleotide primers designed using a dithp of the Sequence Listing are used to extend  
 25 the nucleic acid sequence. One primer is synthesized to initiate 5' extension of the template, and the  
 other primer, to initiate 3' extension of the template. The initial primers may be designed using  
 OLIGO 4.06 software (National Biosciences, Inc. (National Biosciences), Plymouth MN), or another  
 appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50%  
 or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any  
 30 stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations are  
 avoided. Selected human cDNA libraries are used to extend the sequence. If more than one  
 extension is necessary or desired, additional or nested sets of primers are designed.

High fidelity amplification is obtained by PCR using methods well known in the art. PCR is  
 performed in 96-well plates using the PTC-200 thermal cycler (MJ Research). The reaction mix  
 35 contains DNA template, 200 nmol of each primer, reaction buffer containing  $Mg^{2+}$ ,  $(NH_4)_2SO_4$ , and B-  
 mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life

Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ are as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

The concentration of DNA in each well is determined by dispensing 100 µl PICOGREEN quantitation reagent (0.25% (v/v); Molecular Probes) dissolved in 1X Tris-EDTA (TE) and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Incorporated (Corning), Corning NY), allowing the DNA to bind to the reagent. The plate is scanned in a FLUOROSKAN II (Labsystems Oy) to measure the fluorescence of the sample and to quantify the concentration of DNA. A 5 µl to 10 µl aliquot of the reaction mixture is analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions are successful in extending the sequence.

The extended nucleotides are desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides are separated on low concentration (0.6 to 0.8%) agarose gels, fragments are excised, and agar digested with AGAR ACE (Promega). Extended clones are religated using T4 ligase (New England Biolabs, Inc., Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells are selected on antibiotic-containing media, individual colonies are picked and cultured overnight at 37°C in 384-well plates in LB/2x carbenicillin liquid media.

The cells are lysed, and DNA is amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA is quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries are reamplified using the same conditions as described above. Samples are diluted with 20% dimethylsulfoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Applied Biosystems).

In like manner, the dithp is used to obtain regulatory sequences (promoters, introns, and enhancers) using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

**IX. Labeling of Probes and Southern Hybridization Analyses**

Hybridization probes derived from the dithp of the Sequence Listing are employed for screening cDNAs, mRNAs, or genomic DNA. The labeling of probe nucleotides between 100 and 1000 nucleotides in length is specifically described, but essentially the same procedure may be used with larger cDNA fragments. Probe sequences are labeled at room temperature for 30 minutes using a T4 polynucleotide kinase,  $\gamma^{32}\text{P}$ -ATP, and 0.5X One-Phor-All Plus (Amersham Pharmacia Biotech) buffer and purified using a ProbeQuant G-50 Microcolumn (Amersham Pharmacia Biotech). The probe mixture is diluted to  $10^7$  dpm/ $\mu\text{g/ml}$  hybridization buffer and used in a typical membrane-based hybridization analysis.

The DNA is digested with a restriction endonuclease such as Eco RV and is electrophoresed through a 0.7% agarose gel. The DNA fragments are transferred from the agarose to nylon membrane (NYTRAN Plus, Schleicher & Schuell, Inc., Keene NH) using procedures specified by the manufacturer of the membrane. Prehybridization is carried out for three or more hours at  $68^\circ\text{C}$ , and hybridization is carried out overnight at  $68^\circ\text{C}$ . To remove non-specific signals, blots are sequentially washed at room temperature under increasingly stringent conditions, up to 0.1x saline sodium citrate (SSC) and 0.5% sodium dodecyl sulfate. After the blots are placed in a PHOSPHORIMAGER cassette (Molecular Dynamics) or are exposed to autoradiography film, hybridization patterns of standard and experimental lanes are compared. Essentially the same procedure is employed when screening RNA.

**X. Chromosome Mapping of dithp**

The cDNA sequences which were used to assemble SEQ ID NO:1-670 are compared with sequences from the Incyte LIFESEQ database and public domain databases using BLAST and other implementations of the Smith-Waterman algorithm. Sequences from these databases that match SEQ ID NO:1-670 are assembled into clusters of contiguous and overlapping sequences using assembly algorithms such as PHRAP (Table 8). Radiation hybrid and genetic mapping data available from public resources such as the Stanford Human Genome Center (SHGC), Whitehead Institute for Genome Research (WIGR), and Généthon are used to determine if any of the clustered sequences have been previously mapped. Inclusion of a mapped sequence in a cluster will result in the assignment of all sequences of that cluster, including its particular SEQ ID NO., to that map location. The genetic map locations of SEQ ID NO:1-670 are described as ranges, or intervals, of human chromosomes. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Généthon which provide

boundaries for radiation hybrid markers whose sequences were included in each of the clusters.

## XI. Microarray Analysis

### Probe Preparation from Tissue or Cell Samples

5 Total RNA is isolated from tissue samples using the guanidinium thiocyanate method and polyA<sup>+</sup> RNA is purified using the oligo (dT) cellulose method. Each polyA<sup>+</sup> RNA sample is reverse transcribed using MMLV reverse-transcriptase, 0.05 pg/ $\mu$ l oligo-dT primer (21mer), 1X first strand buffer, 0.03 units/ $\mu$ l RNase inhibitor, 500  $\mu$ M dATP, 500  $\mu$ M dGTP, 500  $\mu$ M dTTP, 40  $\mu$ M dCTP, 40  $\mu$ M dCTP-Cy3 (BDS) or dCTP-Cy5 (Amersham Pharmacia Biotech). The reverse transcription  
10 reaction is performed in a 25 ml volume containing 200 ng polyA<sup>+</sup> RNA with GEMBRIGHT kits (Incyte). Specific control polyA<sup>+</sup> RNAs are synthesized by in vitro transcription from non-coding yeast genomic DNA (W. Lei, unpublished). As quantitative controls, the control mRNAs at 0.002 ng, 0.02 ng, 0.2 ng, and 2 ng are diluted into reverse transcription reaction at ratios of 1:100,000, 1:10,000, 1:1000, 1:100 (w/w) to sample mRNA respectively. The control mRNAs are diluted into  
15 reverse transcription reaction at ratios of 1:3, 3:1, 1:10, 10:1, 1:25, 25:1 (w/w) to sample mRNA differential expression patterns. After incubation at 37° C for 2 hr, each reaction sample (one with Cy3 and another with Cy5 labeling) is treated with 2.5 ml of 0.5M sodium hydroxide and incubated for 20 minutes at 85° C to the stop the reaction and degrade the RNA. Probes are purified using two successive CHROMA SPIN 30 gel filtration spin columns (CLONTECH Laboratories, Inc.  
20 (CLONTECH), Palo Alto CA) and after combining, both reaction samples are ethanol precipitated using 1 ml of glycogen (1 mg/ml), 60 ml sodium acetate, and 300 ml of 100% ethanol. The probe is then dried to completion using a SpeedVAC (Savant Instruments Inc., Holbrook NY) and resuspended in 14  $\mu$ l 5X SSC/0.2% SDS.

### 25 Microarray Preparation

Sequences of the present invention are used to generate array elements. Each array element is amplified from bacterial cells containing vectors with cloned cDNA inserts. PCR amplification uses primers complementary to the vector sequences flanking the cDNA insert. Array elements are amplified in thirty cycles of PCR from an initial quantity of 1-2 ng to a final quantity greater than 5  
30  $\mu$ g. Amplified array elements are then purified using SEPHACRYL-400 (Amersham Pharmacia Biotech).

Purified array elements are immobilized on polymer-coated glass slides. Glass microscope slides (Corning) are cleaned by ultrasound in 0.1% SDS and acetone, with extensive distilled water washes between and after treatments. Glass slides are etched in 4% hydrofluoric acid (VWR  
35 Scientific Products Corporation (VWR), West Chester, PA), washed extensively in distilled water, and coated with 0.05% aminopropyl silane (Sigma) in 95% ethanol. Coated slides are cured in a

110°C oven.

Array elements are applied to the coated glass substrate using a procedure described in US Patent No. 5,807,522, incorporated herein by reference. 1  $\mu$ l of the array element DNA, at an average concentration of 100 ng/ $\mu$ l, is loaded into the open capillary printing element by a high-speed robotic apparatus. The apparatus then deposits about 5 nl of array element sample per slide.

Microarrays are UV-crosslinked using a STRATALINKER UV-crosslinker (Stratagene). Microarrays are washed at room temperature once in 0.2% SDS and three times in distilled water. Non-specific binding sites are blocked by incubation of microarrays in 0.2% casein in phosphate buffered saline (PBS) (Tropix, Inc., Bedford, MA) for 30 minutes at 60°C followed by washes in 0.2% SDS and distilled water as before.

#### Hybridization

Hybridization reactions contain 9  $\mu$ l of probe mixture consisting of 0.2  $\mu$ g each of Cy3 and Cy5 labeled cDNA synthesis products in 5X SSC, 0.2% SDS hybridization buffer. The probe mixture is heated to 65°C for 5 minutes and is aliquoted onto the microarray surface and covered with an 1.8 cm<sup>2</sup> coverslip. The arrays are transferred to a waterproof chamber having a cavity just slightly larger than a microscope slide. The chamber is kept at 100% humidity internally by the addition of 140  $\mu$ l of 5x SSC in a corner of the chamber. The chamber containing the arrays is incubated for about 6.5 hours at 60°C. The arrays are washed for 10 min at 45°C in a first wash buffer (1X SSC, 0.1% SDS), three times for 10 minutes each at 45°C in a second wash buffer (0.1X SSC), and dried.

#### Detection

Reporter-labeled hybridization complexes are detected with a microscope equipped with an Innova 70 mixed gas 10 W laser (Coherent, Inc., Santa Clara CA) capable of generating spectral lines at 488 nm for excitation of Cy3 and at 632 nm for excitation of Cy5. The excitation laser light is focused on the array using a 20X microscope objective (Nikon, Inc., Melville NY). The slide containing the array is placed on a computer-controlled X-Y stage on the microscope and raster-scanned past the objective. The 1.8 cm x 1.8 cm array used in the present example is scanned with a resolution of 20 micrometers.

In two separate scans, a mixed gas multiline laser excites the two fluorophores sequentially. Emitted light is split, based on wavelength, into two photomultiplier tube detectors (PMT R1477, Hamamatsu Photonics Systems, Bridgewater NJ) corresponding to the two fluorophores. Appropriate filters positioned between the array and the photomultiplier tubes are used to filter the signals. The emission maxima of the fluorophores used are 565 nm for Cy3 and 650 nm for Cy5. Each array is typically scanned twice, one scan per fluorophore using the appropriate filters at the laser source, although the apparatus is capable of recording the spectra from both fluorophores simultaneously.

The sensitivity of the scans is typically calibrated using the signal intensity generated by a cDNA control species added to the probe mix at a known concentration. A specific location on the array contains a complementary DNA sequence, allowing the intensity of the signal at that location to be correlated with a weight ratio of hybridizing species of 1:100,000. When two probes from  
5 different sources (e.g., representing test and control cells), each labeled with a different fluorophore, are hybridized to a single array for the purpose of identifying genes that are differentially expressed, the calibration is done by labeling samples of the calibrating cDNA with the two fluorophores and adding identical amounts of each to the hybridization mixture.

The output of the photomultiplier tube is digitized using a 12-bit RTI-835H analog-to-digital  
10 (A/D) conversion board (Analog Devices, Inc., Norwood, MA) installed in an IBM-compatible PC computer. The digitized data are displayed as an image where the signal intensity is mapped using a linear 20-color transformation to a pseudocolor scale ranging from blue (low signal) to red (high signal). The data is also analyzed quantitatively. Where two different fluorophores are excited and measured simultaneously, the data are first corrected for optical crosstalk (due to overlapping  
15 emission spectra) between the fluorophores using each fluorophore's emission spectrum.

A grid is superimposed over the fluorescence signal image such that the signal from each spot is centered in each element of the grid. The fluorescence signal within each element is then integrated to obtain a numerical value corresponding to the average intensity of the signal. The software used for signal analysis is the GEMTOOLS gene expression analysis program (Incyte).

20

## **XII. Complementary Nucleic Acids**

Sequences complementary to the dithp are used to detect, decrease, or inhibit expression of the naturally occurring nucleotide. The use of oligonucleotides comprising from about 15 to 30 base pairs is typical in the art. However, smaller or larger sequence fragments can also be used.

25 Appropriate oligonucleotides are designed from the dithp using OLIGO 4.06 software (National Biosciences) or other appropriate programs and are synthesized using methods standard in the art or ordered from a commercial supplier. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent transcription factor binding to the promoter sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent  
30 ribosomal binding and processing of the transcript.

## **XIII. Expression of DITHP**

Expression and purification of DITHP is accomplished using bacterial or virus-based expression systems. For expression of DITHP in bacteria, cDNA is subcloned into an appropriate  
35 vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*)

hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac* operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express DITHP upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of DITHP in eukaryotic cells is achieved by infecting  
 5 insect or mammalian cell lines with recombinant *Autographica californica* nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of baculovirus is replaced with cDNA encoding DITHP by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to  
 10 infect *Spodoptera frugiperda* (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic modifications to baculovirus. (See e.g., Engelhard, *supra*; and Sandig, *supra*.)

In most expression systems, DITHP is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step,  
 15 affinity-based purification of recombinant fusion protein from crude cell lysates. GST, a 26-kilodalton enzyme from *Schistosoma japonicum*, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from DITHP at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity  
 20 purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak Company, Rochester NY). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, *supra*, Chapters 10 and 16). Purified DITHP obtained by these methods can be used directly in the following activity assay.

25

#### XIV. Demonstration of DITHP Activity

DITHP activity is demonstrated through a variety of specific assays, some of which are outlined below.

Oxidoreductase activity of DITHP is measured by the increase in extinction coefficient of  
 30 NAD(P)H coenzyme at 340 nm for the measurement of oxidation activity, or the decrease in extinction coefficient of NAD(P)H coenzyme at 340 nm for the measurement of reduction activity (Dalziel, K. (1963) J. Biol. Chem. 238:2850-2858). One of three substrates may be used: Asn-βGal, biocytidine, or ubiquinone-10. The respective subunits of the enzyme reaction, for example, cytochrome c<sub>1</sub>-b oxidoreductase and cytochrome c, are reconstituted. The reaction mixture contains  
 35 a) 1-2 mg/ml DITHP; and b) 15 mM substrate, 2.4 mM NAD(P)<sup>+</sup> in 0.1 M phosphate buffer, pH 7.1 (oxidation reaction), or 2.0 mM NAD(P)H, in 0.1 M Na<sub>2</sub>HPO<sub>4</sub> buffer, pH 7.4 (reduction reaction); in



a total volume of 0.1 ml. Changes in absorbance at 340 nm ( $A_{340}$ ) are measured at 23.5° C using a recording spectrophotometer (Shimadzu Scientific Instruments, Inc., Pleasanton CA). The amount of NAD(P)H is stoichiometrically equivalent to the amount of substrate initially present, and the change in  $A_{340}$  is a direct measure of the amount of NAD(P)H produced;  $\Delta A_{340} = 6620[\text{NADH}]$ .

- 5 Oxidoreductase activity of DITHP activity is proportional to the amount of NAD(P)H present in the assay.

Transferase activity of DITHP is measured through assays such as a methyl transferase assay in which the transfer of radiolabeled methyl groups between a donor substrate and an acceptor substrate is measured (Bokar, J.A. et al. (1994) J. Biol. Chem. 269:17697-17704). Reaction mixtures  
10 (50  $\mu$ l final volume) contain 15 mM HEPES, pH 7.9, 1.5 mM  $\text{MgCl}_2$ , 10 mM dithiothreitol, 3% polyvinylalcohol, 1.5  $\mu$ Ci [*methyl*- $^3\text{H}$ ]AdoMet (0.375  $\mu$ M AdoMet) (DuPont-NEN), 0.6  $\mu$ g DITHP, and acceptor substrate (0.4  $\mu$ g [ $^{35}\text{S}$ ]RNA or 6-mercaptopurine (6-MP) to 1 mM final concentration). Reaction mixtures are incubated at 30° C for 30 minutes, then 65° C for 5 minutes. The products are separated by chromatography or electrophoresis and the level of methyl transferase activity is  
15 determined by quantification of *methyl*- $^3\text{H}$  recovery.

DITHP hydrolase activity is measured by the hydrolysis of appropriate synthetic peptide substrates conjugated with various chromogenic molecules in which the degree of hydrolysis is quantified by spectrophotometric (or fluorometric) absorption of the released chromophore. (Beynon, R.J. and J.S. Bond (1994) Proteolytic Enzymes: A Practical Approach, Oxford University Press, New  
20 York NY, pp. 25-55) Peptide substrates are designed according to the category of protease activity as endopeptidase (serine, cysteine, aspartic proteases), aminopeptidase (leucine aminopeptidase), or carboxypeptidase (Carboxypeptidase A and B, procollagen C-proteinase).

DITHP isomerase activity such as peptidyl prolyl *cis/trans* isomerase activity can be assayed by an enzyme assay described by Rahfeld, J.U., et al. (1994) (FEBS Lett. 352: 180-184). The assay  
25 is performed at 10° C in 35 mM HEPES buffer, pH 7.8, containing chymotrypsin (0.5 mg/ml) and DITHP at a variety of concentrations. Under these assay conditions, the substrate, Suc-Ala-Xaa-Pro-Phe-4-NA, is in equilibrium with respect to the prolyl bond, with 80-95% in *trans* and 5-20% in *cis* conformation. An aliquot (2  $\mu$ l) of the substrate dissolved in dimethyl sulfoxide (10 mg/ml) is added to the reaction mixture described above. Only the *cis* isomer of the substrate is a substrate for  
30 cleavage by chymotrypsin. Thus, as the substrate is isomerized by DITHP, the product is cleaved by chymotrypsin to produce 4-nitroanilide, which is detected by its absorbance at 390 nm. 4-Nitroanilide appears in a time-dependent and a DITHP concentration-dependent manner.

An assay for DITHP activity associated with growth and development measures cell proliferation as the amount of newly initiated DNA synthesis in Swiss mouse 3T3 cells. A plasmid  
35 containing polynucleotides encoding DITHP is transfected into quiescent 3T3 cultured cells using methods well known in the art. The transiently transfected cells are then incubated in the presence of

[<sup>3</sup>H]thymidine, a radioactive DNA precursor. Where applicable, varying amounts of DITHP ligand are added to the transfected cells. Incorporation of [<sup>3</sup>H]thymidine into acid-precipitable DNA is measured over an appropriate time interval, and the amount incorporated is directly proportional to the amount of newly synthesized DNA.

5           Growth factor activity of DITHP is measured by the stimulation of DNA synthesis in Swiss mouse 3T3 cells (McKay, I. and I. Leigh, eds. (1993) Growth Factors: A Practical Approach, Oxford University Press, New York NY). Initiation of DNA synthesis indicates the cells' entry into the mitotic cycle and their commitment to undergo later division. 3T3 cells are competent to respond to most growth factors, not only those that are mitogenic, but also those that are involved in embryonic  
10 induction. This competence is possible because the in vivo specificity demonstrated by some growth factors is not necessarily inherent but is determined by the responding tissue. In this assay, varying amounts of DITHP are added to quiescent 3T3 cultured cells in the presence of [<sup>3</sup>H]thymidine, a radioactive DNA precursor. DITHP for this assay can be obtained by recombinant means or from biochemical preparations. Incorporation of [<sup>3</sup>H]thymidine into acid-precipitable DNA is measured  
15 over an appropriate time interval, and the amount incorporated is directly proportional to the amount of newly synthesized DNA. A linear dose-response curve over at least a hundred-fold DITHP concentration range is indicative of growth factor activity. One unit of activity per milliliter is defined as the concentration of DITHP producing a 50% response level, where 100% represents maximal incorporation of [<sup>3</sup>H]thymidine into acid-precipitable DNA.

20           Alternatively, an assay for cytokine activity of DITHP measures the proliferation of leukocytes. In this assay, the amount of tritiated thymidine incorporated into newly synthesized DNA is used to estimate proliferative activity. Varying amounts of DITHP are added to cultured leukocytes, such as granulocytes, monocytes, or lymphocytes, in the presence of [<sup>3</sup>H]thymidine, a radioactive DNA precursor. DITHP for this assay can be obtained by recombinant means or from  
25 biochemical preparations. Incorporation of [<sup>3</sup>H]thymidine into acid-precipitable DNA is measured over an appropriate time interval, and the amount incorporated is directly proportional to the amount of newly synthesized DNA. A linear dose-response curve over at least a hundred-fold DITHP concentration range is indicative of DITHP activity. One unit of activity per milliliter is conventionally defined as the concentration of DITHP producing a 50% response level, where 100%  
30 represents maximal incorporation of [<sup>3</sup>H]thymidine into acid-precipitable DNA.

          An alternative assay for DITHP cytokine activity utilizes a Boyden micro chamber (Neuroprobe, Cabin John MD) to measure leukocyte chemotaxis (Vicari, supra). In this assay, about 10<sup>5</sup> migratory cells such as macrophages or monocytes are placed in cell culture media in the upper compartment of the chamber. Varying dilutions of DITHP are placed in the lower compartment. The  
35 two compartments are separated by a 5 or 8 micron pore polycarbonate filter (Nucleopore, Pleasanton CA). After incubation at 37°C for 80 to 120 minutes, the filters are fixed in methanol and stained

with appropriate labeling agents. Cells which migrate to the other side of the filter are counted using standard microscopy. The chemotactic index is calculated by dividing the number of migratory cells counted when DITHP is present in the lower compartment by the number of migratory cells counted when only media is present in the lower compartment. The chemotactic index is proportional to the activity of DITHP.

Alternatively, cell lines or tissues transformed with a vector containing dithp can be assayed for DITHP activity by immunoblotting. Cells are denatured in SDS in the presence of  $\beta$ -mercaptoethanol, nucleic acids removed by ethanol precipitation, and proteins purified by acetone precipitation. Pellets are resuspended in 20 mM tris buffer at pH 7.5 and incubated with Protein G-Sepharose pre-coated with an antibody specific for DITHP. After washing, the Sepharose beads are boiled in electrophoresis sample buffer, and the eluted proteins subjected to SDS-PAGE. The SDS-PAGE is transferred to a nitrocellulose membrane for immunoblotting, and the DITHP activity is assessed by visualizing and quantifying bands on the blot using the antibody specific for DITHP as the primary antibody and  $^{125}\text{I}$ -labeled IgG specific for the primary antibody as the secondary antibody.

DITHP kinase activity is measured by phosphorylation of a protein substrate using  $\gamma$ -labeled [ $^{32}\text{P}$ ]-ATP and quantitation of the incorporated radioactivity using a radioisotope counter. DITHP is incubated with the protein substrate, [ $^{32}\text{P}$ ]-ATP, and an appropriate kinase buffer. The [ $^{32}\text{P}$ ] incorporated into the product is separated from free [ $^{32}\text{P}$ ]-ATP by electrophoresis and the incorporated [ $^{32}\text{P}$ ] is counted. The amount of [ $^{32}\text{P}$ ] recovered is proportional to the kinase activity of DITHP in the assay. A determination of the specific amino acid residue phosphorylated is made by phosphoamino acid analysis of the hydrolyzed protein.

In the alternative, DITHP activity is measured by the increase in cell proliferation resulting from transformation of a mammalian cell line such as COS7, HeLa or CHO with an eukaryotic expression vector encoding DITHP. Eukaryotic expression vectors are commercially available, and the techniques to introduce them into cells are well known to those skilled in the art. The cells are incubated for 48-72 hours after transformation under conditions appropriate for the cell line to allow expression of DITHP. Phase microscopy is then used to compare the mitotic index of transformed versus control cells. An increase in the mitotic index indicates DITHP activity.

In a further alternative, an assay for DITHP signaling activity is based upon the ability of GPCR family proteins to modulate G protein-activated second messenger signal transduction pathways (e.g., cAMP; Gaudin, P. et al. (1998) J. Biol. Chem. 273:4990-4996). A plasmid encoding full length DITHP is transfected into a mammalian cell line (e.g., Chinese hamster ovary (CHO) or human embryonic kidney (HEK-293) cell lines) using methods well-known in the art. Transfected cells are grown in 12-well trays in culture medium for 48 hours, then the culture medium is discarded, and the attached cells are gently washed with PBS. The cells are then incubated in culture medium with or without ligand for 30 minutes, then the medium is removed and cells lysed by

treatment with 1 M perchloric acid. The cAMP levels in the lysate are measured by radioimmunoassay using methods well-known in the art. Changes in the levels of cAMP in the lysate from cells exposed to ligand compared to those without ligand are proportional to the amount of DITHP present in the transfected cells.

- 5 Alternatively, an assay for DITHP protein phosphatase activity measures the hydrolysis of P-nitrophenyl phosphate (PNPP). DITHP is incubated together with PNPP in HEPES buffer pH 7.5, in the presence of 0.1%  $\beta$ -mercaptoethanol at 37°C for 60 min. The reaction is stopped by the addition of 6 ml of 10 N NaOH, and the increase in light absorbance of the reaction mixture at 410 nm resulting from the hydrolysis of PNPP is measured using a spectrophotometer. The increase in light  
10 absorbance is proportional to the phosphatase activity of DITHP in the assay (Diamond, R.H. et al (1994) Mol Cell Biol 14:3752-3762).

- An alternative assay measures DITHP-mediated G-protein signaling activity by monitoring the mobilization of  $\text{Ca}^{++}$  as an indicator of the signal transduction pathway stimulation. (See, e.g., Grynkievicz, G. et al. (1985) J. Biol. Chem. 260:3440; McColl, S. et al. (1993) J. Immunol.  
15 150:4550-4555; and Aussel, C. et al. (1988) J. Immunol. 140:215-220). The assay requires preloading neutrophils or T cells with a fluorescent dye such as FURA-2 or BCECF (Universal Imaging Corp, Westchester PA) whose emission characteristics are altered by  $\text{Ca}^{++}$  binding. When the cells are exposed to one or more activating stimuli artificially (e.g., anti-CD3 antibody ligation of the T cell receptor) or physiologically (e.g., by allogeneic stimulation),  $\text{Ca}^{++}$  flux takes place. This  
20 flux can be observed and quantified by assaying the cells in a fluorometer or fluorescent activated cell sorter. Measurements of  $\text{Ca}^{++}$  flux are compared between cells in their normal state and those transfected with DITHP. Increased  $\text{Ca}^{++}$  mobilization attributable to increased DITHP concentration is proportional to DITHP activity.

- DITHP transport activity is assayed by measuring uptake of labeled substrates into Xenopus  
25 laevis oocytes. Oocytes at stages V and VI are injected with DITHP mRNA (10 ng per oocyte) and incubated for 3 days at 18°C in OR2 medium (82.5mM NaCl, 2.5 mM KCl, 1mM  $\text{CaCl}_2$ , 1mM  $\text{MgCl}_2$ , 1mM  $\text{Na}_2\text{HPO}_4$ , 5 mM Hepes, 3.8 mM NaOH, 50 $\mu\text{g/ml}$  gentamycin, pH 7.8) to allow expression of DITHP protein. Oocytes are then transferred to standard uptake medium (100mM NaCl, 2 mM KCl, 1mM  $\text{CaCl}_2$ , 1mM  $\text{MgCl}_2$ , 10 mM Hepes/Tris pH 7.5). Uptake of various  
30 substrates (e.g., amino acids, sugars, drugs, ions, and neurotransmitters) is initiated by adding labeled substrate (e.g. radiolabeled with  $^3\text{H}$ , fluorescently labeled with rhodamine, etc.) to the oocytes. After incubating for 30 minutes, uptake is terminated by washing the oocytes three times in  $\text{Na}^+$ -free medium, measuring the incorporated label, and comparing with controls. DITHP transport activity is proportional to the level of internalized labeled substrate.

- 35 DITHP transferase activity is demonstrated by a test for galactosyltransferase activity. This can be determined by measuring the transfer of radiolabeled galactose from UDP-galactose to a

GlcNAc-terminated oligosaccharide chain (Kolbinger, F. et al. (1998) *J. Biol. Chem.* 273:58-65). The sample is incubated with 14  $\mu$ l of assay stock solution (180 mM sodium cacodylate, pH 6.5, 1 mg/ml bovine serum albumin, 0.26 mM UDP-galactose, 2  $\mu$ l of UDP-[<sup>3</sup>H]galactose), 1  $\mu$ l of MnCl<sub>2</sub> (500 mM), and 2.5  $\mu$ l of GlcNAc $\beta$ O-(CH<sub>2</sub>)<sub>4</sub>-CO<sub>2</sub>Me (37 mg/ml in dimethyl sulfoxide) for 60 minutes at 37 °C. The reaction is quenched by the addition of 1 ml of water and loaded on a C18 Sep-Pak cartridge (Waters), and the column is washed twice with 5 ml of water to remove unreacted UDP-[<sup>3</sup>H]galactose. The [<sup>3</sup>H]galactosylated GlcNAc $\beta$ O-(CH<sub>2</sub>)<sub>4</sub>-CO<sub>2</sub>Me remains bound to the column during the water washes and is eluted with 5 ml of methanol. Radioactivity in the eluted material is measured by liquid scintillation counting and is proportional to galactosyltransferase activity in the starting sample.

In the alternative, DITHP induction by heat or toxins may be demonstrated using primary cultures of human fibroblasts or human cell lines such as CCL-13, HEK293, or HEP G2 (ATCC). To heat induce DITHP expression, aliquots of cells are incubated at 42 °C for 15, 30, or 60 minutes. Control aliquots are incubated at 37 °C for the same time periods. To induce DITHP expression by toxins, aliquots of cells are treated with 100  $\mu$ M arsenite or 20 mM azetidine-2-carboxylic acid for 0, 3, 6, or 12 hours. After exposure to heat, arsenite, or the amino acid analogue, samples of the treated cells are harvested and cell lysates prepared for analysis by western blot. Cells are lysed in lysis buffer containing 1% Nonidet P-40, 0.15 M NaCl, 50 mM Tris-HCl, 5 mM EDTA, 2 mM N-ethylmaleimide, 2 mM phenylmethylsulfonyl fluoride, 1 mg/ml leupeptin, and 1 mg/ml pepstatin. Twenty micrograms of the cell lysate is separated on an 8% SDS-PAGE gel and transferred to a membrane. After blocking with 5% nonfat dry milk/phosphate-buffered saline for 1 h, the membrane is incubated overnight at 4 °C or at room temperature for 2-4 hours with a 1:1000 dilution of anti-DITHP serum in 2% nonfat dry milk/phosphate-buffered saline. The membrane is then washed and incubated with a 1:1000 dilution of horseradish peroxidase-conjugated goat anti-rabbit IgG in 2% dry milk/phosphate-buffered saline. After washing with 0.1% Tween 20 in phosphate-buffered saline, the DITHP protein is detected and compared to controls using chemiluminescence.

Alternatively, DITHP protease activity is measured by the hydrolysis of appropriate synthetic peptide substrates conjugated with various chromogenic molecules in which the degree of hydrolysis is quantified by spectrophotometric (or fluorometric) absorption of the released chromophore (Beynon, R.J. and J.S. Bond (1994) Proteolytic Enzymes: A Practical Approach, Oxford University Press, New York, NY, pp.25-55). Peptide substrates are designed according to the category of protease activity as endopeptidase (serine, cysteine, aspartic proteases, or metalloproteases), aminopeptidase (leucine aminopeptidase), or carboxypeptidase (carboxypeptidases A and B, procollagen C-proteinase). Commonly used chromogens are 2-naphthylamine, 4-nitroaniline, and furylacrylic acid. Assays are performed at ambient temperature and contain an aliquot of the enzyme and the appropriate substrate in a suitable buffer. Reactions are carried out in an optical cuvette, and

the increase/decrease in absorbance of the chromogen released during hydrolysis of the peptide substrate is measured. The change in absorbance is proportional to the DITHP protease activity in the assay.

In the alternative, an assay for DITHP protease activity takes advantage of fluorescence resonance energy transfer (FRET) that occurs when one donor and one acceptor fluorophore with an appropriate spectral overlap are in close proximity. A flexible peptide linker containing a cleavage site specific for PRTS is fused between a red-shifted variant (RSGFP4) and a blue variant (BFP5) of Green Fluorescent Protein. This fusion protein has spectral properties that suggest energy transfer is occurring from BFP5 to RSGFP4. When the fusion protein is incubated with DITHP, the substrate is cleaved, and the two fluorescent proteins dissociate. This is accompanied by a marked decrease in energy transfer which is quantified by comparing the emission spectra before and after the addition of DITHP (Mitra, R.D. et al (1996) *Gene* 173:13-17). This assay can also be performed in living cells. In this case the fluorescent substrate protein is expressed constitutively in cells and DITHP is introduced on an inducible vector so that FRET can be monitored in the presence and absence of DITHP (Sagot, I. et al (1999) *FEBS Lett.* 447:53-57).

A method to determine the nucleic acid binding activity of DITHP involves a polyacrylamide gel mobility-shift assay. In preparation for this assay, DITHP is expressed by transforming a mammalian cell line such as COS7, HeLa or CHO with a eukaryotic expression vector containing DITHP cDNA. The cells are incubated for 48-72 hours after transformation under conditions appropriate for the cell line to allow expression and accumulation of DITHP. Extracts containing solubilized proteins can be prepared from cells expressing DITHP by methods well known in the art. Portions of the extract containing DITHP are added to [<sup>32</sup>P]-labeled RNA or DNA. Radioactive nucleic acid can be synthesized *in vitro* by techniques well known in the art. The mixtures are incubated at 25°C in the presence of RNase- and DNase-inhibitors under buffered conditions for 5-10 minutes. After incubation, the samples are analyzed by polyacrylamide gel electrophoresis followed by autoradiography. The presence of a band on the autoradiogram indicates the formation of a complex between DITHP and the radioactive transcript. A band of similar mobility will not be present in samples prepared using control extracts prepared from untransformed cells.

In the alternative, a method to determine the methylase activity of a DITHP measures transfer of radiolabeled methyl groups between a donor substrate and an acceptor substrate. Reaction mixtures (50 µl final volume) contain 15 mM HEPES, pH 7.9, 1.5 mM MgCl<sub>2</sub>, 10 mM dithiothreitol, 3% polyvinylalcohol, 1.5 µCi [*methyl*-<sup>3</sup>H]AdoMet (0.375 µM AdoMet) (DuPont-NEN), 0.6 µg DITHP, and acceptor substrate (e.g., 0.4 µg [<sup>35</sup>S]RNA, or 6-mercaptopurine (6-MP) to 1 mM final concentration). Reaction mixtures are incubated at 30 °C for 30 minutes, then 65 °C for 5 minutes. Analysis of [*methyl*-<sup>3</sup>H]RNA is as follows: 1) 50 µl of 2 x loading buffer (20 mM Tris-HCl, pH 7.6, 1 M LiCl, 1 mM EDTA, 1% sodium dodecyl sulphate (SDS)) and 50 µl oligo d(T)-cellulose (10 mg/ml

in 1 x loading buffer) are added to the reaction mixture, and incubated at ambient temperature with shaking for 30 minutes. 2) Reaction mixtures are transferred to a 96-well filtration plate attached to a vacuum apparatus. 3) Each sample is washed sequentially with three 2.4 ml aliquots of 1 x oligo d(T) loading buffer containing 0.5% SDS, 0.1% SDS, or no SDS. and 4) RNA is eluted with 300  $\mu$ l of water into a 96-well collection plate, transferred to scintillation vials containing liquid scintillant, and radioactivity determined. Analysis of [*methyl*- $^3$ H]6-MP is as follows: 1) 500  $\mu$ l 0.5 M borate buffer, pH 10.0, and then 2.5 ml of 20% (v/v) isoamyl alcohol in toluene are added to the reaction mixtures. 2) The samples mixed by vigorous vortexing for ten seconds. 3) After centrifugation at 700g for 10 minutes, 1.5 ml of the organic phase is transferred to scintillation vials containing 0.5 ml absolute ethanol and liquid scintillant, and radioactivity determined. and 4) Results are corrected for the extraction of 6-MP into the organic phase (approximately 41%).

An assay for adhesion activity of DITHP measures the disruption of cytoskeletal filament networks upon overexpression of DITHP in cultured cell lines (Reznicek, G.A. et al. (1998) J. Cell Biol. 141:209-225). cDNA encoding DITHP is subcloned into a mammalian expression vector that drives high levels of cDNA expression. This construct is transfected into cultured cells, such as rat kangaroo PtK2 or rat bladder carcinoma 804G cells. Actin filaments and intermediate filaments such as keratin and vimentin are visualized by immunofluorescence microscopy using antibodies and techniques well known in the art. The configuration and abundance of cytoskeletal filaments can be assessed and quantified using confocal imaging techniques. In particular, the bundling and collapse of cytoskeletal filament networks is indicative of DITHP adhesion activity.

Alternatively, an assay for DITHP activity measures the expression of DITHP on the cell surface. cDNA encoding DITHP is transfected into a non-leukocytic cell line. Cell surface proteins are labeled with biotin (de la Fuente, M.A. et al. (1997) Blood 90:2398-2405). Immunoprecipitations are performed using DITHP-specific antibodies, and immunoprecipitated samples are analyzed using SDS-PAGE and immunoblotting techniques. The ratio of labeled immunoprecipitant to unlabeled immunoprecipitant is proportional to the amount of DITHP expressed on the cell surface.

Alternatively, an assay for DITHP activity measures the amount of cell aggregation induced by overexpression of DITHP. In this assay, cultured cells such as NIH3T3 are transfected with cDNA encoding DITHP contained within a suitable mammalian expression vector under control of a strong promoter. Cotransfection with cDNA encoding a fluorescent marker protein, such as Green Fluorescent Protein (CLONTECH), is useful for identifying stable transfectants. The amount of cell agglutination, or clumping, associated with transfected cells is compared with that associated with untransfected cells. The amount of cell agglutination is a direct measure of DITHP activity.

DITHP may recognize and precipitate antigen from serum. This activity can be measured by the quantitative precipitin reaction (Golub, E.S. et al. (1987) *Immunology: A Synthesis*, Sinauer Associates, Sunderland MA, pages 113-115). DITHP is isotopically labeled using methods known in

the art. Various serum concentrations are added to constant amounts of labeled DITHP. DITHP-antigen complexes precipitate out of solution and are collected by centrifugation. The amount of precipitable DITHP-antigen complex is proportional to the amount of radioisotope detected in the precipitate. The amount of precipitable DITHP-antigen complex is plotted against the serum concentration. For various serum concentrations, a characteristic precipitation curve is obtained, in which the amount of precipitable DITHP-antigen complex initially increases proportionately with increasing serum concentration, peaks at the equivalence point, and then decreases proportionately with further increases in serum concentration. Thus, the amount of precipitable DITHP-antigen complex is a measure of DITHP activity which is characterized by sensitivity to both limiting and excess quantities of antigen.

A microtubule motility assay for DITHP measures motor protein activity. In this assay, recombinant DITHP is immobilized onto a glass slide or similar substrate. Taxol-stabilized bovine brain microtubules (commercially available) in a solution containing ATP and cytosolic extract are perfused onto the slide. Movement of microtubules as driven by DITHP motor activity can be visualized and quantified using video-enhanced light microscopy and image analysis techniques. DITHP motor protein activity is directly proportional to the frequency and velocity of microtubule movement.

Alternatively, an assay for DITHP measures the formation of protein filaments *in vitro*. A solution of DITHP at a concentration greater than the "critical concentration" for polymer assembly is applied to carbon-coated grids. Appropriate nucleation sites may be supplied in the solution. The grids are negative stained with 0.7% (w/v) aqueous uranyl acetate and examined by electron microscopy. The appearance of filaments of approximately 25 nm (microtubules), 8 nm (actin), or 10 nm (intermediate filaments) is a demonstration of protein activity.

DITHP electron transfer activity is demonstrated by oxidation or reduction of NADP. Substrates such as Asn- $\beta$ Gal, biocytidine, or ubiquinone-10 may be used. The reaction mixture contains 1-2 mg/ml HORP, 15 mM substrate, and 2.4 mM NAD(P)<sup>+</sup> in 0.1 M phosphate buffer, pH 7.1 (oxidation reaction), or 2.0 mM NAD(P)H, in 0.1 M Na<sub>2</sub>HPO<sub>4</sub> buffer, pH 7.4 (reduction reaction); in a total volume of 0.1 ml. FAD may be included with NAD, according to methods well known in the art. Changes in absorbance are measured using a recording spectrophotometer. The amount of NAD(P)H is stoichiometrically equivalent to the amount of substrate initially present, and the change in A<sub>340</sub> is a direct measure of the amount of NAD(P)H produced;  $\Delta A_{340} = 6620[\text{NADH}]$ . DITHP activity is proportional to the amount of NAD(P)H present in the assay. The increase in extinction coefficient of NAD(P)H coenzyme at 340 nm is a measure of oxidation activity, or the decrease in extinction coefficient of NAD(P)H coenzyme at 340 nm is a measure of reduction activity (Dalziel, K. (1963) J. Biol. Chem. 238:2850-2858).

DITHP transcription factor activity is measured by its ability to stimulate transcription of a



reporter gene (Liu, H.Y. et al. (1997) EMBO J. 16:5289-5298). The assay entails the use of a well characterized reporter gene construct, LexA<sub>op</sub>-LacZ, that consists of LexA DNA transcriptional control elements (LexA<sub>op</sub>) fused to sequences encoding the *E. coli* LacZ enzyme. The methods for constructing and expressing fusion genes, introducing them into cells, and measuring LacZ enzyme activity, are well known to those skilled in the art. Sequences encoding DITHP are cloned into a plasmid that directs the synthesis of a fusion protein, LexA-DITHP, consisting of DITHP and a DNA binding domain derived from the LexA transcription factor. The resulting plasmid, encoding a LexA-DITHP fusion protein, is introduced into yeast cells along with a plasmid containing the LexA<sub>op</sub>-LacZ reporter gene. The amount of LacZ enzyme activity associated with LexA-DITHP transfected cells, relative to control cells, is proportional to the amount of transcription stimulated by the DITHP.

Chromatin activity of DITHP is demonstrated by measuring sensitivity to DNase I (Dawson, B.A. et al. (1989) J. Biol. Chem. 264:12830-12837). Samples are treated with DNase I, followed by insertion of a cleavable biotinylated nucleotide analog, 5-[(N-biotinamido)hexanoamido-ethyl-1,3-thiopropionyl-3-aminoallyl]-2'-deoxyuridine 5'-triphosphate using nick-repair techniques well known to those skilled in the art. Following purification and digestion with EcoRI restriction endonuclease, biotinylated sequences are affinity isolated by sequential binding to streptavidin and biotincellulose.

Another specific assay demonstrates the ion conductance capacity of DITHP using an electrophysiological assay. DITHP is expressed by transforming a mammalian cell line such as COS7, HeLa or CHO with a eukaryotic expression vector encoding DITHP. Eukaryotic expression vectors are commercially available, and the techniques to introduce them into cells are well known to those skilled in the art. A small amount of a second plasmid, which expresses any one of a number of marker genes such as  $\beta$ -galactosidase, is co-transformed into the cells in order to allow rapid identification of those cells which have taken up and expressed the foreign DNA. The cells are incubated for 48-72 hours after transformation under conditions appropriate for the cell line to allow expression and accumulation of DITHP and  $\beta$ -galactosidase. Transformed cells expressing  $\beta$ -galactosidase are stained blue when a suitable colorimetric substrate is added to the culture media under conditions that are well known in the art. Stained cells are tested for differences in membrane conductance due to various ions by electrophysiological techniques that are well known in the art. Untransformed cells, and/or cells transformed with either vector sequences alone or  $\beta$ -galactosidase sequences alone, are used as controls and tested in parallel. The contribution of DITHP to cation or anion conductance can be shown by incubating the cells using antibodies specific for either DITHP. The respective antibodies will bind to the extracellular side of DITHP, thereby blocking the pore in the ion channel, and the associated conductance.

#### 35 XV. Functional Assays

DITHP function is assessed by expressing dithp at physiologically elevated levels in

mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen Corporation, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10  $\mu$ g of recombinant vector are transiently transfected into  
5 a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2  $\mu$ g of an additional plasmid containing sequences encoding a marker protein are co-transfected.

Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector.  
10 Marker proteins of choice include, e.g., Green Fluorescent Protein (GFP; CLONTECH), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties.

FCM detects and quantifies the uptake of fluorescent molecules that diagnose events  
15 preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific antibodies; and alterations in plasma  
20 membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M. G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of DITHP on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding DITHP and either CD64 or CD64-GFP.  
25 CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Inc., Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding DITHP and other genes of interest can be analyzed by  
30 northern analysis or microarray techniques.

#### XVI. Production of Antibodies

DITHP substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to  
35 immunize rabbits and to produce antibodies using standard protocols.

Alternatively, the DITHP amino acid sequence is analyzed using LASERGENE software

(UNAS'IAK) to determine regions of high immunogenicity, and a corresponding peptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, supra, Chapter 11.)

- 5 Typically, peptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Applied Biosystems) using fmoc-chemistry and coupled to KLH (Sigma) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, supra.) Rabbits are immunized with the peptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for anti-peptide activity by, for example, binding the peptide to
- 10 plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG. Antisera with anti-peptide activity are tested for anti-DITHP activity using protocols well known in the art, including ELISA, RIA, and immunoblotting.

#### **XVII. Purification of Naturally Occurring DITHP Using Specific Antibodies**

- 15 Naturally occurring or recombinant DITHP is substantially purified by immunoaffinity chromatography using antibodies specific for DITHP. An immunoaffinity column is constructed by covalently coupling anti-DITHP antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.
- 20 Media containing DITHP are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of DITHP (e.g., high ionic strength buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/DITHP binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and DITHP is collected.

25

#### **XVIII. Identification of Molecules Which Interact with DITHP**

- DITHP, or biologically active fragments thereof, are labeled with <sup>125</sup>I Bolton-Hunter reagent. (See, e.g., Bolton, A.E. and W.M. Hunter (1973) Biochem. J. 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled DITHP, washed,
- 30 and any wells with labeled DITHP complex are assayed. Data obtained using different concentrations of DITHP are used to calculate values for the number, affinity, and association of DITHP with the candidate molecules.

- Alternatively, molecules interacting with DITHP are analyzed using the yeast two-hybrid system as described in Fields, S. and O. Song (1989) Nature 340:245-246, or using commercially
- 35 available kits based on the two-hybrid system, such as the MATCHMAKER system (CLONTECH).

DITHP may also be used in the PATHCALLING process (CuraGen Corp., New Haven CT)

which employs the yeast two-hybrid system in a high-throughput manner to determine all interactions between the proteins encoded by two large libraries of genes (Nandabalan, K. et al. (2000) U.S. Patent No. 6,057,101).

- 5           All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred  
10   embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the above-described modes for carrying out the invention which are obvious to those skilled in the field of molecular biology or related fields are intended to be within the scope of the following claims.

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
1	LG:1040626.1:2001MAR30	671	LG:1040626.1.orf3:2001MAR30
2	LG:1041136.7:2001MAR30	672	LG:1041136.7.orf3:2001MAR30
3	LG:1043848.1:2001MAR30	673	LG:1043848.1.orf3:2001MAR30
4	LG:1097673.1:2001MAR30	674	LG:1097673.1.orf1:2001MAR30
5	LG:133991.1:2001MAR30	675	LG:133991.1.orf1:2001MAR30
6	LG:1397110.7:2001MAR30	676	LG:1397110.7.orf3:2001MAR30
7	LG:1512094.1:2001MAR30	677	LG:1512094.1.orf3:2001MAR30
8	LG:230734.53:2001MAR30	678	LG:230734.53.orf1:2001MAR30
9	LG:240154.9:2001MAR30	679	LG:240154.9.orf2:2001MAR30
10	LG:245863.31:2001MAR30	680	LG:245863.31.orf3:2001MAR30
11	LG:257151.4:2001MAR30	681	LG:257151.4.orf2:2001MAR30
12	LG:334053.8:2001MAR30	682	LG:334053.8.orf1:2001MAR30
13	LG:392033.1:2001MAR30	683	LG:392033.1.orf1:2001MAR30
14	LG:401748.16:2001MAR30	684	LG:401748.16.orf3:2001MAR30
15	LG:476084.1:2001MAR30	685	LG:476084.1.orf2:2001MAR30
16	LG:068514.1:2001MAR30	686	LG:068514.1.orf2:2001MAR30
17	LI:010505.1:2001MAY17	687	LI:010505.1.orf1:2001MAY17
18	LI:011664.1:2001MAY17	688	LI:011664.1.orf1:2001MAY17
19	LI:021459.66:2001MAY17	689	LI:021459.66.orf3:2001MAY17
20	LI:1047290.8:2001MAY17	690	LI:1047290.8.orf2:2001MAY17
21	LI:1071608.1:2001MAY17	691	LI:1071608.1.orf2:2001MAY17
22	LI:1077079.4:2001MAY17	692	LI:1077079.4.orf2:2001MAY17
23	LI:1173294.9:2001MAY17	693	LI:1173294.9.orf1:2001MAY17
24	LI:148565.7:2001MAY17	694	LI:148565.7.orf2:2001MAY17
25	LI:2052562.23:2001MAY17	695	LI:2052562.23.orf3:2001MAY17
26	LI:2119354.20:2001MAY17	696	LI:2119354.20.orf1:2001MAY17
27	LI:2209329.1:2001MAY17	697	LI:2209329.1.orf2:2001MAY17
28	LI:240143.12:2001MAY17	698	LI:240143.12.orf2:2001MAY17
29	LI:250855.6:2001MAY17	699	LI:250855.6.orf2:2001MAY17
30	LI:293078.2:2001MAY17	700	LI:293078.2.orf3:2001MAY17
31	LI:351818.62:2001MAY17	701	LI:351818.62.orf3:2001MAY17
32	LI:409990.1:2001MAY17	702	LI:409990.1.orf1:2001MAY17
33	LI:474832.7:2001MAY17	703	LI:474832.7.orf2:2001MAY17
34	LI:814696.11:2001MAY17	704	LI:814696.11.orf2:2001MAY17
35	LI:818488.31:2001MAY17	705	LI:818488.31.orf1:2001MAY17
36	LI:2049834.12:2001MAY17	706	LI:2049834.12.orf3:2001MAY17
37	LI:338956.8:2001MAY17	707	LI:338956.8.orf3:2001MAY17
38	LI:1175083.15:2001MAY17	708	LI:1175083.15.orf3:2001MAY17
39	LI:1189311.14:2001MAY17	709	LI:1189311.14.orf2:2001MAY17
40	LI:330984.6:2001MAY17	710	LI:330984.6.orf3:2001MAY17
41	LG:1093461.22:2001JUN22	711	LG:1093461.22.orf3:2001JUN22
42	LG:1138554.48:2001JUN22	712	LG:1138554.48.orf1:2001JUN22
43	LG:1377369.20:2001JUN22	713	LG:1377369.20.orf1:2001JUN22
44	LG:200050.17:2001JUN22	714	LG:200050.17.orf3:2001JUN22
45	LG:437008.4:2001JUN22	715	LG:437008.4.orf2:2001JUN22
46	LG:7684119.1:2001JUN22	716	LG:7684119.1.orf3:2001JUN22
47	LG:7690376.8:2001JUN22	717	LG:7690376.8.orf2:2001JUN22
48	LG:068514.3:2001JUN22	718	LG:068514.3.orf2:2001JUN22
49	LG:270209.1:2001JUN22	719	LG:270209.1.orf1:2001JUN22
50	LG:1400575.1:2001MAR30	720	LG:1400575.1.orf2:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
51	LG:242968.4:2001MAR30	721	LG:242968.4.orf1:2001MAR30
52	LG:344741.17:2001MAR30	722	LG:344741.17.orf2:2001MAR30
53	LG:443203.7:2001MAR30	723	LG:443203.7.orf2:2001MAR30
54	LG:481492.6:2001MAR30	724	LG:481492.6.orf2:2001MAR30
55	LI:035870.26:2001MAY17	725	LI:035870.26.orf3:2001MAY17
56	LI:2121852.1:2001MAY17	726	LI:2121852.1.orf3:2001MAY17
57	LI:2164765.1:2001MAY17	727	LI:2164765.1.orf1:2001MAY17
58	LI:2167150.1:2001MAY17	728	LI:2167150.1.orf2:2001MAY17
59	LI:230062.10:2001MAY17	729	LI:230062.10.orf2:2001MAY17
60	LI:351749.1:2001MAY17	730	LI:351749.1.orf2:2001MAY17
61	LI:399808.27:2001MAY17	731	LI:399808.27.orf3:2001MAY17
62	LI:401269.13:2001MAY17	732	LI:401269.13.orf3:2001MAY17
63	LI:481492.3:2001MAY17	733	LI:481492.3.orf3:2001MAY17
64	LI:1186340.9:2001MAY17	734	LI:1186340.9.orf3:2001MAY17
65	LG:1324237.7:2001JUN22	735	LG:1324237.7.orf1:2001JUN22
66	LG:142131.16:2001JUN22	736	LG:142131.16.orf3:2001JUN22
67	LG:407723.12:2001JUN22	737	LG:407723.12.orf3:2001JUN22
68	LG:7685000.6:2001JUN22	738	LG:7685000.6.orf3:2001JUN22
69	LG:1395921.6:2001JUN22	739	LG:1395921.6.orf1:2001JUN22
70	LG:230062.16:2001JUN22	740	LG:230062.16.orf2:2001JUN22
71	LG:7690036.1:2001JUN22	741	LG:7690036.1.orf2:2001JUN22
72	LG:044276.1:2001JUN22	742	LG:044276.1.orf3:2001JUN22
73	LG:1091967.34:2001JUN22	743	LG:1091967.34.orf1:2001JUN22
73	LG:1091967.34:2001JUN22	744	LG:1091967.34.orf2:2001JUN22
74	LG:242968.17:2001JUN22	745	LG:242968.17.orf1:2001JUN22
75	LG:081174.1:2001MAR30	746	LG:081174.1.orf1:2001MAR30
76	LG:1385255.10:2001MAR30	747	LG:1385255.10.orf3:2001MAR30
77	LG:1397492.21:2001MAR30	748	LG:1397492.21.orf2:2001MAR30
78	LG:1512330.2:2001MAR30	749	LG:1512330.2.orf3:2001MAR30
79	LG:300009.1:2001MAR30	750	LG:300009.1.orf3:2001MAR30
80	LG:333886.2:2001MAR30	751	LG:333886.2.orf1:2001MAR30
81	LG:349438.18:2001MAR30	752	LG:349438.18.orf2:2001MAR30
82	LG:358239.46:2001MAR30	753	LG:358239.46.orf2:2001MAR30
83	LG:250170.3:2001MAR30	754	LG:250170.3.orf2:2001MAR30
84	LG:1383159.5:2001MAR30	755	LG:1383159.5.orf2:2001MAR30
85	LI:044888.1:2001MAY17	756	LI:044888.1.orf2:2001MAY17
86	LI:101277.1:2001MAY17	757	LI:101277.1.orf1:2001MAY17
87	LI:1021852.6:2001MAY17	758	LI:1021852.6.orf2:2001MAY17
88	LI:1072004.14:2001MAY17	759	LI:1072004.14.orf3:2001MAY17
89	LI:1084017.20:2001MAY17	760	LI:1084017.20.orf3:2001MAY17
90	LI:1183158.1:2001MAY17	761	LI:1183158.1.orf3:2001MAY17
91	LI:1188807.9:2001MAY17	762	LI:1188807.9.orf3:2001MAY17
92	LI:206576.15:2001MAY17	763	LI:206576.15.orf2:2001MAY17
93	LI:2120427.4:2001MAY17	764	LI:2120427.4.orf1:2001MAY17
94	LI:2196074.2:2001MAY17	765	LI:2196074.2.orf2:2001MAY17
94	LI:2196074.2:2001MAY17	766	LI:2196074.2.orf3:2001MAY17
95	LI:220797.7:2001MAY17	767	LI:220797.7.orf3:2001MAY17
96	LI:237723.23:2001MAY17	768	LI:237723.23.orf1:2001MAY17
97	LI:817560.12:2001MAY17	769	LI:817560.12.orf1:2001MAY17
98	LI:140935.16:2001MAY17	770	LI:140935.16.orf2:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
99	LI:235333.5:2001MAY17	771	LI:235333.5.orf3:2001MAY17
100	LI:373808.8:2001MAY17	772	LI:373808.8.orf2:2001MAY17
101	LI:424554.1:2001MAY17	773	LI:424554.1.orf2:2001MAY17
102	LG:028634.1:2001JUN22	774	LG:028634.1.orf1:2001JUN22
103	LG:087230.3:2001JUN22	775	LG:087230.3.orf1:2001JUN22
104	LG:1397520.8:2001JUN22	776	LG:1397520.8.orf1:2001JUN22
105	LG:213947.1:2001JUN22	777	LG:213947.1.orf1:2001JUN22
106	LG:218029.8:2001JUN22	778	LG:218029.8.orf3:2001JUN22
107	LG:300009.1:2001JUN22	779	LG:300009.1.orf1:2001JUN22
108	LG:411188.1:2001JUN22	780	LG:411188.1.orf2:2001JUN22
109	LG:481295.21:2001JUN22	781	LG:481295.21.orf3:2001JUN22
110	LG:7684165.8:2001JUN22	782	LG:7684165.8.orf2:2001JUN22
111	LG:7690928.6:2001JUN22	783	LG:7690928.6.orf3:2001JUN22
112	LG:990040.8:2001JUN22	784	LG:990040.8.orf3:2001JUN22
113	LG:126510.8:2001JUN22	785	LG:126510.8.orf3:2001JUN22
114	LG:7692710.8:2001JUN22	786	LG:7692710.8.orf2:2001JUN22
115	LG:044888.1:2001JUN22	787	LG:044888.1.orf1:2001JUN22
116	LG:1447083.2:2001JUN22	788	LG:1447083.2.orf3:2001JUN22
117	LG:7672289.1:2001JUN22	789	LG:7672289.1.orf2:2001JUN22
118	LG:1013021.3:2001MAR30	790	LG:1013021.3.orf2:2001MAR30
119	LG:1096667.17:2001MAR30	791	LG:1096667.17.orf1:2001MAR30
120	LG:1270681.12:2001MAR30	792	LG:1270681.12.orf2:2001MAR30
121	LG:1328242.1:2001MAR30	793	LG:1328242.1.orf3:2001MAR30
122	LG:1396586.4:2001MAR30	794	LG:1396586.4.orf2:2001MAR30
123	LG:1396919.6:2001MAR30	795	LG:1396919.6.orf3:2001MAR30
124	LG:1397751.10:2001MAR30	796	LG:1397751.10.orf1:2001MAR30
125	LG:1450059.4:2001MAR30	797	LG:1450059.4.orf1:2001MAR30
126	LG:1503615.8:2001MAR30	798	LG:1503615.8.orf1:2001MAR30
127	LG:1507027.3:2001MAR30	799	LG:1507027.3.orf3:2001MAR30
128	LG:202892.1:2001MAR30	800	LG:202892.1.orf1:2001MAR30
129	LG:220407.3:2001MAR30	801	LG:220407.3.orf2:2001MAR30
130	LG:242234.11:2001MAR30	802	LG:242234.11.orf1:2001MAR30
131	LG:245181.20:2001MAR30	803	LG:245181.20.orf3:2001MAR30
132	LG:320165.7:2001MAR30	804	LG:320165.7.orf1:2001MAR30
133	LG:333965.2:2001MAR30	805	LG:333965.2.orf2:2001MAR30
134	LG:402431.16:2001MAR30	806	LG:402431.16.orf3:2001MAR30
135	LG:404400.4:2001MAR30	807	LG:404400.4.orf3:2001MAR30
136	LG:406860.73:2001MAR30	808	LG:406860.73.orf1:2001MAR30
137	LG:413797.14:2001MAR30	809	LG:413797.14.orf3:2001MAR30
138	LG:420527.51:2001MAR30	810	LG:420527.51.orf1:2001MAR30
139	LG:277227.1:2001MAR30	811	LG:277227.1.orf2:2001MAR30
140	LG:373260.30:2001MAR30	812	LG:373260.30.orf2:2001MAR30
141	LG:418805.7:2001MAR30	813	LG:418805.7.orf2:2001MAR30
142	LG:1398946.18:2001MAR30	814	LG:1398946.18.orf3:2001MAR30
143	LG:382911.1:2001MAR30	815	LG:382911.1.orf1:2001MAR30
144	LI:028146.27:2001MAY17	816	LI:028146.27.orf3:2001MAY17
145	LI:1072703.6:2001MAY17	817	LI:1072703.6.orf1:2001MAY17
146	LI:1073062.138:2001MAY17	818	LI:1073062.138.orf1:2001MAY17
147	LI:1084954.7:2001MAY17	819	LI:1084954.7.orf2:2001MAY17
148	LI:202892.5:2001MAY17	820	LI:202892.5.orf3:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
149	LI:2030686.1:2001MAY17	821	LI:2030686.1.orf2:2001MAY17
150	LI:2043289.10:2001MAY17	822	LI:2043289.10.orf1:2001MAY17
151	LI:2118426.12:2001MAY17	823	LI:2118426.12.orf3:2001MAY17
152	LI:2118901.10:2001MAY17	824	LI:2118901.10.orf1:2001MAY17
153	LI:213087.4:2001MAY17	825	LI:213087.4.orf1:2001MAY17
154	LI:2155821.1:2001MAY17	826	LI:2155821.1.orf2:2001MAY17
155	LI:2201523.6:2001MAY17	827	LI:2201523.6.orf1:2001MAY17
156	LI:235867.27:2001MAY17	828	LI:235867.27.orf1:2001MAY17
157	LI:238414.1:2001MAY17	829	LI:238414.1.orf2:2001MAY17
158	LI:242234.6:2001MAY17	830	LI:242234.6.orf2:2001MAY17
159	LI:245181.22:2001MAY17	831	LI:245181.22.orf1:2001MAY17
160	LI:245474.13:2001MAY17	832	LI:245474.13.orf2:2001MAY17
161	LI:311661.1:2001MAY17	833	LI:311661.1.orf3:2001MAY17
162	LI:320165.21:2001MAY17	834	LI:320165.21.orf3:2001MAY17
163	LI:337026.1:2001MAY17	835	LI:337026.1.orf1:2001MAY17
164	LI:347977.10:2001MAY17	836	LI:347977.10.orf1:2001MAY17
165	LI:413040.39:2001MAY17	837	LI:413040.39.orf2:2001MAY17
166	LI:467422.1:2001MAY17	838	LI:467422.1.orf3:2001MAY17
167	LI:474596.53:2001MAY17	839	LI:474596.53.orf1:2001MAY17
168	LI:481144.22:2001MAY17	840	LI:481144.22.orf2:2001MAY17
169	LI:725220.1:2001MAY17	841	LI:725220.1.orf2:2001MAY17
170	LI:804636.17:2001MAY17	842	LI:804636.17.orf2:2001MAY17
171	LI:815194.23:2001MAY17	843	LI:815194.23.orf2:2001MAY17
172	LI:817950.6:2001MAY17	844	LI:817950.6.orf2:2001MAY17
173	LI:903485.6:2001MAY17	845	LI:903485.6.orf3:2001MAY17
174	LI:220407.8:2001MAY17	846	LI:220407.8.orf2a:2001MAY17
174	LI:220407.8:2001MAY17	847	LI:220407.8.orf2b:2001MAY17
175	LI:413606.59:2001MAY17	848	LI:413606.59.orf2:2001MAY17
176	LI:202971.33:2001MAY17	849	LI:202971.33.orf1:2001MAY17
177	LI:2209219.4:2001MAY17	850	LI:2209219.4.orf3:2001MAY17
178	LG:1100586.2:2001JUN22	851	LG:1100586.2.orf2:2001JUN22
179	LG:113410.1:2001JUN22	852	LG:113410.1.orf1:2001JUN22
179	LG:113410.1:2001JUN22	853	LG:113410.1.orf3:2001JUN22
180	LG:1500938.10:2001JUN22	854	LG:1500938.10.orf3:2001JUN22
181	LG:303607.15:2001JUN22	855	LG:303607.15.orf1:2001JUN22
182	LG:411148.11:2001JUN22	856	LG:411148.11.orf2:2001JUN22
183	LG:435726.8:2001JUN22	857	LG:435726.8.orf2:2001JUN22
184	LG:475378.4:2001JUN22	858	LG:475378.4.orf2:2001JUN22
185	LG:7692134.1:2001JUN22	859	LG:7692134.1.orf3:2001JUN22
186	LG:985139.2:2001JUN22	860	LG:985139.2.orf1:2001JUN22
187	LG:149419.8:2001JUN22	861	LG:149419.8.orf3:2001JUN22
188	LG:199172.17:2001JUN22	862	LG:199172.17.orf1:2001JUN22
189	LG:256101.6:2001JUN22	863	LG:256101.6.orf2:2001JUN22
190	LG:220407.3:2001JUN22	864	LG:220407.3.orf1:2001JUN22
191	LG:331677.12:2001JUN22	865	LG:331677.12.orf2:2001JUN22
192	LG:367128.7:2001JUN22	866	LG:367128.7.orf3:2001JUN22
193	LG:403176.4:2001JUN22	867	LG:403176.4.orf3:2001JUN22
194	LG:985230.9:2001JUN22	868	LG:985230.9.orf1:2001JUN22
195	LG:005580.6:2001MAR30	869	LG:005580.6.orf3:2001MAR30
196	LG:100653.5:2001MAR30	870	LG:100653.5.orf2:2001MAR30



TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
197	LG:1099240.25:2001MAR30	871	LG:1099240.25.orf3:2001MAR30
198	LG:117947.1:2001MAR30	872	LG:117947.1.orf2:2001MAR30
199	LG:1327967.11:2001MAR30	873	LG:1327967.11.orf1:2001MAR30
200	LG:1395721.9:2001MAR30	874	LG:1395721.9.orf2:2001MAR30
201	LG:210508.1:2001MAR30	875	LG:210508.1.orf2:2001MAR30
202	LG:232313.46:2001MAR30	876	LG:232313.46.orf1:2001MAR30
203	LG:349746.22:2001MAR30	877	LG:349746.22.orf2:2001MAR30
204	LG:350526.1:2001MAR30	878	LG:350526.1.orf3:2001MAR30
205	LG:385569.1:2001MAR30	879	LG:385569.1.orf1:2001MAR30
206	LG:440659.1:2001MAR30	880	LG:440659.1.orf3:2001MAR30
207	LG:1081135.1:2001MAR30	881	LG:1081135.1.orf2:2001MAR30
208	LG:1387341.2:2001MAR30	882	LG:1387341.2.orf2:2001MAR30
209	LG:197915.17:2001MAR30	883	LG:197915.17.orf3:2001MAR30
210	LI:071874.1:2001MAY17	884	LI:071874.1.orf2:2001MAY17
211	LI:1076016.1:2001MAY17	885	LI:1076016.1.orf3:2001MAY17
212	LI:2050098.6:2001MAY17	886	LI:2050098.6.orf1:2001MAY17
213	LI:233360.4:2001MAY17	887	LI:233360.4.orf3:2001MAY17
214	LI:365343.34:2001MAY17	888	LI:365343.34.orf1:2001MAY17
215	LI:757755.14:2001MAY17	889	LI:757755.14.orf3:2001MAY17
216	LI:1086645.2:2001MAY17	890	LI:1086645.2.orf1:2001MAY17
217	LG:1015174.1:2001JUN22	891	LG:1015174.1.orf2:2001JUN22
218	LG:1135945.19:2001JUN22	892	LG:1135945.19.orf3:2001JUN22
219	LG:1382836.16:2001JUN22	893	LG:1382836.16.orf2:2001JUN22
220	LG:228817.5:2001JUN22	894	LG:228817.5.orf1:2001JUN22
221	LG:253987.9:2001JUN22	895	LG:253987.9.orf2:2001JUN22
222	LG:7683993.20:2001JUN22	896	LG:7683993.20.orf3:2001JUN22
223	LG:7691137.1:2001JUN22	897	LG:7691137.1.orf3:2001JUN22
224	LG:977849.6:2001JUN22	898	LG:977849.6.orf3:2001JUN22
225	LG:1088040.17:2001JUN22	899	LG:1088040.17.orf1:2001JUN22
226	LG:1096582.2:2001JUN22	900	LG:1096582.2.orf1:2001JUN22
227	LG:002095.19:2001JUN22	901	LG:002095.19.orf2:2001JUN22
228	LG:227596.1:2001JUN22	902	LG:227596.1.orf3:2001JUN22
229	LG:276154.23:2001JUN22	903	LG:276154.23.orf2:2001JUN22
230	LG:332254.1:2001JUN22	904	LG:332254.1.orf1:2001JUN22
231	LG:1052984.26:2001MAR30	905	LG:1052984.26.orf3:2001MAR30
232	LG:1064250.5:2001MAR30	906	LG:1064250.5.orf3:2001MAR30
233	LG:1065609.1:2001MAR30	907	LG:1065609.1.orf3:2001MAR30
234	LG:1076162.1:2001MAR30	908	LG:1076162.1.orf2:2001MAR30
235	LG:1079476.6:2001MAR30	909	LG:1079476.6.orf3:2001MAR30
236	LG:1080579.9:2001MAR30	910	LG:1080579.9.orf2:2001MAR30
237	LG:1082253.1:2001MAR30	911	LG:1082253.1.orf2:2001MAR30
238	LG:1082263.10:2001MAR30	912	LG:1082263.10.orf3:2001MAR30
239	LG:1092343.1:2001MAR30	913	LG:1092343.1.orf2:2001MAR30
240	LG:1094967.1:2001MAR30	914	LG:1094967.1.orf1:2001MAR30
241	LG:1384132.9:2001MAR30	915	LG:1384132.9.orf3:2001MAR30
242	LG:1384676.4:2001MAR30	916	LG:1384676.4.orf1:2001MAR30
243	LG:1400447.1:2001MAR30	917	LG:1400447.1.orf3:2001MAR30
244	LG:1500260.1:2001MAR30	918	LG:1500260.1.orf1:2001MAR30
245	LG:1500873.3:2001MAR30	919	LG:1500873.3.orf2:2001MAR30
246	LG:1505341.1:2001MAR30	920	LG:1505341.1.orf2:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
247	LG:169863.4:2001MAR30	921	LG:169863.4.orf1:2001MAR30
248	LG:208637.1:2001MAR30	922	LG:208637.1.orf2:2001MAR30
249	LG:234936.67:2001MAR30	923	LG:234936.67.orf1:2001MAR30
250	LG:243305.3:2001MAR30	924	LG:243305.3.orf3:2001MAR30
251	LG:334645.20:2001MAR30	925	LG:334645.20.orf2:2001MAR30
252	LG:349468.13:2001MAR30	926	LG:349468.13.orf3:2001MAR30
253	LG:385145.1:2001MAR30	927	LG:385145.1.orf2:2001MAR30
254	LG:391807.1:2001MAR30	928	LG:391807.1.orf2:2001MAR30
255	LG:399287.10:2001MAR30	929	LG:399287.10.orf2:2001MAR30
256	LG:404157.1:2001MAR30	930	LG:404157.1.orf3:2001MAR30
257	LG:979390.2:2001MAR30	931	LG:979390.2.orf1:2001MAR30
258	LG:981962.1:2001MAR30	932	LG:981962.1.orf3:2001MAR30
259	LG:982976.2:2001MAR30	933	LG:982976.2.orf3:2001MAR30
260	LG:1448087.1:2001MAR30	934	LG:1448087.1.orf3:2001MAR30
261	LG:1449021.1:2001MAR30	935	LG:1449021.1.orf3:2001MAR30
262	LG:144920.1:2001MAR30	936	LG:144920.1.orf1:2001MAR30
263	LG:474725.1:2001MAR30	937	LG:474725.1.orf1:2001MAR30
264	LG:1085952.14:2001MAR30	938	LG:1085952.14.orf3:2001MAR30
265	U:011009.2:2001MAY17	939	U:011009.2.orf3:2001MAY17
266	U:016933.2:2001MAY17	940	U:016933.2.orf2:2001MAY17
267	U:1072014.6:2001MAY17	941	U:1072014.6.orf3:2001MAY17
268	U:1165280.4:2001MAY17	942	U:1165280.4.orf2:2001MAY17
269	U:1167958.4:2001MAY17	943	U:1167958.4.orf2:2001MAY17
270	U:1168073.15:2001MAY17	944	U:1168073.15.orf1:2001MAY17
271	U:1170154.12:2001MAY17	945	U:1170154.12.orf1:2001MAY17
271	U:1170154.12:2001MAY17	946	U:1170154.12.orf3:2001MAY17
272	U:1173769.2:2001MAY17	947	U:1173769.2.orf3:2001MAY17
273	U:1174292.18:2001MAY17	948	U:1174292.18.orf2:2001MAY17
274	U:1177989.1:2001MAY17	949	U:1177989.1.orf1:2001MAY17
275	U:1179173.3:2001MAY17	950	U:1179173.3.orf2:2001MAY17
276	U:1180137.1:2001MAY17	951	U:1180137.1.orf1:2001MAY17
277	U:1181458.2:2001MAY17	952	U:1181458.2.orf3:2001MAY17
278	U:1182817.8:2001MAY17	953	U:1182817.8.orf1:2001MAY17
279	U:1182838.4:2001MAY17	954	U:1182838.4.orf3:2001MAY17
280	U:2053637.1:2001MAY17	955	U:2053637.1.orf1:2001MAY17
281	U:2119713.6:2001MAY17	956	U:2119713.6.orf1:2001MAY17
282	U:2121833.1:2001MAY17	957	U:2121833.1.orf2:2001MAY17
283	U:2121863.1:2001MAY17	958	U:2121863.1.orf2:2001MAY17
284	U:2121899.1:2001MAY17	959	U:2121899.1.orf3:2001MAY17
285	U:2122035.5:2001MAY17	960	U:2122035.5.orf2:2001MAY17
286	U:2122507.3:2001MAY17	961	U:2122507.3.orf3:2001MAY17
287	U:2190152.1:2001MAY17	962	U:2190152.1.orf2:2001MAY17
288	U:2195736.1:2001MAY17	963	U:2195736.1.orf3:2001MAY17
289	U:2195745.2:2001MAY17	964	U:2195745.2.orf1:2001MAY17
290	U:2196327.1:2001MAY17	965	U:2196327.1.orf1:2001MAY17
291	U:2197842.1:2001MAY17	966	U:2197842.1.orf3:2001MAY17
292	U:2202913.1:2001MAY17	967	U:2202913.1.orf1:2001MAY17
293	U:2206159.1:2001MAY17	968	U:2206159.1.orf3:2001MAY17
294	U:2208960.3:2001MAY17	969	U:2208960.3.orf2:2001MAY17
295	U:2209149.1:2001MAY17	970	U:2209149.1.orf2:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
296	U:223050.2:2001MAY17	971	U:223050.2.orf3:2001MAY17
297	U:393468.1:2001MAY17	972	U:393468.1.orf2:2001MAY17
298	U:480324.48:2001MAY17	973	U:480324.48.orf1:2001MAY17
299	U:722634.7:2001MAY17	974	U:722634.7.orf3:2001MAY17
300	U:796992.1:2001MAY17	975	U:796992.1.orf3:2001MAY17
301	U:093337.1:2001MAY17	976	U:093337.1.orf1:2001MAY17
302	U:1081130.3:2001MAY17	977	U:1081130.3.orf1:2001MAY17
303	U:1170908.4:2001MAY17	978	U:1170908.4.orf2:2001MAY17
304	U:1177451.1:2001MAY17	979	U:1177451.1.orf2:2001MAY17
305	U:1180303.18:2001MAY17	980	U:1180303.18.orf1:2001MAY17
306	U:1182999.3:2001MAY17	981	U:1182999.3.orf1:2001MAY17
307	U:1183525.1:2001MAY17	982	U:1183525.1.orf2:2001MAY17
308	U:2121675.1:2001MAY17	983	U:2121675.1.orf3:2001MAY17
309	U:2121766.11:2001MAY17	984	U:2121766.11.orf2:2001MAY17
310	U:2188633.1:2001MAY17	985	U:2188633.1.orf2:2001MAY17
311	U:2188820.2:2001MAY17	986	U:2188820.2.orf2:2001MAY17
312	U:2191871.1:2001MAY17	987	U:2191871.1.orf1:2001MAY17
313	U:2196157.2:2001MAY17	988	U:2196157.2.orf3:2001MAY17
314	U:230109.4:2001MAY17	989	U:230109.4.orf1:2001MAY17
315	U:790409.4:2001MAY17	990	U:790409.4.orf2:2001MAY17
316	LG:084399.1:2001JUN22	991	LG:084399.1.orf3:2001JUN22
317	LG:1079456.3:2001JUN22	992	LG:1079456.3.orf1:2001JUN22
317	LG:1079456.3:2001JUN22	993	LG:1079456.3.orf3:2001JUN22
318	LG:1080406.7:2001JUN22	994	LG:1080406.7.orf3:2001JUN22
319	LG:1505015.1:2001JUN22	995	LG:1505015.1.orf1:2001JUN22
320	LG:208637.1:2001JUN22	996	LG:208637.1.orf1:2001JUN22
321	LG:233311.5:2001JUN22	997	LG:233311.5.orf3:2001JUN22
322	LG:385145.1:2001JUN22	998	LG:385145.1.orf2:2001JUN22
323	LG:404157.1:2001JUN22	999	LG:404157.1.orf3:2001JUN22
324	LG:7684505.1:2001JUN22	1000	LG:7684505.1.orf1:2001JUN22
325	LG:7687730.1:2001JUN22	1001	LG:7687730.1.orf1:2001JUN22
326	LG:7687809.2:2001JUN22	1002	LG:7687809.2.orf3:2001JUN22
327	LG:7690098.1:2001JUN22	1003	LG:7690098.1.orf1:2001JUN22
328	LG:7690113.1:2001JUN22	1004	LG:7690113.1.orf1:2001JUN22
329	LG:7690362.3:2001JUN22	1005	LG:7690362.3.orf2:2001JUN22
330	LG:7691200.3:2001JUN22	1006	LG:7691200.3.orf2:2001JUN22
331	LG:7691277.3:2001JUN22	1007	LG:7691277.3.orf2:2001JUN22
332	LG:7691280.4:2001JUN22	1008	LG:7691280.4.orf2:2001JUN22
333	LG:7691562.2:2001JUN22	1009	LG:7691562.2.orf1:2001JUN22
334	LG:7691685.3:2001JUN22	1010	LG:7691685.3.orf1:2001JUN22
335	LG:7693155.4:2001JUN22	1011	LG:7693155.4.orf2:2001JUN22
336	LG:981962.1:2001JUN22	1012	LG:981962.1.orf3:2001JUN22
337	LG:1449021.1:2001JUN22	1013	LG:1449021.1.orf2:2001JUN22
338	LG:481631.22:2001JUN22	1014	LG:481631.22.orf3:2001JUN22
339	LG:7690406.2:2001JUN22	1015	LG:7690406.2.orf2:2001JUN22
340	LG:7690773.2:2001JUN22	1016	LG:7690773.2.orf3:2001JUN22
341	LG:1347119.1:2001JUN22	1017	LG:1347119.1.orf1:2001JUN22
342	LG:7691570.2:2001JUN22	1018	LG:7691570.2.orf2:2001JUN22
343	LG:023518.3:2001MAR30	1019	LG:023518.3.orf1:2001MAR30
344	LG:1100502.1:2001MAR30	1020	LG:1100502.1.orf3:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
345	LG:235076.6:2001MAR30	1021	LG:235076.6.orf3:2001MAR30
346	LG:270582.4:2001MAR30	1022	LG:270582.4.orf1:2001MAR30
347	LG:334752.12:2001MAR30	1023	LG:334752.12.orf1:2001MAR30
348	LG:425641.11:2001MAR30	1024	LG:425641.11.orf1:2001MAR30
349	LG:980241.4:2001MAR30	1025	LG:980241.4.orf2:2001MAR30
350	LI:1040737.102:2001MAY17	1026	LI:1040737.102.orf2:2001MAY17
351	LI:1072888.10:2001MAY17	1027	LI:1072888.10.orf1:2001MAY17
352	LI:2048255.1:2001MAY17	1028	LI:2048255.1.orf1:2001MAY17
353	LI:330658.1:2001MAY17	1029	LI:330658.1.orf2:2001MAY17
354	LI:410188.4:2001MAY17	1030	LI:410188.4.orf1:2001MAY17
355	LI:902565.38:2001MAY17	1031	LI:902565.38.orf2:2001MAY17
356	LI:2032241.1:2001MAY17	1032	LI:2032241.1.orf2:2001MAY17
357	LI:2192055.1:2001MAY17	1033	LI:2192055.1.orf2:2001MAY17
358	LG:133851.16:2001JUN22	1034	LG:133851.16.orf2:2001JUN22
359	LG:1398822.1:2001JUN22	1035	LG:1398822.1.orf1:2001JUN22
360	LG:1502274.17:2001JUN22	1036	LG:1502274.17.orf1:2001JUN22
361	LG:166400.33:2001JUN22	1037	LG:166400.33.orf2:2001JUN22
362	LG:235076.15:2001JUN22	1038	LG:235076.15.orf1:2001JUN22
363	LG:7689943.1:2001JUN22	1039	LG:7689943.1.orf2:2001JUN22
364	LG:7693319.3:2001JUN22	1040	LG:7693319.3.orf1:2001JUN22
365	LG:980241.4:2001JUN22	1041	LG:980241.4.orf1:2001JUN22
366	LG:226475.15:2001JUN22	1042	LG:226475.15.orf3:2001JUN22
367	LG:422564.11:2001JUN22	1043	LG:422564.11.orf2:2001JUN22
368	LG:026384.13:2001MAR30	1044	LG:026384.13.orf2:2001MAR30
369	LG:1087811.6:2001MAR30	1045	LG:1087811.6.orf1:2001MAR30
370	LG:208877.7:2001MAR30	1046	LG:208877.7.orf1:2001MAR30
371	LG:232959.49:2001MAR30	1047	LG:232959.49.orf2:2001MAR30
372	LG:331078.21:2001MAR30	1048	LG:331078.21.orf3:2001MAR30
373	LG:334345.5:2001MAR30	1049	LG:334345.5.orf2:2001MAR30
374	LG:345279.19:2001MAR30	1050	LG:345279.19.orf3:2001MAR30
375	LG:400109.5:2001MAR30	1051	LG:400109.5.orf2:2001MAR30
376	LG:001294.11:2001MAR30	1052	LG:001294.11.orf1:2001MAR30
377	LG:230895.5:2001MAR30	1053	LG:230895.5.orf1:2001MAR30
378	LI:090657.2:2001MAY17	1054	LI:090657.2.orf2:2001MAY17
379	LI:1072276.1:2001MAY17	1055	LI:1072276.1.orf1:2001MAY17
380	LI:1072654.40:2001MAY17	1056	LI:1072654.40.orf1:2001MAY17
381	LI:123815.12:2001MAY17	1057	LI:123815.12.orf2:2001MAY17
382	LI:198705.6:2001MAY17	1058	LI:198705.6.orf2:2001MAY17
383	LI:2032264.3:2001MAY17	1059	LI:2032264.3.orf1:2001MAY17
384	LI:2070168.1:2001MAY17	1060	LI:2070168.1.orf3:2001MAY17
385	LI:2077540.1:2001MAY17	1061	LI:2077540.1.orf2:2001MAY17
386	LI:207915.45:2001MAY17	1062	LI:207915.45.orf2:2001MAY17
387	LI:2120273.5:2001MAY17	1063	LI:2120273.5.orf3:2001MAY17
388	LI:237520.26:2001MAY17	1064	LI:237520.26.orf3:2001MAY17
389	LI:243892.46:2001MAY17	1065	LI:243892.46.orf2:2001MAY17
390	LI:400590.4:2001MAY17	1066	LI:400590.4.orf1:2001MAY17
391	LI:407084.4:2001MAY17	1067	LI:407084.4.orf2:2001MAY17
392	LI:2052211.9:2001MAY17	1068	LI:2052211.9.orf3:2001MAY17
393	LI:407291.5:2001MAY17	1069	LI:407291.5.orf3:2001MAY17
394	LI:2167560.1:2001MAY17	1070	LI:2167560.1.orf1:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
395	LI:401586.1:2001MAY17	1071	LI:401586.1.orf3:2001MAY17
396	LG:1093982.21:2001JUN22	1072	LG:1093982.21.orf3:2001JUN22
397	LG:1383133.102:2001JUN22	1073	LG:1383133.102.orf1:2001JUN22
398	LG:199121.19:2001JUN22	1074	LG:199121.19.orf3:2001JUN22
399	LG:482411.11:2001JUN22	1075	LG:482411.11.orf3:2001JUN22
400	LG:991986.23:2001JUN22	1076	LG:991986.23.orf3:2001JUN22
401	LG:1500347.6:2001JUN22	1077	LG:1500347.6.orf3:2001JUN22
402	LG:7670971.1:2001JUN22	1078	LG:7670971.1.orf2:2001JUN22
403	LG:010761.6:2001MAR30	1079	LG:010761.6.orf3:2001MAR30
404	LG:104970.6:2001MAR30	1080	LG:104970.6.orf3:2001MAR30
405	LG:1078420.1:2001MAR30	1081	LG:1078420.1.orf2:2001MAR30
406	LG:1094182.9:2001MAR30	1082	LG:1094182.9.orf2:2001MAR30
407	LG:1399075.18:2001MAR30	1083	LG:1399075.18.orf2:2001MAR30
408	LG:1501344.7:2001MAR30	1084	LG:1501344.7.orf3:2001MAR30
409	LI:1144484.3:2001MAY17	1085	LI:1144484.3.orf3:2001MAY17
410	LI:337388.11:2001MAY17	1086	LI:337388.11.orf3:2001MAY17
411	LI:347709.101:2001MAY17	1087	LI:347709.101.orf2:2001MAY17
412	LI:480238.8:2001MAY17	1088	LI:480238.8.orf2:2001MAY17
413	LI:2121656.1:2001MAY17	1089	LI:2121656.1.orf2:2001MAY17
414	LG:1328038.5:2001JUN22	1090	LG:1328038.5.orf3:2001JUN22
415	LG:437443.21:2001JUN22	1091	LG:437443.21.orf3:2001JUN22
416	LG:474165.24:2001JUN22	1092	LG:474165.24.orf2:2001JUN22
417	LG:7689014.1:2001JUN22	1093	LG:7689014.1.orf2:2001JUN22
418	LG:984007.4:2001JUN22	1094	LG:984007.4.orf3:2001JUN22
419	LG:008606.21:2001JUN22	1095	LG:008606.21.orf1:2001JUN22
420	LG:240680.1:2001JUN22	1096	LG:240680.1.orf3:2001JUN22
421	LG:160481.1:2001MAR30	1097	LG:160481.1.orf3:2001MAR30
422	LG:292275.1:2001MAR30	1098	LG:292275.1.orf1:2001MAR30
423	LG:407582.21:2001MAR30	1099	LG:407582.21.orf3:2001MAR30
424	LI:2051428.9:2001MAY17	1100	LI:2051428.9.orf3:2001MAY17
425	LI:355644.50:2001MAY17	1101	LI:355644.50.orf3:2001MAY17
426	LI:375954.18:2001MAY17	1102	LI:375954.18.orf2:2001MAY17
427	LI:480115.132:2001MAY17	1103	LI:480115.132.orf3:2001MAY17
428	LG:1383554.10:2001JUN22	1104	LG:1383554.10.orf2:2001JUN22
429	LG:1135060.33:2001MAR30	1105	LG:1135060.33.orf3:2001MAR30
430	LG:1351716.96:2001MAR30	1106	LG:1351716.96.orf2:2001MAR30
431	LG:1400811.225:2001MAR30	1107	LG:1400811.225.orf3:2001MAR30
432	LG:1401132.92:2001MAR30	1108	LG:1401132.92.orf1:2001MAR30
433	LG:1401165.155:2001MAR30	1109	LG:1401165.155.orf1:2001MAR30
434	LG:1452363.23:2001MAR30	1110	LG:1452363.23.orf1:2001MAR30
435	LG:1503254.1:2001MAR30	1111	LG:1503254.1.orf1:2001MAR30
436	LG:411364.13:2001MAR30	1112	LG:411364.13.orf1:2001MAR30
437	LG:238631.16:2001MAR30	1113	LG:238631.16.orf3:2001MAR30
438	LG:235157.34:2001MAR30	1114	LG:235157.34.orf3:2001MAR30
439	LI:1027765.6:2001MAY17	1115	LI:1027765.6.orf3:2001MAY17
440	LI:105160.28:2001MAY17	1116	LI:105160.28.orf2:2001MAY17
441	LI:1073108.49:2001MAY17	1117	LI:1073108.49.orf1:2001MAY17
442	LI:1189828.21:2001MAY17	1118	LI:1189828.21.orf2:2001MAY17
443	LI:2191073.14:2001MAY17	1119	LI:2191073.14.orf1:2001MAY17
444	LI:2191348.6:2001MAY17	1120	LI:2191348.6.orf1:2001MAY17

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
445	U:2191424.12:2001MAY17	1121	U:2191424.12.orf1:2001MAY17
446	U:2206792.26:2001MAY17	1122	U:2206792.26.orf1:2001MAY17
447	U:255510.1264:2001MAY17	1123	U:255510.1264.orf1:2001MAY17
448	U:392902.48:2001MAY17	1124	U:392902.48.orf2:2001MAY17
449	U:411364.14:2001MAY17	1125	U:411364.14.orf2:2001MAY17
450	U:417464.1:2001MAY17	1126	U:417464.1.orf2:2001MAY17
451	U:439077.1:2001MAY17	1127	U:439077.1.orf1:2001MAY17
452	U:1071390.38:2001MAY17	1128	U:1071390.38.orf3:2001MAY17
453	LG:1225513.19:2001JUN22	1129	LG:1225513.19.orf3:2001JUN22
454	LG:1447752.2:2001JUN22	1130	LG:1447752.2.orf1:2001JUN22
455	LG:239410.21:2001JUN22	1131	LG:239410.21.orf3:2001JUN22
456	LG:7683955.1:2001JUN22	1132	LG:7683955.1.orf2:2001JUN22
457	LG:7691296.7:2001JUN22	1133	LG:7691296.7.orf1:2001JUN22
458	LG:7696542.11:2001JUN22	1134	LG:7696542.11.orf2:2001JUN22
459	LG:7696552.2:2001JUN22	1135	LG:7696552.2.orf2:2001JUN22
460	LG:7696586.3:2001JUN22	1136	LG:7696586.3.orf1:2001JUN22
461	U:1072102.34:2001MAY17	1137	U:1072102.34.orf2:2001MAY17
462	U:2119925.1:2001MAY17	1138	U:2119925.1.orf2:2001MAY17
463	U:2173928.1:2001MAY17	1139	U:2173928.1.orf3:2001MAY17
464	U:2193503.1:2001MAY17	1140	U:2193503.1.orf1:2001MAY17
465	U:368098.26:2001MAY17	1141	U:368098.26.orf3:2001MAY17
466	U:455378.1:2001MAY17	1142	U:455378.1.orf1:2001MAY17
467	U:480845.50:2001MAY17	1143	U:480845.50.orf1:2001MAY17
468	U:2205863.1:2001MAY17	1144	U:2205863.1.orf3:2001MAY17
469	LG:201188.2:2001JUN22	1145	LG:201188.2.orf2:2001JUN22
470	LG:1272496.28:2001MAR30	1146	LG:1272496.28.orf1:2001MAR30
470	LG:1272496.28:2001MAR30	1147	LG:1272496.28.orf3:2001MAR30
471	LG:1500367.1:2001MAR30	1148	LG:1500367.1.orf1:2001MAR30
472	LG:952182.4:2001MAR30	1149	LG:952182.4.orf2:2001MAR30
473	U:197195.10:2001MAY17	1150	U:197195.10.orf2:2001MAY17
474	U:2031121.1:2001MAY17	1151	U:2031121.1.orf1:2001MAY17
475	U:2198279.3:2001MAY17	1152	U:2198279.3.orf3:2001MAY17
476	U:2201248.1:2001MAY17	1153	U:2201248.1.orf1:2001MAY17
477	U:234507.10:2001MAY17	1154	U:234507.10.orf3:2001MAY17
478	U:237999.48:2001MAY17	1155	U:237999.48.orf2:2001MAY17
479	U:244935.47:2001MAY17	1156	U:244935.47.orf3:2001MAY17
480	U:257664.143:2001MAY17	1157	U:257664.143.orf3:2001MAY17
481	U:261900.1:2001MAY17	1158	U:261900.1.orf1:2001MAY17
482	U:346724.22:2001MAY17	1159	U:346724.22.orf1:2001MAY17
483	U:815333.1:2001MAY17	1160	U:815333.1.orf1:2001MAY17
484	U:889399.7:2001MAY17	1161	U:889399.7.orf3:2001MAY17
485	U:1088907.2:2001MAY17	1162	U:1088907.2.orf2:2001MAY17
486	U:218680.7:2001MAY17	1163	U:218680.7.orf2:2001MAY17
487	LG:081189.8:2001JUN22	1164	LG:081189.8.orf2:2001JUN22
488	LG:315445.21:2001JUN22	1165	LG:315445.21.orf3:2001JUN22
489	LG:900035.56:2001JUN22	1166	LG:900035.56.orf2:2001JUN22
490	LG:008513.80:2001MAR30	1167	LG:008513.80.orf3:2001MAR30
491	LG:1384720.130:2001MAR30	1168	LG:1384720.130.orf1:2001MAR30
492	LG:1453611.1:2001MAR30	1169	LG:1453611.1.orf2:2001MAR30
493	LG:1500258.1:2001MAR30	1170	LG:1500258.1.orf2:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
494	LG:1501754.5:2001MAR30	1171	LG:1501754.5.orf3:2001MAR30
495	LG:1502796.1:2001MAR30	1172	LG:1502796.1.orf3:2001MAR30
496	LG:348973.11:2001MAR30	1173	LG:348973.11.orf1:2001MAR30
497	LG:362757.1:2001MAR30	1174	LG:362757.1.orf1:2001MAR30
498	LG:401322.6:2001MAR30	1175	LG:401322.6.orf1:2001MAR30
499	LG:897867.1:2001MAR30	1176	LG:897867.1.orf1:2001MAR30
500	LI:1947939.1:2001MAY17	1177	LI:1947939.1.orf1:2001MAY17
501	LI:245487.16:2001MAY17	1178	LI:245487.16.orf2:2001MAY17
502	LI:257715.58:2001MAY17	1179	LI:257715.58.orf2:2001MAY17
503	LI:333453.9:2001MAY17	1180	LI:333453.9.orf3:2001MAY17
504	LI:412658.111:2001MAY17	1181	LI:412658.111.orf2:2001MAY17
505	LI:720054.1:2001MAY17	1182	LI:720054.1.orf1:2001MAY17
506	LI:765245.9:2001MAY17	1183	LI:765245.9.orf1:2001MAY17
507	LI:814445.58:2001MAY17	1184	LI:814445.58.orf2:2001MAY17
508	LI:897867.1:2001MAY17	1185	LI:897867.1.orf1:2001MAY17
509	LI:311318.6:2001MAY17	1186	LI:311318.6.orf2:2001MAY17
510	LI:401605.12:2001MAY17	1187	LI:401605.12.orf1:2001MAY17
511	LG:1088618.90:2001JUN22	1188	LG:1088618.90.orf2:2001JUN22
512	LG:1446318.6:2001JUN22	1189	LG:1446318.6.orf1:2001JUN22
513	LG:229284.37:2001JUN22	1190	LG:229284.37.orf1:2001JUN22
514	LG:7683471.8:2001JUN22	1191	LG:7683471.8.orf2:2001JUN22
515	LG:7697194.7:2001JUN22	1192	LG:7697194.7.orf1:2001JUN22
516	LG:952407.1:2001JUN22	1193	LG:952407.1.orf1:2001JUN22
517	LG:248005.17:2001JUN22	1194	LG:248005.17.orf1:2001JUN22
518	LG:025007.3:2001MAR30	1195	LG:025007.3.orf1:2001MAR30
519	LG:1510893.1:2001MAR30	1196	LG:1510893.1.orf1:2001MAR30
520	LG:297070.1:2001MAR30	1197	LG:297070.1.orf1:2001MAR30
521	LG:363612.2:2001MAR30	1198	LG:363612.2.orf2:2001MAR30
522	LG:468481.1:2001MAR30	1199	LG:468481.1.orf3:2001MAR30
523	LG:966475.1:2001MAR30	1200	LG:966475.1.orf3:2001MAR30
524	LG:1135422.1:2001MAR30	1201	LG:1135422.1.orf3:2001MAR30
525	LI:1010121.1:2001MAY17	1202	LI:1010121.1.orf1:2001MAY17
526	LI:1072416.19:2001MAY17	1203	LI:1072416.19.orf3:2001MAY17
527	LI:1188564.7:2001MAY17	1204	LI:1188564.7.orf1:2001MAY17
528	LI:2118902.5:2001MAY17	1205	LI:2118902.5.orf3:2001MAY17
529	LI:2206501.1:2001MAY17	1206	LI:2206501.1.orf3:2001MAY17
530	LI:337830.1:2001MAY17	1207	LI:337830.1.orf1:2001MAY17
531	LI:347853.17:2001MAY17	1208	LI:347853.17.orf1:2001MAY17
532	LI:253580.4:2001MAY17	1209	LI:253580.4.orf3:2001MAY17
533	LG:330850.3:2001JUN22	1210	LG:330850.3.orf2:2001JUN22
534	LG:464722.13:2001JUN22	1211	LG:464722.13.orf1:2001JUN22
535	LG:7686119.1:2001JUN22	1212	LG:7686119.1.orf1:2001JUN22
536	LG:903691.14:2001JUN22	1213	LG:903691.14.orf2:2001JUN22
537	LG:1096385.3:2001MAR30	1214	LG:1096385.3.orf3:2001MAR30
538	LG:1101445.1:2001MAR30	1215	LG:1101445.1.orf3:2001MAR30
539	LG:1138457.20:2001MAR30	1216	LG:1138457.20.orf3:2001MAR30
540	LG:1440118.1:2001MAR30	1217	LG:1440118.1.orf2:2001MAR30
541	LG:1443997.1:2001MAR30	1218	LG:1443997.1.orf2:2001MAR30
542	LG:1497707.1:2001MAR30	1219	LG:1497707.1.orf3:2001MAR30
543	LG:1501729.1:2001MAR30	1220	LG:1501729.1.orf1:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
544	LG:1502186.1:2001MAR30	1221	LG:1502186.1.orf2:2001MAR30
545	LG:223142.1:2001MAR30	1222	LG:223142.1.orf3:2001MAR30
546	LG:255713.1:2001MAR30	1223	LG:255713.1.orf1:2001MAR30
547	LG:420283.38:2001MAR30	1224	LG:420283.38.orf2:2001MAR30
548	LG:449413.3:2001MAR30	1225	LG:449413.3.orf3:2001MAR30
549	LG:997599.1:2001MAR30	1226	LG:997599.1.orf2:2001MAR30
550	LG:232776.8:2001MAR30	1227	LG:232776.8.orf1:2001MAR30
551	LI:1045207.1:2001MAY17	1228	LI:1045207.1.orf3:2001MAY17
552	LI:1086565.6:2001MAY17	1229	LI:1086565.6.orf2:2001MAY17
553	LI:1142855.1:2001MAY17	1230	LI:1142855.1.orf1:2001MAY17
554	LI:2188689.1:2001MAY17	1231	LI:2188689.1.orf2:2001MAY17
555	LI:2193411.1:2001MAY17	1232	LI:2193411.1.orf1:2001MAY17
556	LI:2198244.1:2001MAY17	1233	LI:2198244.1.orf1:2001MAY17
557	LI:2198795.4:2001MAY17	1234	LI:2198795.4.orf2:2001MAY17
558	LI:2199688.3:2001MAY17	1235	LI:2199688.3.orf1:2001MAY17
559	LI:790138.64:2001MAY17	1236	LI:790138.64.orf1:2001MAY17
560	LI:757871.10:2001MAY17	1237	LI:757871.10.orf2:2001MAY17
561	LG:1096385.2:2001JUN22	1238	LG:1096385.2.orf1:2001JUN22
562	LG:1100878.1:2001JUN22	1239	LG:1100878.1.orf2:2001JUN22
563	LG:1447560.1:2001JUN22	1240	LG:1447560.1.orf3:2001JUN22
564	LG:1453540.34:2001JUN22	1241	LG:1453540.34.orf2:2001JUN22
565	LG:249518.11:2001JUN22	1242	LG:249518.11.orf3:2001JUN22
566	LG:041656.5:2001JUN22	1243	LG:041656.5.orf3:2001JUN22
567	LI:2208837.4:2001MAY17	1244	LI:2208837.4.orf2:2001MAY17
568	LG:7694341.2:2001JUN22	1245	LG:7694341.2.orf1:2001JUN22
569	LG:016760.1:2001MAR30	1246	LG:016760.1.orf1:2001MAR30
570	LG:1022858.1:2001MAR30	1247	LG:1022858.1.orf2:2001MAR30
571	LG:1135406.15:2001MAR30	1248	LG:1135406.15.orf1:2001MAR30
572	LG:1327517.37:2001MAR30	1249	LG:1327517.37.orf1:2001MAR30
573	LG:1330214.34:2001MAR30	1250	LG:1330214.34.orf2:2001MAR30
574	LG:1384735.5:2001MAR30	1251	LG:1384735.5.orf2:2001MAR30
575	LG:1449837.4:2001MAR30	1252	LG:1449837.4.orf3:2001MAR30
576	LG:1452330.5:2001MAR30	1253	LG:1452330.5.orf3:2001MAR30
577	LG:1510248.1:2001MAR30	1254	LG:1510248.1.orf2:2001MAR30
578	LG:215109.8:2001MAR30	1255	LG:215109.8.orf3:2001MAR30
579	LG:279978.17:2001MAR30	1256	LG:279978.17.orf2:2001MAR30
580	LG:414732.1:2001MAR30	1257	LG:414732.1.orf2:2001MAR30
581	LG:1132208.1:2001MAR30	1258	LG:1132208.1.orf3:2001MAR30
582	LG:1454339.4:2001MAR30	1259	LG:1454339.4.orf1:2001MAR30
583	LI:018342.1:2001MAY17	1260	LI:018342.1.orf1:2001MAY17
584	LI:1177772.36:2001MAY17	1261	LI:1177772.36.orf1:2001MAY17
585	LI:2207152.6:2001MAY17	1262	LI:2207152.6.orf1:2001MAY17
586	LI:244159.24:2001MAY17	1263	LI:244159.24.orf3:2001MAY17
587	LI:405244.8:2001MAY17	1264	LI:405244.8.orf2:2001MAY17
588	LI:270318.18:2001MAY17	1265	LI:270318.18.orf1:2001MAY17
589	LI:154692.45:2001MAY17	1266	LI:154692.45.orf3:2001MAY17
590	LI:411238.31:2001MAY17	1267	LI:411238.31.orf3:2001MAY17
591	LI:814424.6:2001MAY17	1268	LI:814424.6.orf3:2001MAY17
592	LG:1327517.25:2001JUN22	1269	LG:1327517.25.orf1:2001JUN22
593	LG:343949.3:2001JUN22	1270	LG:343949.3.orf3:2001JUN22



TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
594	LG:413000.28:2001JUN22	1271	LG:413000.28.orf1:2001JUN22
595	LG:7692006.3:2001JUN22	1272	LG:7692006.3.orf2:2001JUN22
596	LG:336953.5:2001JUN22	1273	LG:336953.5.orf1:2001JUN22
597	LG:1399785.1:2001JUN22	1274	LG:1399785.1.orf3:2001JUN22
598	LG:425024.5:2001JUN22	1275	LG:425024.5.orf3:2001JUN22
599	LG:482494.10:2001JUN22	1276	LG:482494.10.orf2:2001JUN22
600	LG:978629.6:2001JUN22	1277	LG:978629.6.orf3:2001JUN22
601	LG:005776.12:2001MAR30	1278	LG:005776.12.orf3:2001MAR30
602	LG:029219.1:2001MAR30	1279	LG:029219.1.orf1:2001MAR30
603	LG:091743.1:2001MAR30	1280	LG:091743.1.orf3:2001MAR30
604	LG:1397656.6:2001MAR30	1281	LG:1397656.6.orf3:2001MAR30
605	LG:1500866.5:2001MAR30	1282	LG:1500866.5.orf1:2001MAR30
606	LG:1511332.1:2001MAR30	1283	LG:1511332.1.orf2:2001MAR30
607	LG:233288.31:2001MAR30	1284	LG:233288.31.orf1:2001MAR30
608	LG:269269.24:2001MAR30	1285	LG:269269.24.orf2:2001MAR30
609	LG:331581.5:2001MAR30	1286	LG:331581.5.orf2:2001MAR30
610	LG:481433.4:2001MAR30	1287	LG:481433.4.orf3:2001MAR30
611	LG:246935.4:2001MAR30	1288	LG:246935.4.orf2:2001MAR30
612	LG:475420.1:2001MAR30	1289	LG:475420.1.orf1:2001MAR30
613	LI:1073084.60:2001MAY17	1290	LI:1073084.60.orf2:2001MAY17
614	LI:2040379.1:2001MAY17	1291	LI:2040379.1.orf3:2001MAY17
615	LI:2119526.4:2001MAY17	1292	LI:2119526.4.orf3:2001MAY17
616	LI:213228.1:2001MAY17	1293	LI:213228.1.orf1:2001MAY17
617	LI:2179709.1:2001MAY17	1294	LI:2179709.1.orf1:2001MAY17
618	LI:2208147.1:2001MAY17	1295	LI:2208147.1.orf3:2001MAY17
619	LI:235487.10:2001MAY17	1296	LI:235487.10.orf2:2001MAY17
620	LI:476342.4:2001MAY17	1297	LI:476342.4.orf1:2001MAY17
621	LI:759025.1:2001MAY17	1298	LI:759025.1.orf1:2001MAY17
622	LI:765589.1:2001MAY17	1299	LI:765589.1.orf3:2001MAY17
623	LI:902535.3:2001MAY17	1300	LI:902535.3.orf3:2001MAY17
624	LI:257592.5:2001MAY17	1301	LI:257592.5.orf2:2001MAY17
625	LI:471684.65:2001MAY17	1302	LI:471684.65.orf2:2001MAY17
626	LG:1382838.272:2001JUN22	1303	LG:1382838.272.orf3:2001JUN22
627	LG:142736.1:2001JUN22	1304	LG:142736.1.orf1:2001JUN22
628	LG:221707.43:2001JUN22	1305	LG:221707.43.orf3:2001JUN22
629	LG:7689247.1:2001JUN22	1306	LG:7689247.1.orf1:2001JUN22
630	LG:7693136.5:2001JUN22	1307	LG:7693136.5.orf2:2001JUN22
631	LG:001505.13:2001MAR30	1308	LG:001505.13.orf2:2001MAR30
632	LG:1051541.1:2001MAR30	1309	LG:1051541.1.orf1:2001MAR30
633	LG:1090140.1:2001MAR30	1310	LG:1090140.1.orf3:2001MAR30
634	LG:1094595.2:2001MAR30	1311	LG:1094595.2.orf3:2001MAR30
635	LG:1500340.1:2001MAR30	1312	LG:1500340.1.orf2:2001MAR30
636	LG:1502353.1:2001MAR30	1313	LG:1502353.1.orf3:2001MAR30
637	LG:1511710.6:2001MAR30	1314	LG:1511710.6.orf2:2001MAR30
638	LG:231372.4:2001MAR30	1315	LG:231372.4.orf2:2001MAR30
639	LG:234855.6:2001MAR30	1316	LG:234855.6.orf2:2001MAR30
640	LG:242157.8:2001MAR30	1317	LG:242157.8.orf1:2001MAR30
641	LG:477127.6:2001MAR30	1318	LG:477127.6.orf3:2001MAR30
642	LG:412684.17:2001MAR30	1319	LG:412684.17.orf2:2001MAR30
643	LG:474937.20:2001MAR30	1320	LG:474937.20.orf2:2001MAR30

TABLE 1

SEQ ID NO:	Template ID	SEQ ID NO:	ORF ID
644	LG:1452698.8:2001MAR30	1321	LG:1452698.8.orf2:2001MAR30
645	LG:1503673.1:2001MAR30	1322	LG:1503673.1.orf3:2001MAR30
646	LG:213092.14:2001MAR30	1323	LG:213092.14.orf1:2001MAR30
647	LI:015309.1:2001MAY17	1324	LI:015309.1.orf1:2001MAY17
648	LI:030502.2:2001MAY17	1325	LI:030502.2.orf1:2001MAY17
649	LI:100501.1:2001MAY17	1326	LI:100501.1.orf1:2001MAY17
650	LI:1011706.2:2001MAY17	1327	LI:1011706.2.orf2:2001MAY17
651	LI:1171752.20:2001MAY17	1328	LI:1171752.20.orf2:2001MAY17
652	LI:2049713.6:2001MAY17	1329	LI:2049713.6.orf1:2001MAY17
653	LI:397393.2:2001MAY17	1330	LI:397393.2.orf3:2001MAY17
654	LI:401697.25:2001MAY17	1331	LI:401697.25.orf2:2001MAY17
655	LI:903668.7:2001MAY17	1332	LI:903668.7.orf1:2001MAY17
656	LI:903956.35:2001MAY17	1333	LI:903956.35.orf2:2001MAY17
657	LI:055784.15:2001MAY17	1334	LI:055784.15.orf2:2001MAY17
658	LI:2195792.2:2001MAY17	1335	LI:2195792.2.orf2:2001MAY17
659	LI:2207923.8:2001MAY17	1336	LI:2207923.8.orf3:2001MAY17
660	LI:232953.31:2001MAY17	1337	LI:232953.31.orf3:2001MAY17
661	LI:764674.1:2001MAY17	1338	LI:764674.1.orf2:2001MAY17
662	LI:893532.747:2001MAY17	1339	LI:893532.747.orf2:2001MAY17
663	LG:1121446.8:2001JUN22	1340	LG:1121446.8.orf1:2001JUN22
664	LG:1440335.2:2001JUN22	1341	LG:1440335.2.orf3:2001JUN22
665	LG:370271.9:2001JUN22	1342	LG:370271.9.orf3:2001JUN22
666	LG:414048.16:2001JUN22	1343	LG:414048.16.orf1:2001JUN22
667	LG:7683385.1:2001JUN22	1344	LG:7683385.1.orf3:2001JUN22
668	LG:7697332.3:2001JUN22	1345	LG:7697332.3.orf1:2001JUN22
669	LG:1047075.1:2001JUN22	1346	LG:1047075.1.orf3:2001JUN22
670	LG:331171.2:2001JUN22	1347	LG:331171.2.orf2:2001JUN22

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
1	LG:1040626.1:2001MAR30	g182977	1.00E-110	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) (Homo sapiens)
2	LG:1041136.7:2001MAR30	g17902306	1.00E-103	unnamed protein product (Homo sapiens)
3	LG:1043848.1:2001MAR30	g3133255	3.00E-71	PGP9.5 (Equus caballus)
4	LG:1097673.1:2001MAR30	g12585682	0	chondralin 6-sulfotransferase (Rattus norvegicus)
5	LG:133991.1:2001MAR30	g13359183	8.00E-23	KIAA1655 protein (Homo sapiens)
6	LG:1397110.7:2001MAR30	g6457272	9.00E-53	putative E1-E2 ATPase (Mus musculus)
7	LG:1512094.1:2001MAR30	g13278066	1.00E-136	Similar to uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase) (Mus musculus)
8	LG:230734.53:2001MAR30	g6013149	6.00E-91	aldehyde reductase (Homo sapiens)
9	LG:240154.9:2001MAR30	g10437752	5.00E-08	unnamed protein product (Homo sapiens)
10	LG:245863.31:2001MAR30	g15928817	1.00E-126	Similar to pyroline 5-carboxylate reductase isoform (Homo sapiens)
11	LG:257151.4:2001MAR30	g190818	2.00E-29	quinone oxidoreductase (Homo sapiens)
12	LG:334053.8:2001MAR30	g10437485	2.00E-17	unnamed protein product (Homo sapiens)
13	LG:392033.1:2001MAR30	g951270	6.00E-88	IPP-2 (Homo sapiens)
14	LG:401748.16:2001MAR30	g7768658	3.00E-44	6-pyruvoyl-tetrahydropterin synthase (Homo sapiens)
15	LG:476084.1:2001MAR30	g1654186	0	CTP synthetase homolog (Mus musculus)
16	LG:068514.1:2001MAR30	g6457274	0	putative E1-E2 ATPase (Mus musculus)
17	LI:010505.1:2001MAY17	g14189960	1.00E-25	PRO0764 (Homo sapiens)
18	LI:011664.1:2001MAY17	g11493483	2.00E-18	PRO2550 (Homo sapiens)
19	LI:021459.66:2001MAY17	g9837517	0	cysteinyl-tRNA synthetase (Homo sapiens)
20	LI:1047290.8:2001MAY17	g204495	1.00E-123	glutathione S-transferase Ya subunit (Rattus norvegicus)
21	LI:1071608.1:2001MAY17	g399660	2.00E-55	aldehyde reductase (Rattus norvegicus)
22	LI:1077079.4:2001MAY17	g1488969	6.00E-64	brain acyl-CoA synthetase II (Rattus norvegicus)
23	LI:1173294.9:2001MAY17	g12856270	0	putative (Mus musculus)
24	LI:148565.7:2001MAY17	g1184772	1.00E-155	cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC2 (Zea mays)
25	LI:2052562.23:2001MAY17	g12406973	1.00E-142	alanine-glyoxylate aminotransferase 2 (Homo sapiens)
26	LI:2119354.20:2001MAY17	g7242608	0	clJ510D11.1 (hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)) (Homo sapiens)
27	LI:2209329.1:2001MAY17	g10437485	2.00E-30	unnamed protein product (Homo sapiens)
28	LI:240143.12:2001MAY17	g11545401	0	3 beta-hydroxy-delta 5-C27-steroid oxidoreductase (Mus musculus)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
29	LI:250855.6:2001MAY17	g7023324	1.00E-149	Homo sapiens cDNA FLJ10956 fis, clone PLACE1000420, weakly similar to 7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-).
30	LI:293078.2:2001MAY17	g6457274	0	putative E1-E2 ATPase (Mus musculus)
31	LI:351818.62:2001MAY17	g306812	1.00E-104	glutathione transferase M1 (Homo sapiens)
32	LI:409990.1:2001MAY17	g16549456	9.00E-26	unnamed protein product (Homo sapiens)
33	LI:474832.7:2001MAY17	g7023200	0	unnamed protein product (Homo sapiens)
34	LI:814696.11:2001MAY17	g3191969	0	dJ337O18.2.1 (Lysosomal Protective Protein precursor (EC 3.4.16.5, Cathepsin A, Carboxypeptidase C) (isoform 1)) (Homo sapiens)
35	LI:818488.31:2001MAY17	g450271	0	epoxide hydrolase (Homo sapiens)
36	LI:2049834.12:2001MAY17	g14161726	1.00E-149	putative 1-aminocyclopropane-1-carboxylate synthase (Homo sapiens)
37	LI:338956.8:2001MAY17	g1754714	5.00E-71	oviductin (Xenopus laevis)
38	LI:1175083.15:2001MAY17	g14026730	5.00E-12	homoserine kinase (Mesorhizobium loti)
39	LI:118931.14:2001MAY17	g10435084	0	Homo sapiens cDNA FLJ13178 fis, clone NT2RP3003914, weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-).
40	LI:330984.6:2001MAY17	g6453472	1.00E-115	hypothetical protein (Homo sapiens)
41	LG:1093461.22:2001JUN22	g14602585	6.00E-27	methylentetrahydrofolate dehydrogenase (NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase (Homo sapiens)
42	LG:1138554.48:2001JUN22	g7328960	2.00E-19	Homo sapiens PGFS gene for prostaglandin F synthase (AKR 1C3), exon 1, 2, 3, 4, 5.
43	LG:1377369.20:2001JUN22	g12005726	1.00E-47	DC21 (Homo sapiens)
44	LG:200050.17:2001JUN22	g16924333	1.00E-174	cytosolic acyl coenzyme A thioester hydrolase (Homo sapiens)
45	LG:437008.4:2001JUN22	g7023029	2.00E-10	unnamed protein product (Homo sapiens)
46	LG:7684119.1:2001JUN22	g202842	1.00E-103	aldolase C (Rattus norvegicus)
47	LG:7690376.8:2001JUN22	g6006405	4.00E-14	acetyl-CoA-carboxylase (Bos taurus)
48	LG:068514.3:2001JUN22	g6457274	0	putative E1-E2 ATPase (Mus musculus)
49	LG:270209.1:2001JUN22	g12698182	4.00E-13	hypothetical protein (Macaca fascicularis)
50	LG:1400575.1:2001MAR30	g6467206	1.00E-101	gonadotropin inducible transcription repressor-4 (Homo sapiens)
51	LG:242968.4:2001MAR30	g15797278	0	unnamed protein product (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
52	LG:344741.17:2001MAR30	g5441939	0	Inhibin beta-A chain precursor (Homo sapiens)
53	LG:443203.7:2001MAR30	g6467206	1.00E-110	gonadotropin inducible transcription repressor-4 (Homo sapiens)
54	LG:481492.6:2001MAR30	g12002127	3.00E-60	CKK1 protein (Homo sapiens)
55	LI:035870.26:2001MAY17	g6862560	1.00E-151	endothelial cell growth factor 1 (Homo sapiens)
56	LI:2121852.1:2001MAY17	g6467206	3.00E-30	gonadotropin inducible transcription repressor-4 (Homo sapiens)
57	LI:2164765.1:2001MAY17	g825442	2.00E-12	prosmatostatin (Cnrls familiaris)
58	LI:2167150.1:2001MAY17	g10437569	6.00E-16	unnamed protein product (Homo sapiens)
59	LI:230062.10:2001MAY17	g459811	3.00E-92	basic fibroblast growth factor (ctg start codon); putative (Homo sapiens)
60	LI:351749.1:2001MAY17	g4868435	7.00E-26	apoptosis related protein APR-2 (Homo sapiens)
61	LI:399808.27:2001MAY17	g3452409	1.00E-11	Ribosomal protein kinase B (RSK-B) (Homo sapiens)
62	LI:401269.13:2001MAY17	g6624117	2.00E-19	pre-B cell enhancing factor (Homo sapiens)
63	LI:481492.3:2001MAY17	g12002127	2.00E-71	CKK1 protein (Homo sapiens)
64	LI:1186340.9:2001MAY17	g13559798	6.00E-05	alpha3 type IV collagen (Homo sapiens)
65	LG:1324237.7:2001JUN22	g34663	1.00E-41	macrophage inflammatory protein-2beta precursor (Homo sapiens)
66	LG:142131.16:2001JUN22	g6624117	2.00E-19	pre-B cell enhancing factor (Homo sapiens)
67	LG:407723.12:2001JUN22	g386852	0	kininogen (Homo sapiens)
68	LG:7685000.6:2001JUN22	g265426	5.00E-21	neurotrophin-3 (5' region, promoter) (human, placenta, Genomic, 3821 nt).
69	LG:1395921.6:2001JUN22	g5834566	0	dJ967N21.1.1 (chromogranin B (secretogranin 1, SCG1) (isoform 1)) (Homo sapiens)
70	LG:230062.16:2001JUN22	g459811	3.00E-92	basic fibroblast growth factor (ctg start codon); putative (Homo sapiens)
71	LG:7690036.1:2001JUN22	g6467206	1.00E-176	gonadotropin inducible transcription repressor-4 (Homo sapiens)
72	LG:044276.1:2001JUN22	g10433120	4.00E-20	unnamed protein product (Homo sapiens)
73	LG:1091967.34:2001JUN22	g5468516	2.00E-09	Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; and unknown genes.
74	LG:242968.17:2001JUN22	g15797260	0	unnamed protein product (Homo sapiens)
75	LG:081174.1:2001MAR30	g7020625	9.00E-31	unnamed protein product (Homo sapiens)
76	LG:1385255.10:2001MAR30	g732800	0	receptor tyrosine kinase (Homo sapiens)
77	LG:1397492.21:2001MAR30	g2662434	0	immunoglobulin-like transcript 5 protein (Homo sapiens)
78	LG:1512330.2:2001MAR30	g3861482	0	Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene.

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
79	LG:300009.1:2001MAR30	g9280152	5.00E-26	unnamed protein product (Macaca fascicularis)
80	LG:333886.2:2001MAR30	g558456	3.00E-49	beta 2 thyroid hormone receptor (Mus musculus)
81	LG:349438.18:2001MAR30	g5702091	0	green fluorescent protein-esrogen receptor alpha fusion (Mammalian expression vector pCI-nGL1-HEGO)
82	LG:358239.46:2001MAR30	g35311	1.00E-116	MHC class I promoter binding protein (Homo sapiens)
83	LG:250170.3:2001MAR30	g11022747	0	CRL1 protein (Homo sapiens)
84	LG:1383159.5:2001MAR30	g11226987	8.00E-07	unnamed protein product (synthetic construct)
85	LI:044888.1:2001MAY17	g12698182	2.00E-14	hypothetical protein (Macaca fascicularis)
86	LI:101277.1:2001MAY17	g13517983	0	G-protein coupled receptor 91 (Homo sapiens)
87	LI:1021852.6:2001MAY17	g12214287	1.00E-97	dJ402H5.1 (novel 7 transmembrane receptor of the rhodopsin family) (Homo sapiens)
88	LI:1072004.14:2001MAY17	g1381181	1.00E-142	ubiquitin-conjugating enzyme E2-32k (Oryctolagus cuniculus)
89	LI:1084017.20:2001MAY17	g2343109	8.00E-65	MIR-7 (Homo sapiens)
90	LI:1183158.1:2001MAY17	g10437569	7.00E-22	unnamed protein product (Homo sapiens)
91	LI:118807.9:2001MAY17	g4097253	4.00E-69	calcitonin gene-related peptide receptor component protein (Homo sapiens)
92	LI:206576.15:2001MAY17	g12232595	0	aryl hydrocarbon receptor nuclear translocator, ARNT (Homo sapiens)
93	LI:2120427.4:2001MAY17	g59571	6.00E-05	RS1 (human herpesvirus 1)
94	LI:2196074.2:2001MAY17	g6469324	7.00E-13	purinoceptor P2X6 (Homo sapiens)
95	LI:220797.7:2001MAY17	g1419016	2.00E-56	odorant receptor (Mus musculus)
96	LI:237723.23:2001MAY17	g5442038	1.00E-150	stromal cell-derived receptor-1 alpha (Homo sapiens)
97	LI:817560.12:2001MAY17	g4309953	1.00E-107	T cell receptor gamma chain; similar to PID:g339160 (Homo sapiens)
98	LI:140935.16:2001MAY17	g11226987	1.00E-166	unnamed protein product (synthetic construct)
99	LI:235333.5:2001MAY17	g425148	0	TGF-beta superfamily receptor type I (Homo sapiens)
100	LI:373808.8:2001MAY17	g2690100	4.00E-06	B. burgdorferi predicted coding region BB116 (Borrelia burgdorferi)
101	LI:424554.1:2001MAY17	g13359183	2.00E-28	KIAA1655 protein (Homo sapiens)
102	LG:028634.1:2001JUN22	g9280152	7.00E-12	unnamed protein product (Macaca fascicularis)
103	LG:087230.3:2001JUN22	g7020440	3.00E-12	unnamed protein product (Homo sapiens)
104	LG:1397520.8:2001JUN22	g3064029	7.00E-05	T cell receptor beta chain CDR3 (Mus musculus)
105	LG:213947.1:2001JUN22	g7262613	3.00E-24	candidate taste receptor T2R7 (Homo sapiens)
106	LG:218029.8:2001JUN22	g13528954	2.00E-93	putative receptor protein (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
107	LG:300009.1:2001JUN22	g9280152	6.00E-26	unnamed protein product (Macaca fascicularis)
108	LG:411188.1:2001JUN22	g204400	5.00E-65	glutamate receptor (GluR-D) (Rattus norvegicus)
109	LG:481295.21:2001JUN22	g2218074	0	glucocorticoid receptor alpha (Homo sapiens)
110	LG:7684165.8:2001JUN22	g12654658	0	Homo sapiens, retinoid X receptor, beta, clone MGC:1831 IMAGE:3502936, mRNA, complete cds.
111	LG:7690928.6:2001JUN22	g16930377	9.00E-16	leukocyte immunoglobulin-like receptor b (Pan troglodytes)
112	LG:990040.8:2001JUN22	g3861488	1.00E-71	vesicle soluble NSF attachment protein receptor Vti2 (Homo sapiens)
113	LG:126510.8:2001JUN22	g6006811	6.00E-22	serpentine receptor (Mus musculus)
114	LG:7692710.8:2001JUN22	g4159884	1.00E-122	similar to mouse olfactory receptor 13; similar to P34984 (PID:g464305) (Homo sapiens)
115	LG:044888.1:2001JUN22	g12698182	2.00E-14	hypothetical protein (Macaca fascicularis)
116	LG:1447083.2:2001JUN22	g1732344	2.00E-13	Human orphan G-protein coupled receptor Dez isoform b mRNA, complete cds.
117	LG:7672289.1:2001JUN22	g10433120	8.00E-19	unnamed protein product (Homo sapiens)
118	LG:1013021.3:2001MAR30	g202752	5.00E-26	adenylyl cyclase type II (Rattus norvegicus)
119	LG:1096667.17:2001MAR30	g8250239	6.00E-80	protein phosphatase 4 regulatory subunit 2 (Homo sapiens)
120	LG:1270681.12:2001MAR30	g986879	3.00E-95	cyclin-dependent kinase (Homo sapiens)
121	LG:1328242.1:2001MAR30	g10047261	0	KIAA1593 protein (Homo sapiens)
122	LG:1396586.4:2001MAR30	g189956	0	Human pim-1 oncogene mRNA, complete cds.
123	LG:1396919.6:2001MAR30	g12654002	5.00E-46	Homo sapiens, RAB13, member RAS oncogene family, clone MGC:5074 IMAGE:3451945, mRNA, complete cds.
124	LG:1397751.10:2001MAR30	g12832961	0	putative (Mus musculus)
125	LG:1450059.4:2001MAR30	g10437485	7.00E-17	unnamed protein product (Homo sapiens)
126	LG:1503615.8:2001MAR30	g397935	0	a2-chimaerin (Homo sapiens)
127	LG:1507027.3:2001MAR30	g14043783	1.00E-143	Unknown (protein for MGC:14256) (Homo sapiens)
128	LG:202892.1:2001MAR30	g14041850	3.00E-89	unnamed protein product (Homo sapiens)
129	LG:220407.3:2001MAR30	g12830335	0	bA550O8.2 (novel protein kinase) (Homo sapiens)
130	LG:242234.11:2001MAR30	g10443732	0	calcium/calmodulin-dependent protein kinase II delta12 subunit (Xenopus)
131	LG:245181.20:2001MAR30	g407075	4.00E-17	MAP kinase activated protein kinase-2 (Homo sapiens)
132	LG:320165.7:2001MAR30	g8331757	1.00E-162	Ca2+/Calmodulin-dependent protein kinase I (Homo sapiens)
133	LG:333965.2:2001MAR30	g2736151	0	myotonic dystrophy kinase-related Cdc42-binding kinase (Rattus norvegicus)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
134	LG:402431.16:2001MAR30	g2961199	1.00E-98	tyrosine phosphatase (Homo sapiens)
135	LG:404400.4:2001MAR30	g14794515	0	interleukin-4 induced gene-1 protein (Homo sapiens)
136	LG:406860.73:2001MAR30	g10435919	0	unnamed protein product (Homo sapiens)
137	LG:413797.14:2001MAR30	g1463127	0	JNK3 alpha1 protein kinase (Homo sapiens)
138	LG:420527.51:2001MAR30	g632964	1.00E-130	ck11; putative (Homo sapiens)
139	LG:277227.1:2001MAR30	g12653099	0	Similar to RAB2, member RAS oncogene family-like (Homo sapiens)
140	LG:373260.30:2001MAR30	g7263960	1.00E-130	bA395L14.11.1 (RAB, member of RAS oncogene family-like 2A (isoform 1)) (Homo sapiens)
141	LG:418805.7:2001MAR30	g2735857	0	cAMP-specific phosphodiesterase PDE4D5 (Homo sapiens)
142	LG:1398946.18:2001MAR30	g15213263	3.00E-93	RAS guanyl releasing protein 4 (Homo sapiens)
143	LG:382911.1:2001MAR30	g7020538	0	unnamed protein product (Homo sapiens)
144	LJ:028146.27:2001MAY17	g13592175	2.00E-08	ppg3 (Leishmania major)
145	LJ:1072703.6:2001MAY17	g11493483	4.00E-12	PRO2550 (Homo sapiens)
146	LJ:1073062.138:2001MAY17	g6010438	3.00E-14	protein phosphatase type-1 catalytic subunit delta isoform (Homo sapiens)
147	LJ:1084954.7:2001MAY17	g12837642	2.00E-89	putative (Mus musculus)
148	LJ:202892.5:2001MAY17	g14041850	1.00E-101	unnamed protein product (Homo sapiens)
149	LJ:2030686.1:2001MAY17	g10437569	1.00E-28	unnamed protein product (Homo sapiens)
150	LJ:2043289.10:2001MAY17	g16511330	4.00E-69	unnamed protein product (Homo sapiens)
151	LJ:2118426.12:2001MAY17	g12830367	0	serine/threonine kinase 33 (Homo sapiens)
152	LJ:2118901.10:2001MAY17	g2586413	2.00E-08	protein phosphatase with EF-hands-2 long form (Homo sapiens)
153	LJ:213087.4:2001MAY17	g15795911	1.00E-42	unnamed protein product (Homo sapiens)
154	LJ:2155821.1:2001MAY17	g6164867	6.00E-22	G-protein gamma 8 subunit (Homo sapiens)
155	LJ:2201523.6:2001MAY17	g763130	1.00E-121	YPT3 (Homo sapiens)
156	LJ:235867.27:2001MAY17	g12407081	0	protein kinase/ribonuclease IRE1 beta (Homo sapiens)
157	LJ:238414.1:2001MAY17	g14189960	2.00E-28	PRO0764 (Homo sapiens)
158	LJ:242234.6:2001MAY17	g3088551	5.00E-61	calcium/calmodulin-dependent protein kinase II delta (Mus musculus)
159	LJ:245181.22:2001MAY17	g530090	0	MAP kinase activated protein kinase 2 (Homo sapiens)
160	LJ:245474.13:2001MAY17	g189510	3.00E-83	p70 ribosomal S6 kinase alpha-II (Homo sapiens)
161	LJ:311661.1:2001MAY17	g10437569	1.00E-21	unnamed protein product (Homo sapiens)
162	LJ:320165.21:2001MAY17	g8331757	1.00E-151	Ca2+/Calmodulin-dependent protein kinase I (Homo sapiens)



Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
163	LI:337026.1:2001MAY17	g1872200	5.00E-13	alternatively spliced product using exon 13A (Homo sapiens)
164	LI:347977.10:2001MAY17	g4995956	1.00E-180	map kinase phosphatase-like protein MK-STYX (Homo sapiens)
165	LI:413040.39:2001MAY17	g211368	4.00E-35	calmodulin-like protein (Gallus gallus)
166	LI:467422.1:2001MAY17	g7768768	0	Homo sapiens genomic DNA, chromosome 21q, section 91/105.
167	LI:474596.53:2001MAY17	g15042611	0	Ser/Thr protein kinase PAR-1Balpha (Homo sapiens)
168	LI:481144.22:2001MAY17	g1016005	1.00E-128	serine/threonine kinase (Rattus norvegicus)
169	LI:725220.1:2001MAY17	g1304169	3.00E-79	protein tyrosine phosphatase (Mus musculus)
170	LI:804636.17:2001MAY17	g10437485	3.00E-21	unnamed protein product (Homo sapiens)
171	LI:815194.23:2001MAY17	g665588	2.00E-79	ccilmodulin (Homo sapiens)
172	LI:817950.6:2001MAY17	g10505346	5.00E-31	guanine nucleotide binding protein beta subunit 4 (Homo sapiens)
173	LI:903485.6:2001MAY17	g3068752	0	Jak2 kinase (Homo sapiens)
174	LI:220407.8:2001MAY17	g12830335	2.00E-82	ba55008.2 (novel protein kinase) (Homo sapiens)
175	LI:413606.59:2001MAY17	g31744	1.00E-151	G protein alpha-subunit (AA 1-355) (Homo sapiens)
176	LI:202971.33:2001MAY17	g14149100	6.00E-40	PTEN induced putative kinase 1 (Homo sapiens)
177	LI:2209219.4:2001MAY17	g14571717	5.00E-10	myosin light chain kinase (MLCK) (Homo sapiens)
178	LG:1100586.2:2001JUN22	g3646067	2.00E-41	MEK5 (MAP/ERK kinase kinase 5 (ASK1, MAPKK5, Mitogen Activated Protein kinase kinase kinase 5)) (Homo sapiens)
179	LG:113410.1:2001JUN22	g6650810	9.00E-21	PRO1902 (Homo sapiens)
180	LG:1500938.10:2001JUN22	g403007	1.00E-130	PHAPI (Putative HLA DR Associated Protein 1) (Homo sapiens)
181	LG:303607.15:2001JUN22	g177993	0	Human casein kinase II alpha subunit mRNA, complete cds.
182	LG:411148.11:2001JUN22	g32131	2.00E-17	putative p33 (Homo sapiens)
183	LG:435726.8:2001JUN22	g4153873	3.00E-24	similar to wee 1-like protein kinase; similar to P30291 (PID:g1351419) (Homo sapiens)
184	LG:475378.4:2001JUN22	g7023688	2.00E-12	unnamed protein product (Homo sapiens)
185	LG:7692134.1:2001JUN22	g15213263	1.00E-120	RAS guanyl releasing protein 4 (Homo sapiens)
186	LG:985139.2:2001JUN22	g10437569	6.00E-16	unnamed protein product (Homo sapiens)
187	LG:149419.8:2001JUN22	g15706262	0	O14.1.1 (bromodomain-containing protein 2 (RING3, KIAA9001), isoform 1) (Homo sapiens)
188	LG:199172.17:2001JUN22	g15186754	0	RaIGDS-related effector protein of M-Ras (Mus musculus)
189	LG:256101.6:2001JUN22	g17390126	1.00E-122	Ric (Drosophila)-like, expressed in neurons (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
190	LG:220407.3:2001JUN22	g12830335	0	bA550O8.2 (novel protein kinase) (Homo sapiens)
191	LG:331677.12:2001JUN22	g9367828	0	protein phosphatase 2A 72 kDa regulatory subunit (Homo sapiens)
192	LG:367128.7:2001JUN22	g13311007	1.00E-144	protein kinase NYD-SP15 (Homo sapiens)
193	LG:403176.4:2001JUN22	g2653311	2.00E-06	very large virion protein (tegument) (Bovine herpesvirus type 1.1)
194	LG:985230.9:2001JUN22	g7959159	2.00E-84	KIAA1450 protein (Homo sapiens)
195	LG:005580.6:2001MAR30	g2317723	1.00E-101	Polycomb 2 homolog (Homo sapiens)
196	LG:100653.5:2001MAR30	g7020488	1.00E-164	unnamed protein product (Homo sapiens)
197	LG:1099240.25:2001MAR30	g5737759	8.00E-83	polyamine modulated factor-1 (Homo sapiens)
198	LG:117947.1:2001MAR30	g483430	1.00E-112	Jun-D (Rattus norvegicus)
199	LG:1327967.11:2001MAR30	g12583650	1.00E-167	leucine-zipper protein (Homo sapiens)
200	LG:1395721.9:2001MAR30	g10437569	2.00E-25	unnamed protein product (Homo sapiens)
201	LG:210508.1:2001MAR30	g9280152	6.00E-31	unnamed protein product (Macaca fascicularis)
202	LG:232313.46:2001MAR30	g9714266	0	DRBP76 alpha (Homo sapiens)
203	LG:349746.22:2001MAR30	g15524590	0	unnamed protein product (Homo sapiens)
204	LG:350526.1:2001MAR30	g5052951	1.00E-12	unknown (Homo sapiens)
205	LG:385569.1:2001MAR30	g16550231	2.00E-26	unnamed protein product (Homo sapiens)
206	LG:440659.1:2001MAR30	g12804963	6.00E-48	Similar to ubiquitin-cytochrome c reductase hinge protein (Homo sapiens)
207	LG:1081135.1:2001MAR30	g4165087	1.00E-121	Williams-Beuren syndrome deletion transcript 9 (Homo sapiens)
208	LG:1387341.2:2001MAR30	g12314067	1.00E-104	dJ1167H4.1.1 (novel protein, isoform 1) (Homo sapiens)
209	LG:197915.17:2001MAR30	g10435455	1.00E-44	unnamed protein product (Homo sapiens)
210	LI:071874.1:2001MAY17	g10436387	1.00E-12	unnamed protein product (Homo sapiens)
211	LI:1076016.1:2001MAY17	g7341372	4.00E-76	retinoblastoma-binding protein 1-related protein (Rattus norvegicus)
212	LI:2050098.6:2001MAY17	g12654881	3.00E-29	Unknown (protein for MGC:5149) (Homo sapiens)
213	LI:233360.4:2001MAY17	g11493409	1.00E-15	PRO0898 (Homo sapiens)
214	LI:365343.34:2001MAY17	g5565859	0	epithelium-restricted Ets protein ESX (Homo sapiens)
215	LI:757755.14:2001MAY17	g13529308	8.00E-21	Unknown (protein for IMAGE:3461492) (Homo sapiens)
216	LI:1086645.2:2001MAY17	g2317723	1.00E-26	Polycomb 2 homolog (Homo sapiens)
217	LG:1015174.1:2001JUN22	g2224559	0	KIAA0309 (Homo sapiens)
218	LG:1135945.19:2001JUN22	g2460124	6.00E-63	putative transcription factor CA150 (Homo sapiens)
219	LG:1382836.16:2001JUN22	g6683492	9.00E-27	bromodomain PHD finger transcription factor (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number - Probability Score	Annotation
220	LG:228817.5:2001JUN22	g13938329 2.00E-86	H2.0 (Drosophila)-like homeo box 1 (Homo sapiens)
221	LG:253987.9:2001JUN22	g490013 2.00E-73	ORF, HEIR-1, pot. neuroblastoma-associated regulator (Homo sapiens)
222	LG:7683993.20:2001JUN22	g1045655 1.00E-42	silencing mediator of retinoid and thyroid hormone action (Homo sapiens)
223	LG:7691137.1:2001JUN22	g882393 7.00E-76	TBP-associated factor TAFI31 (Homo sapiens)
224	LG:977849.6:2001JUN22	g13529308 1.00E-38	Unknown (protein for IMAGE:3461492) (Homo sapiens)
225	LG:1088040.17:2001JUN22	g4049922 0	transcription factor WSTF (Homo sapiens)
226	LG:1096582.2:2001JUN22	g12001942 0	Myo01 protein (Homo sapiens)
227	LG:002095.19:2001JUN22	g7019877 3.00E-19	unnamed protein product (Homo sapiens)
228	LG:227596.1:2001JUN22	g6690167 9.00E-13	PRO0117 (Homo sapiens)
229	LG:276154.23:2001JUN22	g5163089 0	P38IP (Homo sapiens)
230	LG:332254.1:2001JUN22	g11493483 2.00E-28	PRO2550 (Homo sapiens)
231	LG:1052984.26:2001MAR30	g13938351 1.00E-164	Similar to zinc finger protein 268 (Homo sapiens)
232	LG:1064250.5:2001MAR30	g11181880 0	bA1021O19.1 (zinc finger protein 33a (KOX 31)) (Homo sapiens)
233	LG:1065609.1:2001MAR30	g7023216 4.00E-65	unnamed protein product (Homo sapiens)
234	LG:1076162.1:2001MAR30	g5730196 3.00E-50	Kruppel-type zinc finger (Homo sapiens)
235	LG:1079476.6:2001MAR30	g13752754 0	zinc finger 1111 (Homo sapiens)
236	LG:1080579.9:2001MAR30	g347906 8.00E-33	zinc finger protein (Homo sapiens)
237	LG:1082253.1:2001MAR30	g10436807 7.00E-94	unnamed protein product (Homo sapiens)
238	LG:1082263.10:2001MAR30	g5441615 1.00E-83	zinc finger protein (Carls familiaris)
239	LG:1092343.1:2001MAR30	g488555 3.00E-71	zinc finger protein ZNF135 (Homo sapiens)
240	LG:1094967.1:2001MAR30	g6007769 0	KID1 (Mus musculus)
241	LG:1384132.9:2001MAR30	g1020145 1.00E-126	DNA binding protein (Homo sapiens)
242	LG:1384676.4:2001MAR30	g10440081 3.00E-29	unnamed protein product (Homo sapiens)
243	LG:1400447.1:2001MAR30	g16550223 9.00E-34	unnamed protein product (Homo sapiens)
244	LG:1500260.1:2001MAR30	g2739353 1.00E-46	ZNF91L (Homo sapiens)
245	LG:1500873.3:2001MAR30	g2739353 0	ZNF91L (Homo sapiens)
246	LG:1505341.1:2001MAR30	g6693371 1.00E-114	ZNF225 (Homo sapiens)
247	LG:169863.4:2001MAR30	g498152 4.00E-22	ha0946 protein is Kruppel-related. (Homo sapiens)
248	LG:208637.1:2001MAR30	g2085786 0	similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185) (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
249	LG:234936.67:2001MAR30	g644871	3.00E-93	DNA/RNA-binding protein (Homo sapiens)
250	LG:243305.3:2001MAR30	g3378094	2.00E-47	KRAB domain zinc finger protein (Homo sapiens)
251	LG:334645.20:2001MAR30	g12853416	3.00E-23	putative (Mus musculus)
252	LG:349468.13:2001MAR30	g6649546	5.00E-51	zinc finger protein neuro-d4 (Mus musculus)
253	LG:385145.1:2001MAR30	g12584159	0	zinc finger protein 268 (Homo sapiens)
254	LG:391807.1:2001MAR30	g1488275	2.00E-44	zinc finger protein basophilin (Homo sapiens)
255	LG:399287.10:2001MAR30	g1480005	1.00E-166	Zic4 protein (Mus musculus)
256	LG:404157.1:2001MAR30	g5441615	1.00E-121	zinc finger protein (Canis familiaris)
257	LG:979390.2:2001MAR30	g12852573	8.00E-17	putative (Mus musculus)
258	LG:981962.1:2001MAR30	g9502404	1.00E-112	Hypothetical zinc finger-like protein (Homo sapiens)
259	LG:982976.2:2001MAR30	g1020145	1.00E-147	DNA binding protein (Homo sapiens)
260	LG:1448087.1:2001MAR30	g5262560	3.00E-16	hypothetical protein (Homo sapiens)
261	LG:1449021.1:2001MAR30	g13937909	9.00E-44	Similar to KIAA0961 protein (Homo sapiens)
262	LG:144920.1:2001MAR30	g2689444	1.00E-141	ZNF134 (Homo sapiens)
263	LG:474725.1:2001MAR30	g1572600	0	Zik1 (Mus musculus)
264	LG:1085952.14:2001MAR30	g6088099	5.00E-08	Homo sapiens mRNA for zinc finger protein (ZFD25), complete cds.
265	U:011009.2:2001MAY17	g9367763	0	zinc finger protein Cezanne (Homo sapiens)
266	U:016933.2:2001MAY17	g13359183	4.00E-19	KIAA1655 protein (Homo sapiens)
267	U:1072014.6:2001MAY17	g12848204	0	putative (Mus musculus)
268	U:1165280.4:2001MAY17	g16306806	0	zinc finger protein 43 (HTF6) (Homo sapiens)
269	U:1167958.4:2001MAY17	g14602838	1.00E-140	zinc-finger protein ZBRK1 (Homo sapiens)
270	U:1168073.15:2001MAY17	g3342002	2.00E-69	hematopoietic cell derived zinc finger protein (Homo sapiens)
271	U:1170154.12:2001MAY17	g16552172	2.00E-46	unnamed protein product (Homo sapiens)
272	U:1173769.2:2001MAY17	g8099348	0	zinc finger protein (Homo sapiens)
273	U:1174292.18:2001MAY17	g2384653	0	Kruppel family zinc finger protein (Homo sapiens)
274	U:1177989.1:2001MAY17	g16551429	0	unnamed protein product (Homo sapiens)
275	U:1179173.3:2001MAY17	g6118383	0	zinc finger protein ZNF223 (Homo sapiens)
276	U:1180137.1:2001MAY17	g16552123	2.00E-59	unnamed protein product (Homo sapiens)
277	U:1181458.2:2001MAY17	g186774	1.00E-159	zinc finger protein (Homo sapiens)
278	U:1182817.8:2001MAY17	g498152	0	ha0946 protein is Kruppel-related. (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
279	U:1182838.4:2001MAY17	g13752754	0	zinc finger 1111 (Homo sapiens)
280	U:12053637.1:2001MAY17	g2739353	1.00E-72	ZNF91L (Homo sapiens)
281	U:12119713.6:2001MAY17	g14042190	0	unnamed protein product (Homo sapiens)
282	U:12121833.1:2001MAY17	g9502402	1.00E-118	ZNF225 (amino acids 79-706) (Homo sapiens)
283	U:12121863.1:2001MAY17	g14456631	1.00E-84	CU54820.4 (novel KRAB box containing C2H2 type zinc finger protein) (Homo sapiens)
284	U:12121899.1:2001MAY17	g13623607	4.00E-50	zinc finger protein 136 (clone pHZ-20) (Homo sapiens)
285	U:12122035.5:2001MAY17	g2739353	2.00E-55	ZNF91L (Homo sapiens)
286	U:12122507.3:2001MAY17	g7023216	1.00E-45	unnamed protein product (Homo sapiens)
287	U:12190152.1:2001MAY17	g3342002	8.00E-37	hematopoietic cell derived zinc finger protein (Homo sapiens)
288	U:12195736.1:2001MAY17	g488557	7.00E-56	zinc finger protein ZNF137 (Homo sapiens)
289	U:12195745.2:2001MAY17	g9502404	7.00E-28	Hypothetical zinc finger-like protein (Homo sapiens)
290	U:12196327.1:2001MAY17	g15081398	0	kruppel-like zinc finger protein (Homo sapiens)
291	U:12197842.1:2001MAY17	g3511122	0	zinc finger protein (Homo sapiens)
292	U:12202913.1:2001MAY17	g1017722	2.00E-32	repressor transcriptional factor (Homo sapiens)
293	U:12206159.1:2001MAY17	g6088100	2.00E-97	zinc finger protein (ZFD25) (Homo sapiens)
294	U:12208960.3:2001MAY17	g38032	0	ZNF43 (Homo sapiens)
295	U:12209149.1:2001MAY17	g32071	4.00E-26	HF.10 finger protein (AA 1-491) (Homo sapiens)
296	U:1223050.2:2001MAY17	g12483902	2.00E-57	zinc finger protein HIT-10 (Rattus norvegicus)
297	U:1393468.1:2001MAY17	g2618752	1.00E-160	zinc finger protein (Takifugu rubripes)
298	U:1480324.48:2001MAY17	g14042190	1.00E-137	unnamed protein product (Homo sapiens)
299	U:1722634.7:2001MAY17	g15081398	7.00E-34	kruppel-like zinc finger protein (Homo sapiens)
300	U:1796992.1:2001MAY17	g15012179	1.00E-121	zinc finger protein 16 (KIX 9) (Homo sapiens)
301	U:1093337.1:2001MAY17	g12652727	2.00E-31	Unknown (protein for IMAGE:3352566) (Homo sapiens)
302	U:1081130.3:2001MAY17	g4309888	2.00E-53	similar to zinc finger proteins; similar to protein S47071 (PID:g631503), match to EST AA339462 (NID:g1991774) (Homo sapiens)
303	U:1170908.4:2001MAY17	g12052983	0	hypothetical protein (Homo sapiens)
304	U:1177451.1:2001MAY17	g4159888	0	zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333) (Homo sapiens)
305	U:1180303.18:2001MAY17	g16306806	0	zinc finger protein 43 (HIF6) (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
306	LI:1182999.3:2001MAY17	g13543419	0	Similar to zinc finger protein 304 (Homo sapiens)
307	LI:1183525.1:2001MAY17	g4235144	9.00E-96	BC39498_1 (Homo sapiens)
308	LI:2121675.1:2001MAY17	g14043841	2.00E-50	Unknown (protein for MGC:14429) (Homo sapiens)
309	LI:2121766.1:2001MAY17	g3282513	7.00E-76	C2H2 zinc finger protein (Homo sapiens)
310	LI:2188633.1:2001MAY17	g14042822	1.00E-120	unnamed protein product (Homo sapiens)
311	LI:2188820.2:2001MAY17	g13623607	1.00E-141	zinc finger protein 136 (clone pHZ-20) (Homo sapiens)
312	LI:2191871.1:2001MAY17	g14042293	2.00E-71	unnamed protein product (Homo sapiens)
313	LI:2196157.2:2001MAY17	g13543419	6.00E-13	Similar to zinc finger protein 304 (Homo sapiens)
314	LI:230109.4:2001MAY17	g12584159	0	zinc finger protein 268 (Homo sapiens)
315	LI:790409.4:2001MAY17	g13752754	1.00E-150	zinc finger 1111 (Homo sapiens)
316	LG:084399.1:2001JUN22	g6760445	6.00E-14	Smad- and Olf-interacting zinc finger protein (Homo sapiens)
317	LG:1079456.3:2001JUN22	g7023703	3.00E-29	unnamed protein product (Homo sapiens)
318	LG:1080406.7:2001JUN22	g14041991	5.00E-71	unnamed protein product (Homo sapiens)
319	LG:1505015.1:2001JUN22	g488555	3.00E-77	zinc finger protein ZNF135 (Homo sapiens)
320	LG:208637.1:2001JUN22	g2085786	0	similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185) (Homo sapiens)
321	LG:233311.5:2001JUN22	g9714522	1.00E-38	bA162G10.3 (zinc finger protein) (Homo sapiens)
322	LG:385145.1:2001JUN22	g12804011	0	KIAA0798 gene product (Homo sapiens)
323	LG:404157.1:2001JUN22	g15012179	1.00E-121	zinc finger protein 16 (KOX 9) (Homo sapiens)
324	LG:7684505.1:2001JUN22	g488557	1.00E-59	zinc finger protein ZNF137 (Homo sapiens)
325	LG:7687730.1:2001JUN22	g6007771	0	KID2 (Mus musculus)
326	LG:7687809.2:2001JUN22	g15081398	0	kruppel-like zinc finger protein (Homo sapiens)
327	LG:7690098.1:2001JUN22	g1017722	1.00E-151	repressor transcriptional factor (Homo sapiens)
328	LG:7690113.1:2001JUN22	g186774	0	zinc finger protein (Homo sapiens)
329	LG:7690362.3:2001JUN22	g14042293	2.00E-79	unnamed protein product (Homo sapiens)
330	LG:7691200.3:2001JUN22	g13752754	0	zinc finger 1111 (Homo sapiens)
331	LG:7691277.3:2001JUN22	g10835284	1.00E-120	Zinc finger protein ZNF223 (amino acids 82-482) (Homo sapiens)
332	LG:7691280.4:2001JUN22	g2739353	1.00E-81	ZNF91L (Homo sapiens)
333	LG:7691562.2:2001JUN22	g1017722	1.00E-128	repressor transcriptional factor (Homo sapiens)
334	LG:7691685.3:2001JUN22	g7023216	6.00E-53	unnamed protein product (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
335	LG:7693155.4:2001JUN22	g1480005	2.00E-47	Zic4 protein (Mus musculus)
336	LG:981962.1:2001JUN22	g9502404	1.00E-112	Hypothetical zinc finger-like protein (Homo sapiens)
337	LG:1449021.1:2001JUN22	g13937909	1.00E-43	Similar to KIAA0961 protein (Homo sapiens)
338	LG:481631.22:2001JUN22	g14042253	0	unnamed protein product (Homo sapiens)
339	LG:7690406.2:2001JUN22	g14042590	1.00E-144	unnamed protein product (Homo sapiens)
340	LG:7690773.2:2001JUN22	g14042293	2.00E-79	unnamed protein product (Homo sapiens)
341	LG:1347119.1:2001JUN22	g7280338	0	LIM domain ZNF185 peptide (Homo sapiens)
342	LG:7691570.2:2001JUN22	g13752754	4.00E-63	zinc finger 1111 (Homo sapiens)
343	LG:023518.3:2001MAR30	g736727	1.00E-140	32 kd accessory protein (Bos taurus)
344	LG:1100502.1:2001MAR30	g12842190	5.00E-53	putative (Mus musculus)
345	LG:235076.6:2001MAR30	g2317723	1.00E-29	Polycomb 2 homolog (Homo sapiens)
346	LG:270582.4:2001MAR30	g9622335	0	two-pore domain potassium channel TREK-1 (Homo sapiens)
347	LG:334752.12:2001MAR30	g11125153	0	sodium-dependent vitamin C transporter (Homo sapiens)
348	LG:425641.11:2001MAR30	g3970725	0	glycoprotein-associated amino acid transporter (Homo sapiens)
349	LG:980241.4:2001MAR30	g12698192	8.00E-22	hypothetical protein (Macaca fascicularis)
350	LI:1040737.102:2001MAY17	g5457150	2.00E-82	Na,K-ATPase alpha-4 subunit (Mus musculus)
351	LI:1072888.10:2001MAY17	g8927560	2.00E-69	glucose transporter 3 (Homo sapiens)
352	LI:2048255.1:2001MAY17	g531469	0	renal osmotic stress-induced Na-Cl organic solute cotransporter (Rattus norvegicus)
353	LI:330658.1:2001MAY17	g14189960	1.00E-29	PRO0764 (Homo sapiens)
354	LI:410188.4:2001MAY17	g184039	0	sodium channel alpha subunit (Homo sapiens)
355	LI:902565.38:2001MAY17	g4165326	1.00E-115	plasma membrane calcium ATPase isoform 1 (Homo sapiens)
356	LI:2032241.1:2001MAY17	g10437485	2.00E-11	unnamed protein product (Homo sapiens)
357	LI:2192055.1:2001MAY17	g10834776	1.00E-13	PNAS-110 (Homo sapiens)
358	LG:133851.16:2001JUN22	g17512130	7.00E-22	Unknown (protein for MGC:20634) (Homo sapiens)
359	LG:1398822.1:2001JUN22	g685001	1.00E-152	water-channel aquaporin 2; AQP2 (Homo sapiens)
360	LG:1502274.17:2001JUN22	g8810220	4.00E-57	voltage-dependent anion channel 1 (Bos taurus)
361	LG:166400.33:2001JUN22	g1809220	6.00E-33	K+ channel beta 2 subunit (Homo sapiens)
362	LG:235076.15:2001JUN22	g7801278	6.00E-07	putative translation initiation factor IF-2(fragment) (Streptomyces coelicolor)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
363	LG:7689943.1:2001JUN22	g1049231	2.00E-26	Method: conceptual translation supplied by author; putative hybrid protein similar to HERV-H protease and HERV-E integrase (Human endogenous cJ1003J2.3.2 (potassium voltage-gated channel, Shaw-related subfamily, member 4) (Homo sapiens)
364	LG:7693319.3:2001JUN22	g12313899	2.00E-92	hypothetical protein (Macaca fascicularis)
365	LG:980241.4:2001JUN22	g12698192	2.00E-21	channel interacting PDZ domain protein (Mus musculus)
366	LG:226475.15:2001JUN22	g3108057	0	Homo sapiens channel-kinase 1 (CHAK1) mRNA, complete cds.
367	LG:422564.11:2001JUN22	g13562152	0	calpain (Rattus norvegicus)
368	LG:026384.13:2001MAR30	g495222	4.00E-38	cyclophilin 18 (Oryctolagus cuniculus)
369	LG:108781.6:2001MAR30	g6651171	1.00E-31	zinc metalloprotease ADAMTS6 (Homo sapiens)
370	LG:208877.7:2001MAR30	g5923786	7.00E-21	neutral protease alpha subunit (Homo sapiens)
371	LG:232959.49:2001MAR30	g179909	1.00E-63	hepsin (Homo sapiens)
372	LG:331078.21:2001MAR30	g32064	0	Similar to distal intestinal serine protease (Mus musculus)
373	LG:334345.5:2001MAR30	g15012124	3.00E-42	Similar to peptidylprolyl isomerase (cyclophilin)-like 2 (Homo sapiens)
374	LG:345279.19:2001MAR30	g13366579	0	hypothetical protein (Macaca fascicularis)
375	LG:400109.5:2001MAR30	g12698182	2.00E-28	Ran binding protein 2 (Homo sapiens)
376	LG:001294.11:2001MAR30	g2293556	0	UDP-GalNAc:polypeptide N-acetylglactosaminyl transferase (Homo sapiens)
377	LG:230895.5:2001MAR30	g971459	0	Homo sapiens serine protease DESC1 (DESC1) mRNA, complete cds.
378	LI:090657.2:2001MAY17	g6137096	1.00E-30	CARS-Cyp (Homo sapiens)
379	LI:1072276.1:2001MAY17	g1117968	1.00E-141	calpain 12 (Mus musculus)
380	LI:1072654.40:2001MAY17	g441200	1.00E-112	calpain 12 (Mus musculus)
381	LI:123815.12:2001MAY17	g10303331	1.00E-126	calpain (Rattus norvegicus)
382	LI:198705.6:2001MAY17	g495222	1.00E-156	hypothetical protein (Macaca fascicularis)
383	LI:2032264.3:2001MAY17	g9929935	2.00E-08	unnamed protein product (Homo sapiens)
384	LI:2070168.1:2001MAY17	g10436743	7.00E-21	a disintegrin-like and metalloprotease domain with thrombospondin type I motifs-like 3 (Homo sapiens)
385	LI:2077540.1:2001MAY17	g13183078	1.00E-166	zinc metalloendopeptidase (Homo sapiens)
386	LI:207915.45:2001MAY17	g11493589	4.00E-60	saccular collagen (Lepomis macrochirus)
387	LI:2120273.5:2001MAY17	g687606	6.00E-47	Unknown (protein for MGC:9299) (Homo sapiens)
388	LI:237520.26:2001MAY17	g16307229	1.00E-107	anionic trypsinogen (Homo sapiens)
389	LI:243892.46:2001MAY17	g2275595	1.00E-144	



Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
390	LI:400590.4:2001MAY17	g557646	0	meprin a (Homo sapiens)
391	LI:407084.4:2001MAY17	g13661813	1.00E-09	Homo sapiens alpha-2-macroglobulin (A2M) gene, exon 18 and partial cds.
392	LI:2052211.9:2001MAY17	g15593890	0	unnamed protein product (Homo sapiens)
393	LI:407291.5:2001MAY17	g6525045	3.00E-85	thyroxine-binding globulin (Sus scrofa)
394	LI:2167560.1:2001MAY17	g7770139	8.00E-25	PRO1722 (Homo sapiens)
395	LI:401586.1:2001MAY17	g15593888	0	unnamed protein product (Homo sapiens)
396	LG:1093982.21:2001JUN22	g12804335	1.00E-32	Unknown (protein for IMAGE:2823490) (Homo sapiens)
397	LG:1383133.102:2001JUN22	g35741	1.00E-108	precursor polypeptide (AA -17 to 244) (Homo sapiens)
398	LG:199121.19:2001JUN22	g3510507	0	metallic protease-disintegrin (Xenopus laevis)
399	LG:482411.1:2001JUN22	g886050	0	Ich-2 (Homo sapiens)
400	LG:991986.23:2001JUN22	g17390251	1.00E-161	ubiquitin specific protease 3 (Homo sapiens)
401	LG:1500347.6:2001JUN22	g11992277	2.00E-09	NUDE-like protein (Mus musculus)
402	LG:7670971.1:2001JUN22	g9280152	6.00E-21	unnamed protein product (Macaca fascicularis)
403	LG:010761.6:2001MAR30	g12803835	5.00E-21	adenosine deaminase, tRNA-specific 1 (Homo sapiens)
404	LG:104970.6:2001MAR30	g3776076	0	poly(A)-specific ribonuclease (Homo sapiens)
405	LG:1078420.1:2001MAR30	g1263081	1.00E-82	mariner transposase (Homo sapiens)
406	LG:1094182.9:2001MAR30	g14141216	7.00E-86	Srp46 splicing factor (Homo sapiens)
407	LG:1399075.18:2001MAR30	g531243	1.00E-20	DNA helicase Q1 (Homo sapiens)
408	LG:1501344.7:2001MAR30	g14198360	2.00E-28	U1 small nuclear ribonucleoprotein 1C (Mus musculus)
409	LI:1144484.3:2001MAY17	g10437569	1.00E-31	unnamed protein product (Homo sapiens)
410	LI:337388.11:2001MAY17	g355568	2.00E-19	DNA polymerase alpha-subunit (AA 1 - 1462) (Homo sapiens)
411	LI:347709.101:2001MAY17	g31395	6.00E-87	fibrillarin (Homo sapiens)
412	LI:480238.8:2001MAY17	g12654217	4.00E-79	Similar to poly (A) polymerase (Homo sapiens)
413	LI:2121656.1:2001MAY17	g2226004	3.00E-39	ORF1; MER37, putative transposase similar to pogo element (Homo sapiens)
414	LG:1328038.5:2001JUN22	g807817	1.00E-18	RNA helicase (HRH1) (Homo sapiens)
415	LG:437443.21:2001JUN22	g182174	2.00E-83	excision repair protein (Homo sapiens)
416	LG:474165.24:2001JUN22	g3005587	2.00E-95	Ser/Arg-related nuclear matrix protein (Homo sapiens)
417	LG:7689014.1:2001JUN22	g1263081	1.00E-108	mariner transposase (Homo sapiens)
418	LG:984007.4:2001JUN22	g2228750	4.00E-40	RNA polymerase III subunit (Homo sapiens)
419	LG:008606.21:2001JUN22	g56520	6.00E-05	L1 retroposon, a portion of its ORF2 sequence (Rattus norvegicus)

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SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
420	LG:240680.1:2001JUN22	g2226004	4.00E-39	ORF1; MER37; putative transposase similar to pogo element (Homo sapiens)
421	LG:160481.1:2001MAR30	g9280152	4.00E-12	unnamed protein product (Macaca fascicularis)
422	LG:292275.1:2001MAR30	g6688786	1.00E-167	mouse fat 1 cadherin (Mus musculus)
423	LG:407582.21:2001MAR30	g7023112	1.00E-163	unnamed protein product (Homo sapiens)
424	LI:2051428.9:2001MAY17	g13161066	0	protocadherin 11 (Homo sapiens)
425	LI:355644.50:2001MAY17	g4699891	1.00E-154	integrin alpha 7 chain (Homo sapiens)
426	LI:375954.18:2001MAY17	g506407	1.00E-157	Homo sapiens cadherin-13 mRNA, complete cds.
427	LI:480115.132:2001MAY17	g190670	3.00E-06	pulmonary surfactant-associated protein (Homo sapiens)
428	LG:1383554.10:2001JUN22	g9652246	1.00E-05	leukocyte surface protein precursor (Homo sapiens)
429	LG:1135060.33:2001MAR30	g33742	4.00E-61	immunoglobulin lambda light chain (Homo sapiens)
430	LG:1351716.96:2001MAR30	g567121	2.00E-42	immunoglobulin heavy chain (Homo sapiens)
431	LG:1400811.225:2001MAR30	g3170879	5.00E-56	immunoglobulin heavy chain variable region (Homo sapiens)
432	LG:1401132.92:2001MAR30	g185985	1.00E-66	immunoglobulin kappa light chain VC region (Homo sapiens)
433	LG:1401165.155:2001MAR30	g16974102	2.00E-52	anti-peptide/MHC complex HLA-A1/MAGE-A1 monoclonal antibody heavy chain (Homo sapiens)
434	LG:1452363.23:2001MAR30	g6691521	3.00E-17	hMYHalpha1 (Homo sapiens)
435	LG:1503254.1:2001MAR30	g3954893	2.00E-74	Immunoglobulin kappa light chain (Homo sapiens)
436	LG:411364.13:2001MAR30	g11493483	1.00E-14	PRO2550 (Homo sapiens)
437	LG:238631.16:2001MAR30	g12803995	2.00E-40	Similar to HLA class II region expressed gene KE2 (Homo sapiens)
438	LG:235157.34:2001MAR30	g12841350	0	putative (Mus musculus)
439	LI:1027765.6:2001MAY17	g17045933	1.00E-154	unnamed protein product (Homo sapiens)
440	LI:105160.28:2001MAY17	g1399328	3.00E-37	Macaca mulatta MHC class I antigen Mamu A*06 mRNA, complete cds.
441	LI:1073108.49:2001MAY17	g16741061	1.00E-120	Similar to immunoglobulin kappa constant (Homo sapiens)
442	LI:1189828.21:2001MAY17	g6468391	7.00E-12	dJ365O12.1 (KIAA0758 protein) (Homo sapiens)
443	LI:2191073.14:2001MAY17	g15777271	1.00E-25	immunoglobulin alpha heavy chain variable region (Homo sapiens)
444	LI:2191348.6:2001MAY17	g9367869	3.00E-25	immunoglobulin heavy chain variant (Homo sapiens)
445	LI:2191424.12:2001MAY17	g5834016	4.00E-25	immunoglobulin heavy chain variable region precursor (Homo sapiens)
446	LI:2206792.26:2001MAY17	g15149823	6.00E-19	immunoglobulin lambda-3 surrogate light chain (Homo sapiens)
447	LI:255510.1264:2001MAY17	g33742	7.00E-36	immunoglobulin lambda light chain (Homo sapiens)
448	LI:392902.48:2001MAY17	g2980663	0	FSH (Homo sapiens)

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SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
449	LI:411364.14:2001MAY17	g12847527	5.00E-38	putative (Mus musculus)
450	LI:417464.1:2001MAY17	g1196425	2.00E-29	envelope protein (Homo sapiens)
451	LI:439077.1:2001MAY17	g12698182	8.00E-12	hypothetical protein (Macaca fascicularis)
452	LI:1071390.38:2001MAY17	g13185197	9.00E-49	unnamed protein product (Homo sapiens)
453	LI:1225513.19:2001JUN22	g583510	1.00E-126	3D6 antibody light chain (synthetic construct)
454	LG:1447752.2:2001JUN22	g5833974	8.00E-38	immunoglobulin heavy chain variable region precursor (Homo sapiens)
455	LG:239410.21:2001JUN22	g15779199	0	NG22 protein (Homo sapiens)
456	LG:7683955.1:2001JUN22	g441355	1.00E-27	Ig kappa light chain (VJ) (Homo sapiens)
457	LG:7691296.7:2001JUN22	g567128	2.00E-24	immunoglobulin heavy chain (Homo sapiens)
458	LG:7696542.11:2001JUN22	g583510	1.00E-109	3D6 antibody light chain (synthetic construct)
459	LG:7696552.2:2001JUN22	g492350	1.00E-101	Y22 light chain antifibrin antibody (unidentified)
460	LG:7696586.3:2001JUN22	g516489	6.00E-53	Ig light chain V11 region (Homo sapiens)
461	LI:1072102.34:2001MAY17	g30184	1.00E-101	I1beta-hydrolase precursor (Homo sapiens)
462	LI:211925.1:2001MAY17	g11414998	0	NADPH-cytochrome P-450 reductase (Homo sapiens)
463	LI:2173928.1:2001MAY17	g165098	7.00E-20	hepatic flavin-containing monooxygenase (EC 1.14.13.8) (Oryctolagus)
464	LI:2193503.1:2001MAY17	g12858580	1.00E-63	putative (Mus musculus)
465	LI:368098.26:2001MAY17	g13161409	2.00E-96	family 4 cytochrome P450 (Mus musculus)
466	LI:455378.1:2001MAY17	g1809135	1.00E-70	thioredoxin (Homo sapiens)
467	LI:480845.50:2001MAY17	g517252	2.00E-88	cytochrome-c oxidase subunit IV (Homo sapiens)
468	LI:2205863.1:2001MAY17	g15680169	3.00E-83	cytochrome b5 outer mitochondrial membrane precursor (Homo sapiens)
469	LG:201188.2:2001JUN22	g13161409	2.00E-21	family 4 cytochrome P450 (Mus musculus)
470	LG:1272496.28:2001MAR30	g886299	4.00E-58	thrombospondin 3 (Homo sapiens)
471	LG:1500367.1:2001MAR30	g178847	9.00E-52	apolipoprotein D precursor (Homo sapiens)
472	LG:952182.4:2001MAR30	g6647302	2.00E-05	matrilysin (Homo sapiens)
473	LI:197195.10:2001MAY17	g1418929	2.00E-17	H-sapiens mRNA for prepro-alpha2(I) collagen.
474	LI:2031121.1:2001MAY17	g14017771	0	fibrillin3 (Homo sapiens)
475	LI:2198279.3:2001MAY17	g5102836	2.00E-23	bK150C2.5 (PUTATIVE novel protein similar to APOBEC1 (Apolipoprotein B mRNA editing protein) and Phorbol) (Homo sapiens)
476	LI:2201248.1:2001MAY17	g188882	0	unnamed protein product (Homo sapiens)
477	LI:234507.10:2001MAY17	g15524596	1.00E-154	

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
478	LI:237999.48:2001MAY17	g348912	1.00E-135	glycoprotein (Homo sapiens)
479	LI:244935.47:2001MAY17	g2388555	0	alpha2(I) collagen (Homo sapiens)
480	LI:257664.143:2001MAY17	g386744	1.00E-103	guanine nucleotide-binding protein G-s-alpha-2 (Homo sapiens)
481	LI:261900.1:2001MAY17	g11493483	7.00E-31	PRO2550 (Homo sapiens)
482	LI:346724.22:2001MAY17	g508729	0	thymopoietin gamma (Homo sapiens)
483	LI:815333.1:2001MAY17	g762831	0	fibrillin 2 (Mus musculus)
484	LI:889399.7:2001MAY17	g187152	1.00E-105	lysosomal acid lipase/cholesterol esterase (Homo sapiens)
485	LI:1088907.2:2001MAY17	g4680715	7.00E-13	CGI-38 protein (Homo sapiens)
486	LI:218680.7:2001MAY17	g5917666	1.00E-07	extensin-like protein (Zea mays)
487	LG:081189.8:2001JUN22	g14017771	0	fibrillin3 (Homo sapiens)
488	LG:315445.21:2001JUN22	g1911490	5.00E-16	Con1 (Homo sapiens)
489	LG:900035.56:2001JUN22	g1888409	0	collagen type I alpha 1 (Homo sapiens)
490	LG:008513.80:2001MAR30	g13904996	0	Unknown (protein for MGC:8116) (Mus musculus)
491	LG:1384720.130:2001MAR30	g28335	1.00E-146	H.sapiens ACTB mRNA for mutant beta-actin (beta'-actin).
492	LG:145361.1:2001MAR30	g7689897	2.00E-38	myosin light chain-2 (Homo sapiens)
493	LG:1500258.1:2001MAR30	g15076511	1.00E-39	nonmuscle myosin light chain 2 (Homo sapiens)
494	LG:1501754.5:2001MAR30	g338441	0	beta-spectrin (Homo sapiens)
495	LG:1502796.1:2001MAR30	g12861068	6.00E-95	putative (Mus musculus)
496	LG:348973.11:2001MAR30	g3550977	0	beta-spectrin III (Homo sapiens)
497	LG:362757.1:2001MAR30	g1419370	8.00E-74	actin depolymerizing factor (Zea mays)
498	LG:401322.6:2001MAR30	g159725	1.00E-23	alpha tubulin (Octopus dofleini)
499	LG:897867.1:2001MAR30	g14250822	9.00E-22	kinesin 2 (60-70kD) (Homo sapiens)
500	LI:1947939.1:2001MAY17	g6176550	1.00E-104	dyncactin subunit p25 (Mus musculus)
501	LI:245487.16:2001MAY17	g16307401	0	Unknown (protein for MGC:12143) (Mus musculus)
502	LI:257715.58:2001MAY17	g2501855	2.00E-12	22 kDa actin-binding protein (Homo sapiens)
503	LI:333453.9:2001MAY17	g2072425	0	non-lens beta gamma-crystallin like protein (Homo sapiens)
504	LI:412658.11:2001MAY17	g13097756	0	actinin, alpha 1 (Homo sapiens)
505	LI:720054.1:2001MAY17	g13506797	1.00E-117	myosin-VIb (Mus musculus)
506	LI:765245.9:2001MAY17	g1526432	0	neutral calponin (Homo sapiens)
507	LI:814445.58:2001MAY17	g307082	0	keratin type II (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
508	LI:897867.1:2001MAY17	g14250822	6.00E-22	kinesin 2 (60-70kD) (Homo sapiens)
509	LI:311318.6:2001MAY17	g338441	0	beta-spectrin (Homo sapiens)
510	LI:401605.12:2001MAY17	g9910111	0	myosin X (Homo sapiens)
511	LG:1088618.90:2001JUN22	g3157976	0	alpha actinin (Homo sapiens)
512	LG:1446318.6:2001JUN22	g407339	0	Kif1b (Mus musculus)
513	LG:229284.37:2001JUN22	g6683745	1.00E-112	HOITL protein (Homo sapiens)
514	LG:7683471.8:2001JUN22	g1532191	5.00E-11	alpha-1 tubulin (Hirudo medicinalis)
515	LG:7697194.7:2001JUN22	g553858	7.00E-77	alpha-cardiac actin (Mus musculus)
516	LG:952407.1:2001JUN22	g13506797	1.00E-105	myosin-VIb (Mus musculus)
517	LG:248005.17:2001JUN22	g1147783	0	myosin-Xb (Homo sapiens)
518	LG:025007.3:2001MAR30	g487906	8.00E-42	VMO-1 (Gallus gallus)
519	LG:1510893.1:2001MAR30	g1212917	1.00E-141	axonal transporter of synaptic vesicles (Homo sapiens)
520	LG:297070.1:2001MAR30	g9650954	2.00E-83	beta-1,6-N-acetylglucosaminyltransferase B (Mus musculus)
521	LG:363612.2:2001MAR30	g1526556	1.00E-155	syntaxin 1B (Mus musculus)
522	LG:468481.1:2001MAR30	g4151805	2.00E-33	membrane-associated guanylate kinase-interacting protein 1 Maguin-1 (Rattus norvegicus)
523	LG:966475.1:2001MAR30	g14189960	9.00E-11	PRO0764 (Homo sapiens)
524	LG:1135422.1:2001MAR30	g13810306	1.00E-140	transmembrane protein 7 (Homo sapiens)
525	LI:1010121.1:2001MAY17	g777776	5.00E-29	apical endosomal glycoprotein (Rattus norvegicus)
526	LI:1072416.19:2001MAY17	g439295	0	H.sapiens gap gene mRNA, complete CDS.
527	LI:1188564.7:2001MAY17	g396170	9.00E-59	CMRF-35 antigen (Homo sapiens)
528	LI:2118902.5:2001MAY17	g7406853	0	clathrin-associated adaptor medium chain mu 1A (Mus musculus)
529	LI:2206501.1:2001MAY17	g10433120	4.00E-22	unnamed protein product (Homo sapiens)
530	LI:337830.1:2001MAY17	g7708438	1.00E-110	dJ885A10.1 (similar to cerebellin precursor) (Homo sapiens)
531	LI:347853.17:2001MAY17	g7020783	3.00E-90	unnamed protein product (Homo sapiens)
532	LI:253580.4:2001MAY17	g14042242	1.00E-128	unnamed protein product (Homo sapiens)
533	LG:330850.3:2001JUN22	g288448	1.00E-139	bcl2lg fusion gene (Homo sapiens)
534	LG:464722.13:2001JUN22	g12803531	4.00E-69	dolichyl-diphosphooligosaccharide-protein glycosyltransferase (Homo sapiens)
535	LG:7686119.1:2001JUN22	g396170	1.00E-30	CMRF-35 antigen (Homo sapiens)
536	LG:903691.14:2001JUN22	g439296	0	gap (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
537	LG:1096385.3:2001MAR30	g14043204	1.00E-42	ribosomal protein, large, P1 (Homo sapiens)
538	LG:1101445.1:2001MAR30	g206736	1.00E-106	ribosomal protein L7 (Rattus norvegicus)
539	LG:1138457.20:2001MAR30	g36114	6.00E-28	H.sapiens mRNA for ribosomal protein L26.
540	LG:1440118.1:2001MAR30	g338447	2.00E-74	RPS16 (Homo sapiens)
541	LG:1443997.1:2001MAR30	g57698	2.00E-95	ribosomal protein L3 (Rattus rattus)
542	LG:1497707.1:2001MAR30	g12858199	1.00E-70	putative (Mus musculus)
543	LG:1501729.1:2001MAR30	g13960133	2.00E-62	ribosomal protein S20 (Homo sapiens)
544	LG:1502186.1:2001MAR30	g12851192	1.00E-48	putative (Mus musculus)
545	LG:223142.1:2001MAR30	g57682	2.00E-26	ribosomal protein L17 (Rattus rattus)
546	LG:255713.1:2001MAR30	g14198321	3.00E-25	ribosomal protein L31 (Mus musculus)
547	LG:420283.38:2001MAR30	g36647	1.00E-89	ribosomal protein L7a (Homo sapiens)
548	LG:449413.3:2001MAR30	g643074	9.00E-76	putative 40S ribosomal protein s12 (Fragaria x ananassa)
549	LG:997599.1:2001MAR30	g15680000	1.00E-127	Similar to ribosomal protein L10 (Homo sapiens)
550	LG:232776.8:2001MAR30	g4165247	1.00E-107	dJ69E11.3 (Yeast YPR037W and worm C02C2.6 predicted proteins LIKE (Homo sapiens)
551	LI:1045207.1:2001MAY17	g15213784	6.00E-35	ribosomal protein L32 (Spodoptera frugiperda)
552	LI:1086565.6:2001MAY17	g387057	7.00E-05	ribosomal protein S14 (Cricetulus griseus)
553	LI:1142855.1:2001MAY17	g14043204	2.00E-42	ribosomal protein, large, P1 (Homo sapiens)
554	LI:2188689.1:2001MAY17	g550015	7.00E-64	ribosomal protein L21 (Homo sapiens)
555	LI:2193411.1:2001MAY17	g13489168	1.00E-76	60S ribosomal protein L17 (Oryza sativa)
556	LI:2198244.1:2001MAY17	g550025	2.00E-48	ribosomal protein S10 (Homo sapiens)
557	LI:2198795.4:2001MAY17	g14198321	2.00E-33	ribosomal protein L31 (Mus musculus)
558	LI:2199688.3:2001MAY17	g517222	1.00E-28	ribosomal protein S24 (Homo sapiens)
559	LI:790138.64:2001MAY17	g12653502	5.00E-15	Homo sapiens, Similar to ribosomal protein S24, clone MGC:8595 IMAGE:2961125, mRNA, complete cds.
560	LI:757871.10:2001MAY17	g15214837	6.00E-92	Unknown (protein for MGC:13410) (Homo sapiens)
561	LG:1096385.2:2001JUN22	g13097207	4.00E-33	ribosomal protein, large, P1 (Homo sapiens)
562	LG:1100878.1:2001JUN22	g6519820	5.00E-79	ribosomal protein S4X (RPS4X) (Macaca fuscata)
563	LG:1447560.1:2001JUN22	g387057	8.00E-16	ribosomal protein S14 (Cricetulus griseus)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
564	LG:1453540.34:2001JUN22	g7022717	6.00E-61	Homo sapiens cDNA FLJ10589 fis, clone NT2RP2004389, weakly similar to PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.
565	LG:249518.11:2001JUN22	g5815233	5.00E-07	60S acidic ribosomal protein PO (Homo sapiens)
566	LG:041656.5:2001JUN22	g4678751	1.00E-136	hypothetical protein (Homo sapiens)
567	LI:2208837.4:2001MAY17	g4379067	7.00E-47	CU240C2.1 (Core histone H2A/H2B/H3/H4) (Homo sapiens)
568	LG:7694341.2:2001JUN22	g12654707	3.00E-67	H2A histone family, member L (Homo sapiens)
569	LG:016760.1:2001MAR30	g178281	1.00E-31	AHNK nucleoprotein (Homo sapiens)
570	LG:1022858.1:2001MAR30	g4454682	3.00E-23	NADH-ubiquinone oxidoreductase subunit B9 homolog (Homo sapiens)
571	LG:1135406.15:2001MAR30	g189306	1.00E-144	nucleolin (Homo sapiens)
572	LG:1327517.37:2001MAR30	g8101070	0	Homo sapiens golgin-like protein (GLP) gene, complete cds.
573	LG:1330214.34:2001MAR30	g14043791	1.00E-157	Similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (Homo sapiens)
574	LG:1384735.5:2001MAR30	g8099669	8.00E-24	golgin-like protein (Homo sapiens)
575	LG:1449837.4:2001MAR30	g1652625	0	isoleucyl-tRNA synthetase (Synechocystis sp. PCC 6803)
576	LG:1452330.5:2001MAR30	g2827205	0	general transcription factor 2-1 (Homo sapiens)
577	LG:1510248.1:2001MAR30	g313287	2.00E-89	cysteine-rich protein (Gallus gallus)
578	LG:215109.8:2001MAR30	g10803415	1.00E-170	Golgi protein (Homo sapiens)
579	LG:279978.17:2001MAR30	g5070357	0	xenobiotic/medium-chain fatty acid:CoA ligase form XL-III (Bos taurus)
580	LG:414732.1:2001MAR30	g183233	4.00E-57	beta-glucuronidase precursor (EC 3.2.1.31) (Homo sapiens)
581	LG:1132208.1:2001MAR30	g3219503	2.00E-65	putative short-chain type dehydrogenase/reductase (Homo sapiens)
582	LG:1454339.4:2001MAR30	g7022046	6.00E-75	unnamed protein product (Homo sapiens)
583	LI:018342.1:2001MAY17	g214747	5.00E-50	ribonucleoprotein (Xenopus laevis)
584	LI:1177772.36:2001MAY17	g8099669	5.00E-53	golgin-like protein (Homo sapiens)
585	LI:2207152.6:2001MAY17	g178281	6.00E-61	AHNK nucleoprotein (Homo sapiens)
586	LI:244159.24:2001MAY17	g7292499	4.00E-15	CG15021 gene product (Drosophila melanogaster)
587	LI:405244.8:2001MAY17	g4938296	3.00E-81	clj64K7.3.1 (heterogenous nuclear ribonucleoprotein RALY or autoantigen P542, isoform 1) (Homo sapiens)
588	LI:270318.18:2001MAY17	g7578783	1.00E-155	HT015 protein (Homo sapiens)
589	LI:154692.45:2001MAY17	g14424773	1.00E-141	MMS19 (MET18 S. cerevisiae)-like (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
590	LI:411238.31:2001MAY17	g14042547	0	Homo sapiens cDNA FLJ14778 fis, clone NT2RP4000370, moderately similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR.
591	LI:814424.6:2001MAY17	g7021981	1.00E-20	unnamed protein product (Homo sapiens)
592	LG:1327517.25:2001JUN22	g8099669	4.00E-54	golgin-like protein (Homo sapiens)
593	LG:343949.3:2001JUN22	g7453117	1.00E-31	peroxisome assembly factor-2 (Homo sapiens)
594	LG:413000.28:2001JUN22	g190787	0	Human prollyl 4-hydroxylase alpha subunit mRNA, complete cds, clone PA-15.
595	LG:7692006.3:2001JUN22	g1125021	2.00E-11	Human U2AF1-RS2 mRNA, complete cds.
596	LG:336953.5:2001JUN22	g15636917	0	homolog of Human holocarboxylase synthetase gene HLCS (Mus musculus)
597	LG:1399785.1:2001JUN22	g3342234	1.00E-07	nuclear antigen EBNA-1 (Cercopithecine herpesvirus 15)
598	LG:425024.5:2001JUN22	g3851160	4.00E-34	cp431 (Rattus norvegicus)
599	LG:482494.10:2001JUN22	g9652082	4.00E-54	nucleolar protein 5 (Homo sapiens)
600	LG:978629.6:2001JUN22	g13540302	2.00E-61	nucleolar protein C7C (Rattus norvegicus)
601	LG:005776.12:2001MAR30	g8493519	2.00E-06	nuclear localization signal binding protein (Mus musculus)
602	LG:029219.1:2001MAR30	g7020625	1.00E-29	unnamed protein product (Homo sapiens)
603	LG:091743.1:2001MAR30	g1495464	3.00E-23	Metallothionein 1R (Homo sapiens)
604	LG:1397656.6:2001MAR30	g3336972	0	cdJ45P21.1 (butyrophilin, subfamily 3, member A3 (BTF3)) (Homo sapiens)
605	LG:1500866.5:2001MAR30	g951233	2.00E-23	MLN 70, S100 C (Homo sapiens)
606	LG:1511332.1:2001MAR30	g14189960	6.00E-24	PRO0764 (Homo sapiens)
607	LG:233288.31:2001MAR30	g15341763	0	Unknown (protein for MGC:17103) (Homo sapiens)
608	LG:269269.24:2001MAR30	g337756	0	sphingolipid activator precursor (Homo sapiens)
609	LG:331581.5:2001MAR30	g10434110	1.00E-149	unnamed protein product (Homo sapiens)
610	LG:481433.4:2001MAR30	g3091280	0	Importin alpha 7 subunit (Homo sapiens)
611	LG:246935.4:2001MAR30	g12620408	7.00E-80	UPF3X (Homo sapiens)
612	LG:475420.1:2001MAR30	g386835	0	Interstitial retinol-binding protein precursor (Homo sapiens)
613	LI:1073084.60:2001MAY17	g182514	7.00E-55	ferritin light chain (Homo sapiens)
614	LI:2040379.1:2001MAY17	g1163174	1.00E-129	similar to yeast Sec6p, Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author (Rattus norvegicus)
615	LI:2119526.4:2001MAY17	g517351	4.00E-11	metallothionein IX (Homo sapiens)
616	LI:2132228.1:2001MAY17	g7020625	3.00E-23	unnamed protein product (Homo sapiens)



Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
617	U:2179709.1:2001MAY17	g9967319	2.00E-14	hypothetical protein (Macaca fascicularis)
618	U:2208147.1:2001MAY17	g10437569	1.00E-33	unnamed protein product (Homo sapiens)
619	U:235487.10:2001MAY17	g1176422	3.00E-89	rhophilin (Mus musculus)
620	U:476342.4:2001MAY17	g790641	3.00E-25	gamma-thionin (Hordeum vulgare)
621	U:759025.1:2001MAY17	g7020440	2.00E-14	unnamed protein product (Homo sapiens)
622	U:765589.1:2001MAY17	g15215290	1.00E-105	Similar to RIKEN cDNA 2810405111 gene (Homo sapiens)
623	U:902535.3:2001MAY17	g204559	2.00E-79	major alpha-hemoglobin (Rattus norvegicus)
624	U:257592.5:2001MAY17	g3327142	4.00E-52	KIAA0664 protein (Homo sapiens)
625	U:471684.65:2001MAY17	g1071681	5.00E-90	unnamed protein product (Homo sapiens)
626	LG:1382838.272:2001JUN22	g28435	5.00E-93	apoferritin H chain (Homo sapiens)
627	LG:142736.1:2001JUN22	g10437569	7.00E-23	unnamed protein product (Homo sapiens)
628	LG:221707.43:2001JUN22	g12232321	2.00E-17	Homo sapiens hUPF3A mRNA, complete cds.
629	LG:7689247.1:2001JUN22	g7770139	6.00E-22	PRO1722 (Homo sapiens)
630	LG:7693136.5:2001JUN22	g9719420	5.00E-99	SNARE Vti1a protein (Rattus norvegicus)
631	LG:001505.13:2001MAR30	g5926671	4.00E-07	Homo sapiens genomic DNA, chromosome 3p21.3, clone:301 to 308, anti-oncogene region, section 2/5.
632	LG:1051541.1:2001MAR30	g2393894	3.00E-14	gag (Fowlpox virus)
633	LG:1090140.1:2001MAR30	g6572954	2.00E-31	NU-interacting factor isoform T2; NU/Ldb1/CLIM interacting factor (Gallus)
634	LG:1094595.2:2001MAR30	g1731809	6.00E-88	c-myc binding protein (Homo sapiens)
635	LG:1500340.1:2001MAR30	g914925	6.00E-58	DAD-1 (Mesocricetus auratus)
636	LG:1502353.1:2001MAR30	g10436424	2.00E-11	unnamed protein product (Homo sapiens)
637	LG:1511710.6:2001MAR30	g3550080	0	formin binding protein 21 (Homo sapiens)
638	LG:231372.4:2001MAR30	g14250095	1.00E-134	uncharacterized hematopoietic stem/progenitor cells protein MDS032 (Homo sapiens)
639	LG:234855.6:2001MAR30	g16877739	6.00E-80	cell division protein FtsJ (Homo sapiens)
640	LG:242157.8:2001MAR30	g2853265	1.00E-84	Jun dimerization protein 2 (Rattus norvegicus)
641	LG:477127.6:2001MAR30	g15430745	1.00E-37	SEPTIN6 type II (Homo sapiens)
642	LG:412684.17:2001MAR30	g14042913	1.00E-120	unnamed protein product (Homo sapiens)
643	LG:474937.20:2001MAR30	g12005511	2.00E-82	HT027 (Homo sapiens)

Table 2

SEQ ID NO:	Template ID	GI Number	Probability Score	Annotation
644	LG:1452698.8:2001MAR30	g13543880	0	Homo sapiens, hairy/enhancer-of-split related with YRPW motif-like, clone MGC:12623 IMAGE:2964729, mRNA, complete cds.
645	LG:1503673.1:2001MAR30	g13477307	1.00E-126	adipose differentiation-related protein (Homo sapiens)
646	LG:213092.14:2001MAR30	g6539606	0	metastasis suppressor protein (Homo sapiens)
647	LI:015309.1:2001MAY17	g1177607	3.00E-11	pvc1 (Plasmodium vivax)
648	LI:030502.2:2001MAY17	g16553789	6.00E-28	unnamed protein product (Homo sapiens)
649	LI:100501.1:2001MAY17	g7770237	2.00E-20	PRO2822 (Homo sapiens)
650	LI:1011706.2:2001MAY17	g310100	0	developmentally regulated protein (Rattus norvegicus)
651	LI:1171752.20:2001MAY17	g4587965	0	JAW1-related protein MRV1A long isoform (Homo sapiens)
652	LI:2049713.6:2001MAY17	g4689203	4.00E-48	glia maturation factor gamma (Homo sapiens)
653	LI:397393.2:2001MAY17	g3882998	2.00E-17	myotubularin related protein 7 (Homo sapiens)
654	LI:401697.25:2001MAY17	g4101480	1.00E-157	recombination and sister chromatid cohesion protein homolog (Homo sapiens)
655	LI:903668.7:2001MAY17	g4165083	0	growth factor independence-1B (Homo sapiens)
656	LI:903956.35:2001MAY17	g5852976	0	NUMB isoform 4 (Homo sapiens)
657	LI:055784.15:2001MAY17	g1841314	0	neurofibromin (Rattus norvegicus)
658	LI:2195792.2:2001MAY17	g293321	5.00E-87	CDC42Mm (Mus musculus)
659	LI:2207923.8:2001MAY17	g7271471	2.00E-98	Rab-related GTP-binding protein RabJ (Homo sapiens)
660	LI:232953.31:2001MAY17	g5106557	0	MLL septin-like fusion protein (Homo sapiens)
661	LI:764674.1:2001MAY17	g7770153	1.00E-10	PRO1866 (Homo sapiens)
662	LI:893532.747:2001MAY17	g14042419	0	unnamed protein product (Homo sapiens)
663	LG:1121446.8:2001JUN22	g50188	6.00E-94	bfg1 (Mus musculus)
664	LG:1440335.2:2001JUN22	g2570351	4.00E-50	notch homolog (Lytechinus variegatus)
665	LG:370271.9:2001JUN22	g11877205	2.00E-11	dJ77O19.1 (NB thymosin beta) (Homo sapiens)
666	LG:414048.16:2001JUN22	g37332	8.00E-53	H.sapiens mRNA for tre oncogene (clone 213).
667	LG:7683385.1:2001JUN22	g339697	2.00E-18	thymosin beta-10 (Homo sapiens)
668	LG:7697332.3:2001JUN22	g13310191	6.00E-27	recombinant envelope protein (multiple sclerosis associated retrovirus)
669	LG:1047075.1:2001JUN22	g2228759	9.00E-27	Pol (Rauscher murine leukemia virus)
670	LG:331171.2:2001JUN22	g6650377	1.00E-142	pecanex 1 (Mus musculus)

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
1	LG:1040626.1:2001MAR30	210	650	forward 3	gpdh	Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain	1.90E-23
1	LG:1040626.1:2001MAR30	728	1135	forward 2	gpdh_C	Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain	4.90E-09
1	LG:1040626.1:2001MAR30	652	1110	forward 1	gpdh_C	Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain	7.40E-05
2	LG:1041136.7:2001MAR30	252	1160	forward 3	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomerase family	3.40E-58
3	LG:1043848.1:2001MAR30	228	641	forward 3	Peptidase_C12	Ubiquitin carboxyl-terminal hydrolase, family 1	1.30E-23
3	LG:1043848.1:2001MAR30	26	556	forward 2	Peptidase_C12	Ubiquitin carboxyl-terminal hydrolase, family 1	1.10E-20
7	LG:1512094.1:2001MAR30	63	848	forward 3	OMPdecase	Orotidine 5'-phosphate decarboxylase	6.80E-69
7	LG:1512094.1:2001MAR30	46	771	forward 1	OMPdecase	Orotidine 5'-phosphate decarboxylase	6.70E-09
8	LG:230734.53:2001MAR30	151	792	forward 1	aldo_ket_red	Aldo/keto reductase family	1.20E-38
10	LG:245863.31:2001MAR30	480	1217	forward 3	P5CR	Delta 1-pyrroline-5-carboxylate	1.40E-93
14	LG:401748.16:2001MAR30	657	968	forward 3	PTPS	6-pyruvoyl tetrahydropterin synthase	4.50E-50
15	LG:476084.1:2001MAR30	1154	1867	forward 2	GATase	Glutamine amidotransferase class-I	1.30E-67
19	LI:021459.66:2001MAY17	1293	3053	forward 3	tRNA-synt_1e	tRNA synthetases class I (C)	2.20E-185
20	LI:1047290.8:2001MAY17	341	670	forward 2	GST_C	Glutathione S-transferase, C-terminal domain	3.00E-31
20	LI:1047290.8:2001MAY17	104	325	forward 2	GST_N	Glutathione S-transferase, N-terminal domain	1.80E-24
23	LI:1173294.9:2001MAY17	502	696	forward 1	zf-DHHC	DHHC zinc finger domain	2.30E-38
24	LI:148565.7:2001MAY17	35	490	forward 2	gpdh	Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain	1.60E-94
24	LI:148565.7:2001MAY17	493	927	forward 1	gpdh_C	Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain	6.80E-47
25	LI:2052562.23:2001MAY17	228	860	forward 3	aminoIran_3	Aminotransferase class-III	5.80E-05
26	LI:2119354.20:2001MAY17	289	1182	forward 1	G6PD_C	Glucose-6-phosphate dehydrogenase, C-terminal domain	2.10E-10

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
26	U:2119354.20:2001MAY17	1327	2025	forward 1	Glucosamine_iso	Glucosamine-6-phosphate isomerases/6-	3.90E-04
27	U:2209329.1:2001MAY17	42	110	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.20E-04
28	U:240143.12:2001MAY17	290	1381	forward 2	3Beta_HSD	3-beta hydroxysteroid dehydrogenase/isomerase family	5.70E-199
31	U:351818.62:2001MAY17	1194	1508	forward 3	GST_C	Glutathione S-transferase, C-terminal domain	2.90E-29
31	U:351818.62:2001MAY17	77	331	forward 2	GST_N	Glutathione S-transferase, N-terminal domain	4.70E-14
31	U:351818.62:2001MAY17	730	933	forward 1	GST_N	Glutathione S-transferase, N-terminal domain	2.50E-05
31	U:351818.62:2001MAY17	453	656	forward 3	GST_N	Glutathione S-transferase, N-terminal domain	2.50E-05
33	U:474832.7:2001MAY17	182	829	forward 2	PCMT	Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PCMT)	3.80E-10
34	U:814696.11:2001MAY17	326	1600	forward 2	serine_carbpept	Serine carboxypeptidase	8.30E-162
34	U:814696.11:2001MAY17	289	1389	forward 1	serine_carbpept	Serine carboxypeptidase	7.90E-11
35	U:818488.31:2001MAY17	964	1626	forward 1	abhydrolase	alpha/beta hydrolase fold	7.20E-29
36	U:2049834.12:2001MAY17	1593	2492	forward 3	aminoitrans_1_2	Aminotransferase class I and II	2.40E-06
37	U:338956.8:2001MAY17	321	1049	forward 3	trypsin	Trypsin	1.70E-80
44	LG:200050.17:2001JUN22	663	1073	forward 3	Acyl-CoA_hydro	Cytosolic long-chain acyl-CoA thioester hydrolase	1.40E-61
46	LG:7684119.1:2001JUN22	93	632	forward 3	glycolytic_enz	Fructose-bisphosphate aldolase class-I	4.80E-33
50	LG:1400575.1:2001MAR30	149	271	forward 2	KRAB	KRAB box	7.10E-24
50	LG:1400575.1:2001MAR30	437	505	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.40E-07
52	LG:344741.17:2001MAR30	1199	1525	forward 2	TGF-beta	Transforming growth factor beta like domain	3.00E-62
52	LG:344741.17:2001MAR30	371	1069	forward 2	TGFb_propeptide	TGF-beta propeptide	6.00E-55
53	LG:443203.7:2001MAR30	11	79	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.50E-06
55	U:035870.26:2001MAY17	2709	2909	forward 3	Glycos_transf_3N	Glycosyl transferase family, helical bundle domain	4.90E-22
55	U:035870.26:2001MAY17	2934	3479	forward 3	Glycos_transf_3	Glycosyl transferase family, a/b	2.10E-23

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
57	LI:2164765.1:2001MAY17	382	435	forward 1	Somatostatin	Somatostatin/Coristatin family	2.60E-04
59	LI:230062.10:2001MAY17	413	793	forward 2	FGF	Fibroblast growth factor	5.50E-84
65	LG:1324237.7:2001JUN22	210	377	forward 3	IL8	Small cytokines (interctine/chemokine), interleukin-8 like	2.30E-04
67	LG:407723.12:2001JUN22	3	251	forward 3	cystatin	Cystatin domain	5.00E-16
69	LG:1395921.6:2001JUN22	1	1269	forward 1	Granlin	Granlin (chromogranin or	4.20E-102
70	LG:230062.16:2001JUN22	413	793	forward 2	FGF	Fibroblast growth factor	5.50E-84
71	LG:7690036.1:2001JUN22	105	173	forward 3	zf-C2H2	Zinc finger, C2H2 type	9.60E-07
71	LG:7690036.1:2001JUN22	868	936	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.10E-06
71	LG:7690036.1:2001JUN22	1073	1147	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.40E-06
76	LG:1385255.10:2001MAR30	687	1136	forward 3	F5_F8_type_C	F5/8 type C domain	9.50E-69
76	LG:1385255.10:2001MAR30	2277	3137	forward 3	pklnase	Protein kinase domain	1.90E-76
81	LG:349438.18:2001MAR30	1406	1987	forward 2	hormone_rec	Ligand-binding domain of nuclear hormone receptor	1.60E-49
81	LG:349438.18:2001MAR30	356	898	forward 2	Oest_recep.	Oestrogen receptor	3.10E-136
81	LG:349438.18:2001MAR30	902	1129	forward 2	zf-C4	Zinc finger, C4 type (two domains)	3.50E-50
82	LG:358239.46:2001MAR30	116	676	forward 2	hormone_rec	Ligand-binding domain of nuclear hormone receptor	8.10E-67
83	LG:250170.3:2001MAR30	1091	1351	forward 2	fn3	Fibronectin type III domain	8.20E-07
86	LI:101277.1:2001MAY17	229	996	forward 1	7tm_1	7 transmembrane receptor (rhodopsin family)	8.00E-41
88	LI:1072004.14:2001MAY17	210	707	forward 3	UQ_con	Ubiquitin-conjugating enzyme	9.20E-74
92	LI:206576.15:2001MAY17	320	481	forward 2	HLH	Helix-loop-helix DNA-binding domain	1.30E-06
92	LI:206576.15:2001MAY17	539	736	forward 2	PAS	PAS domain	1.50E-11
97	LI:817560.12:2001MAY17	349	594	forward 1	Ig	Immunoglobulin domain	1.60E-05
98	LI:140935.16:2001MAY17	416	1051	forward 2	Neur_chan_LBD	Neurotransmitter-gated ion-channel ligand binding domain	3.80E-75
99	LI:235333.5:2001MAY17	426	680	forward 3	Activin_rec	Activin types I and II receptor domain	4.30E-23
99	LI:235333.5:2001MAY17	975	1844	forward 3	pklnase	Protein kinase domain	6.10E-61
109	LG:481295.21:2001JUN22	486	1613	forward 3	GCR	Glucocorticoid receptor	0.00E+00
109	LG:481295.21:2001JUN22	2115	2672	forward 3	hormone_rec	Ligand-binding domain of nuclear hormone receptor	4.10E-44

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
109	LG:481295.21:2001JUN22	1665	1895	forward 3	zf-C4	Zinc finger, C4 type (two domains)	2.20E-43
113	LG:126510.8:2001JUN22	648	800	forward 3	GPS	Latrophilin/CL-1-like GPS domain	4.20E-07
114	LG:7692710.8:2001JUN22	1331	2077	forward 2	7tm_1	7 transmembrane receptor (rhodopsin family)	5.30E-35
120	LG:1270681.12:2001MAR30	812	1111	forward 2	CDI	Cyclin-dependent kinase inhibitor	3.70E-54
121	LG:1328242.1:2001MAR30	2301	3188	forward 3	HECT	HECT-domain (ubiquitin-transferase)	7.70E-34
121	LG:1328242.1:2001MAR30	735	884	forward 3	RCC1	Regulator of chromosome condensation (RCC1)	1.80E-08
124	LG:1397751.10:2001MAR30	829	939	forward 1	WD40	WD domain, G-beta repeat	2.00E-08
126	LG:1503615.8:2001MAR30	952	1101	forward 1	DAG_PE-bind	Phorbol esters/diacylglycerol binding domain (C1 domain)	1.50E-24
126	LG:1503615.8:2001MAR30	1180	1647	forward 1	RhoGAP	RhoGAP domain	1.60E-78
126	LG:1503615.8:2001MAR30	481	696	forward 1	SH2	SH2 domain	2.70E-14
127	LG:1507027.3:2001MAR30	1371	1625	forward 3	EF1BD	EF-1 guanine nucleotide exchange domain	2.70E-40
128	LG:202892.1:2001MAR30	355	852	forward 1	arf	ADP-ribosylation factor family	1.00E-73
129	LG:220407.3:2001MAR30	2	967	forward 2	pkkinase	Protein kinase domain	6.60E-53
130	LG:242234.11:2001MAR30	40	816	forward 1	pkkinase	Protein kinase domain	5.30E-93
132	LG:320165.7:2001MAR30	181	984	forward 1	pkkinase	Protein kinase domain	3.50E-57
134	LG:402431.16:2001MAR30	663	1112	forward 3	Y_phosphatase	Protein-tyrosine phosphatase	3.00E-07
135	LG:404400.4:2001MAR30	9	1112	forward 3	Amino_oxidase	Flavin containing amine	1.00E-41
136	LG:406860.73:2001MAR30	298	477	forward 1	lg	Immunoglobulin domain	1.70E-06
137	LG:413797.14:2001MAR30	450	1337	forward 3	pkkinase	Protein kinase domain	6.30E-74
138	LG:420527.51:2001MAR30	1669	2457	forward 1	pkkinase	Protein kinase domain	2.20E-54
139	LG:277227.1:2001MAR30	1977	2729	forward 3	RasGEF	RasGEF domain	2.30E-16
139	LG:277227.1:2001MAR30	1286	1459	forward 2	RasGEFN	Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	8.60E-06
140	LG:373260.30:2001MAR30	560	1141	forward 2	ras	Ras family	2.10E-26
141	LG:418805.7:2001MAR30	1535	2269	forward 2	PDEase	3',5'-cyclic nucleotide	1.50E-158
147	LI:1084954.7:2001MAY17	59	586	forward 2	arf	ADP-ribosylation factor family	1.00E-03
147	LI:1084954.7:2001MAY17	98	691	forward 2	ras	Ras family	1.20E-93
148	LI:202892.5:2001MAY17	222	755	forward 3	arf	ADP-ribosylation factor family	1.10E-89

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
151	LI:2118426.12:2001MAY17	543	1340	forward 3	pkkinase	Protein kinase domain	3.40E-84
154	LI:2155821.1:2001MAY17	203	349	forward 2	G-gamma	GGL domain	1.50E-17
155	LI:2201523.6:2001MAY17	556	1173	forward 1	ras	Ras family	6.50E-107
156	LI:235867.27:2001MAY17	142	927	forward 1	pkkinase	Protein kinase domain	2.60E-50
159	LI:245181.22:2001MAY17	64	849	forward 1	pkkinase	Protein kinase domain	7.30E-76
160	LI:245474.13:2001MAY17	-554	763	forward 2	pkkinase_C	Protein kinase C terminal domain	5.10E-09
162	LI:320165.21:2001MAY17	96	737	forward 3	pkkinase	Protein kinase domain	4.10E-28
163	LI:337026.1:2001MAY17	795	1121	forward 3	ras	Ras family	7.80E-05
164	LI:347977.10:2001MAY17	669	1088	forward 3	DSPC	Dual specificity phosphatase, catalytic domain	1.80E-18
165	LI:413040.39:2001MAY17	353	439	forward 2	efhand	EF hand	1.80E-08
167	LI:474596.53:2001MAY17	2135	2284	forward 2	KA1	Kinase associated domain 1	4.00E-21
167	LI:474596.53:2001MAY17	201	1274	forward 3	pkkinase	Protein kinase domain	9.30E-39
167	LI:474596.53:2001MAY17	253	900	forward 1	pkkinase	Protein kinase domain	6.80E-05
167	LI:474596.53:2001MAY17	958	1077	forward 1	UBA	UBA/TS-N domain	8.20E-05
168	LI:481144.22:2001MAY17	209	961	forward 2	pkkinase	Protein kinase domain	1.90E-71
169	LI:725220.1:2001MAY17	631	846	forward 1	SH2	SH2 domain	3.30E-28
169	LI:725220.1:2001MAY17	926	1105	forward 2	SH2	SH2 domain	3.50E-04
171	LI:815194.23:2001MAY17	377	463	forward 2	efhand	EF hand	3.20E-09
172	LI:817950.6:2001MAY17	250	360	forward 1	WD40	WD domain, G-beta repeat	1.90E-06
173	LI:903485.6:2001MAY17	14	157	forward 2	Kelch	Kelch motif	1.70E-06
173	LI:903485.6:2001MAY17	2940	3773	forward 3	pkkinase	Protein kinase domain	3.20E-82
173	LI:903485.6:2001MAY17	1596	1838	forward 3	SH2	SH2 domain	9.50E-04
175	LI:413606.59:2001MAY17	941	1390	forward 2	arf	ADP-ribosylation factor family	6.00E-04
175	LI:413606.59:2001MAY17	662	1531	forward 2	G-alpha	G-protein alpha subunit	6.30E-149
187	LG:149419.8:2001JUN22	2022	2291	forward 3	bromodomain	Bromodomain	2.30E-42
187	LG:149419.8:2001JUN22	2993	3202	forward 2	bromodomain	Bromodomain	1.00E-04
188	LG:199172.17:2001JUN22	802	1434	forward 1	RasGEF	RasGEF domain	1.20E-64
189	LG:256101.6:2001JUN22	230	814	forward 2	ras	Ras family	4.20E-66
196	LG:100653.5:2001MAR30	308	481	forward 2	HLH	Helix-loop-helix DNA-binding domain	3.10E-14
198	LG:117947.1:2001MAR30	522	716	forward 3	bZIP	bZIP transcription factor	6.80E-20
199	LG:1327967.11:2001MAR30	1558	1752	forward 1	bZIP	bZIP transcription factor	3.60E-11

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
202	LG:232313.46:2001MAR30	1312	1503	forward 1	dsm	Double-stranded RNA binding motif	9.50E-22
203	LG:349746.22:2001MAR30	418	594	forward 1	SRF-1F	SRF-type transcription factor (DNA-binding and dimerisation domain)	1.40E-37
205	LG:385569.1:2001MAR30	106	225	forward 1	KRAB	KRAB box	2.40E-19
206	LG:440659.1:2001MAR30	207	401	forward 3	UCR_hinge	Ubiquinol-cytochrome C reductase hinge protein	1.70E-45
207	LG:1081135.1:2001MAR30	206	472	forward 2	bromodomain	Bromodomain	2.30E-24
214	LI:365343.34:2001MAY17	982	1239	forward 1	Ets	Ets-domain	6.00E-35
214	LI:365343.34:2001MAY17	310	564	forward 1	SAM_PNT	Sterile alpha motif (SAM)/Pointed domain	1.00E-33
216	LI:1086645.2:2001MAY17	1	120	forward 1	chromo	'chromo' (CHR)romatin Organization Modifier) domain	6.20E-16
217	LG:1015174.1:2001JUN22	6485	6706	forward 2	helicase_C	Helicase conserved C-terminal domain	6.60E-25
217	LG:1015174.1:2001JUN22	2285	3145	forward 2	SNF2_N	SNF2 and others N-terminal domain	1.00E-110
218	LG:1135945.19:2001JUN22	673	822	forward 1	FF	FF domain	6.40E-12
218	LG:1135945.19:2001JUN22	498	644	forward 3	FF	FF domain	3.00E-11
223	LG:7691137.1:2001JUN22	311	628	forward 2	TFIID-31	Transcription initiation factor IID, 31kD subunit	5.20E-41
223	LG:7691137.1:2001JUN22	348	665	forward 3	TFIID-31	Transcription initiation factor IID, 31kD subunit	8.10E-06
225	LG:1088040.17:2001JUN22	4121	4387	forward 2	bromodomain	Bromodomain	2.30E-24
225	LG:1088040.17:2001JUN22	3650	3796	forward 2	PHD	PHD-finger	3.30E-19
226	LG:1096582.2:2001JUN22	2938	3084	forward 1	PHD	PHD-finger	1.60E-14
231	LG:1052984.26:2001MAR30	531	599	forward 3	zf-C2H2	Zinc finger, C2H2 type	3.20E-07
232	LG:1064250.5:2001MAR30	198	320	forward 3	KRAB	KRAB box	8.10E-28
232	LG:1064250.5:2001MAR30	1401	1469	forward 3	zf-C2H2	Zinc finger, C2H2 type	5.80E-07
234	LG:1076162.1:2001MAR30	379	450	forward 1	zf-C2H2	Zinc finger, C2H2 type	9.90E-07
235	LG:1079476.6:2001MAR30	765	833	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.10E-07
235	LG:1079476.6:2001MAR30	11	79	forward 2	zf-C2H2	Zinc finger, C2H2 type	6.00E-06
236	LG:1080579.9:2001MAR30	170	292	forward 2	KRAB	KRAB box	1.50E-25
237	LG:1082253.1:2001MAR30	74	142	forward 2	zf-C2H2	Zinc finger, C2H2 type	5.20E-07
238	LG:1082263.10:2001MAR30	75	143	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.70E-07



TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
239	LG:1092343.1:2001MAR30	446	514	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.00E-08
240	LG:1094967.1:2001MAR30	934	1056	forward 1	KRAB	KRAB box	1.50E-26
240	LG:1094967.1:2001MAR30	1786	1854	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.40E-07
241	LG:1384132.9:2001MAR30	712	780	forward 1	zf-C2H2	Zinc finger, C2H2 type	8.80E-08
241	LG:1384132.9:2001MAR30	135	203	forward 3	zf-C2H2	Zinc finger, C2H2 type	8.80E-08
243	LG:1400447.1:2001MAR30	343	465	forward 1	KRAB	KRAB box	3.80E-28
243	LG:1400447.1:2001MAR30	812	880	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.40E-07
243	LG:1400447.1:2001MAR30	948	1016	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.50E-04
245	LG:1500873.3:2001MAR30	1114	1236	forward 1	KRAB	KRAB box	5.30E-24
245	LG:1500873.3:2001MAR30	2522	2590	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.10E-07
245	LG:1500873.3:2001MAR30	3780	3845	forward 3	zf-C2H2	Zinc finger, C2H2 type	5.50E-04
246	LG:1505341.1:2001MAR30	479	547	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.20E-05
249	LG:234936.67:2001MAR30	1028	1102	forward 2	zf-C2H2	Zinc finger, C2H2 type	6.60E-06
249	LG:234936.67:2001MAR30	628	696	forward 1	zf-C2H2	Zinc finger, C2H2 type	7.40E-05
250	LG:243305.3:2001MAR30	207	275	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.50E-04
251	LG:334645.20:2001MAR30	455	577	forward 2	KRAB	KRAB box	3.00E-24
252	LG:349468.13:2001MAR30	172	318	forward 1	PHD	PHD-finger	2.50E-15
253	LG:385145.1:2001MAR30	272	394	forward 2	KRAB	KRAB box	1.00E-25
253	LG:385145.1:2001MAR30	977	1045	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.60E-06
255	LG:399287.10:2001MAR30	740	814	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.60E-07
256	LG:404157.1:2001MAR30	879	947	forward 3	zf-C2H2	Zinc finger, C2H2 type	6.50E-08
257	LG:979390.2:2001MAR30	85	207	forward 1	KRAB	KRAB box	3.00E-23
258	LG:981962.1:2001MAR30	12	80	forward 3	zf-C2H2	Zinc finger, C2H2 type	5.40E-07
259	LG:982976.2:2001MAR30	750	818	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.00E-08
260	LG:1448087.1:2001MAR30	39	161	forward 3	KRAB	KRAB box	1.60E-27
261	LG:1449021.1:2001MAR30	180	302	forward 3	KRAB	KRAB box	5.90E-22
261	LG:1449021.1:2001MAR30	543	611	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.00E-06
262	LG:144920.1:2001MAR30	550	618	forward 1	zf-C2H2	Zinc finger, C2H2 type	8.90E-08
263	LG:474725.1:2001MAR30	64	186	forward 1	KRAB	KRAB box	1.40E-21
263	LG:474725.1:2001MAR30	952	1020	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.70E-07
267	Li:1072014.6:2001MAY17	243	560	forward 3	BTB	BTB/POZ domain	4.80E-28
268	Li:1165280.4:2001MAY17	236	358	forward 2	KRAB	KRAB box	7.40E-24

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
268	U:1165280.4:2001MAY17	1064	1132	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.00E-07
269	U:1167958.4:2001MAY17	272	394	forward 2	KRAB	KRAB box	1.00E-25
269	U:1167958.4:2001MAY17	977	1045	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.60E-06
270	U:1168073.15:2001MAY17	727	849	forward 1	KRAB	KRAB box	2.70E-23
271	U:1170154.12:2001MAY17	97	165	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.30E-06
271	U:1170154.12:2001MAY17	246	314	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.10E-05
272	U:1173769.2:2001MAY17	150	272	forward 3	KRAB	KRAB box	9.20E-09
272	U:1173769.2:2001MAY17	1362	1430	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.00E-07
273	U:1174292.18:2001MAY17	115	237	forward 1	KRAB	KRAB box	1.10E-25
273	U:1174292.18:2001MAY17	1478	1546	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.00E-06
274	U:1177989.1:2001MAY17	109	231	forward 1	KRAB	KRAB box	3.10E-19
274	U:1177989.1:2001MAY17	1372	1440	forward 1	zf-C2H2	Zinc finger, C2H2 type	5.70E-08
275	U:1179173.3:2001MAY17	221	343	forward 2	KRAB	KRAB box	9.10E-25
275	U:1179173.3:2001MAY17	1229	1297	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.20E-06
276	U:1180137.1:2001MAY17	286	354	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.90E-06
277	U:1181458.2:2001MAY17	64	132	forward 1	zf-C2H2	Zinc finger, C2H2 type	3.50E-07
277	U:1181458.2:2001MAY17	924	992	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.30E-06
277	U:1181458.2:2001MAY17	1079	1147	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.90E-04
278	U:1182817.8:2001MAY17	205	327	forward 1	KRAB	KRAB box	8.10E-28
278	U:1182817.8:2001MAY17	1408	1476	forward 1	zf-C2H2	Zinc finger, C2H2 type	5.80E-07
279	U:1182838.4:2001MAY17	765	833	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.10E-07
279	U:1182838.4:2001MAY17	11	79	forward 2	zf-C2H2	Zinc finger, C2H2 type	6.00E-06
280	U:2053637.1:2001MAY17	363	431	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.70E-07
280	U:2053637.1:2001MAY17	139	207	forward 1	zf-C2H2	Zinc finger, C2H2 type	4.80E-04
282	U:2121833.1:2001MAY17	557	625	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.20E-05
283	U:2121863.1:2001MAY17	230	298	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.00E-08
283	U:2121863.1:2001MAY17	78	146	forward 3	zf-C2H2	Zinc finger, C2H2 type	9.90E-06
284	U:2121899.1:2001MAY17	273	341	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.40E-06
285	U:2122035.5:2001MAY17	125	247	forward 2	KRAB	KRAB box	7.90E-25
286	U:2122507.3:2001MAY17	128	250	forward 2	KRAB	KRAB box	3.80E-28
287	U:2190152.1:2001MAY17	122	244	forward 2	KRAB	KRAB box	4.20E-25
288	U:2195736.1:2001MAY17	183	251	forward 3	zf-C2H2	Zinc finger, C2H2 type	3.60E-06

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
288	LI:2195736.1:2001MAY17	586	654	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.20E-05
289	LI:2195745.2:2001MAY17	247	369	forward 1	KRAB	KRAB box	2.00E-22
290	LI:2196327.1:2001MAY17	958	1026	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.20E-08
291	LI:2197842.1:2001MAY17	129	251	forward 3	KRAB	KRAB box	2.30E-24
291	LI:2197842.1:2001MAY17	1065	1133	forward 3	zf-C2H2	Zinc finger, C2H2 type	6.90E-08
293	LI:2206159.1:2001MAY17	531	599	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.70E-07
294	LI:2208960.3:2001MAY17	1114	1236	forward 1	KRAB	KRAB box	5.30E-24
294	LI:2208960.3:2001MAY17	2522	2590	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.10E-07
296	LI:223050.2:2001MAY17	369	491	forward 3	KRAB	KRAB box	3.10E-16
296	LI:223050.2:2001MAY17	13	258	forward 1	SCAN	SCAN domain	1.60E-13
297	LI:393468.1:2001MAY17	1045	1113	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.70E-05
297	LI:393468.1:2001MAY17	557	625	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.30E-04
298	LI:480324.48:2001MAY17	202	552	forward 1	ArfGap	Putative GTP-ase activating protein for Arf	9.80E-47
299	LI:722634.7:2001MAY17	426	548	forward 3	KRAB	KRAB box	4.50E-27
300	LI:796992.1:2001MAY17	879	947	forward 3	zf-C2H2	Zinc finger, C2H2 type	6.50E-08
301	LI:093337.1:2001MAY17	379	501	forward 1	KRAB	KRAB box	2.10E-25
302	LI:1081130.3:2001MAY17	512	634	forward 2	KRAB	KRAB box	4.90E-23
303	LI:1170908.4:2001MAY17	1283	1351	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.10E-07
303	LI:1170908.4:2001MAY17	1834	1902	forward 1	zf-C2H2	Zinc finger, C2H2 type	8.30E-04
304	LI:1177451.1:2001MAY17	1070	1138	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.90E-07
305	LI:1180303.18:2001MAY17	925	993	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.60E-07
305	LI:1180303.18:2001MAY17	1400	1468	forward 2	zf-C2H2	Zinc finger, C2H2 type	9.10E-05
306	LI:1182999.3:2001MAY17	469	591	forward 1	KRAB	KRAB box	1.40E-22
306	LI:1182999.3:2001MAY17	1387	1455	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.50E-05
307	LI:1183525.1:2001MAY17	941	1009	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.90E-06
308	LI:2121675.1:2001MAY17	17	85	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.70E-06
308	LI:2121675.1:2001MAY17	99	167	forward 3	zf-C2H2	Zinc finger, C2H2 type	9.20E-04
309	LI:2121766.11:2001MAY17	956	1024	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.40E-06
310	LI:2188633.1:2001MAY17	409	477	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.00E-05
310	LI:2188633.1:2001MAY17	104	172	forward 2	zf-C2H2	Zinc finger, C2H2 type	9.90E-04
311	LI:2188820.2:2001MAY17	452	520	forward 2	zf-C2H2	Zinc finger, C2H2 type	5.20E-07

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
312	LI:2191871.1:2001MAY17	313	381	forward 1	zf-C2H2	Zinc finger, C2H2 type	4.00E-06
313	LI:2196157.2:2001MAY17	228	350	forward 3	KRAB	KRAB box	4.30E-22
314	LI:230109.4:2001MAY17	1303	1371	forward 1	zf-C2H2	Zinc finger, C2H2 type	4.50E-08
315	LI:790409.4:2001MAY17	485	553	forward 2	zf-C2H2	Zinc finger, C2H2 type	4.70E-08
317	LG:1079456.3:2001JUN22	238	360	forward 1	KRAB	KRAB box	1.00E-28
317	LG:1079456.3:2001JUN22	120	242	forward 3	KRAB	KRAB box	4.00E-24
318	LG:1080406.7:2001JUN22	236	304	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.50E-06
319	LG:1505015.1:2001JUN22	505	573	forward 1	zf-C2H2	Zinc finger, C2H2 type	8.00E-07
320	LG:208637.1:2001JUN22	143	457	forward 2	BTB	BTB/POZ domain	1.20E-05
321	LG:233311.5:2001JUN22	558	680	forward 3	KRAB	KRAB box	2.40E-25
322	LG:385145.1:2001JUN22	272	394	forward 2	KRAB	KRAB box	1.00E-25
322	LG:385145.1:2001JUN22	977	1045	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.60E-06
322	LG:385145.1:2001JUN22	2022	2090	forward 3	zf-C2H2	Zinc finger, C2H2 type	4.80E-06
323	LG:404157.1:2001JUN22	879	947	forward 3	zf-C2H2	Zinc finger, C2H2 type	6.50E-08
324	LG:7684505.1:2001JUN22	401	469	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.20E-05
325	LG:7687730.1:2001JUN22	934	1056	forward 1	KRAB	KRAB box	1.50E-26
325	LG:7687730.1:2001JUN22	1786	1854	forward 1	zf-C2H2	Zinc finger, C2H2 type	2.40E-07
326	LG:7687809.2:2001JUN22	1029	1097	forward 3	zf-C2H2	Zinc finger, C2H2 type	2.20E-08
327	LG:7690098.1:2001JUN22	430	498	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.00E-07
327	LG:7690098.1:2001JUN22	1233	1301	forward 3	zf-C2H2	Zinc finger, C2H2 type	4.90E-05
328	LG:7690113.1:2001JUN22	2021	2089	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.00E-07
328	LG:7690113.1:2001JUN22	913	981	forward 1	zf-C2H2	Zinc finger, C2H2 type	3.50E-07
329	LG:7690362.3:2001JUN22	41	109	forward 2	zf-C2H2	Zinc finger, C2H2 type	5.30E-06
330	LG:7691200.3:2001JUN22	743	811	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.00E-07
330	LG:7691200.3:2001JUN22	1161	1229	forward 3	zf-C2H2	Zinc finger, C2H2 type	1.40E-04
331	LG:7691277.3:2001JUN22	173	241	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.20E-06
332	LG:7691280.4:2001JUN22	146	268	forward 2	KRAB	KRAB box	7.90E-25
333	LG:7691562.2:2001JUN22	487	555	forward 1	zf-C2H2	Zinc finger, C2H2 type	1.80E-07
335	LG:7693155.4:2001JUN22	413	487	forward 2	zf-C2H2	Zinc finger, C2H2 type	3.80E-06
336	LG:981962.1:2001JUN22	12	80	forward 3	zf-C2H2	Zinc finger, C2H2 type	5.40E-07
337	LG:1449021.1:2001JUN22	260	382	forward 2	KRAB	KRAB box	5.90E-22
337	LG:1449021.1:2001JUN22	623	691	forward 2	zf-C2H2	Zinc finger, C2H2 type	2.00E-06

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
338	LG:481631.22:2001JUN22	389	511	forward 2	KRAB	KRAB box	3.80E-28
338	LG:481631.22:2001JUN22	183	305	forward 3	KRAB	KRAB box	4.00E-24
338	LG:481631.22:2001JUN22	1224	1292	forward 3	zf-C2H2	Zinc finger, C2H2 type	4.80E-07
339	LG:7690406.2:2001JUN22	377	445	forward 2	zf-C2H2	Zinc finger, C2H2 type	1.50E-06
340	LG:7690773.2:2001JUN22	263	331	forward 2	zf-C2H2	Zinc finger, C2H2 type	4.50E-05
343	LG:023518.3:2001MAR30	190	1191	forward 1	vATP-synt_AC39	ATP synthase (C/AC39) subunit	2.50E-128
345	LG:235076.6:2001MAR30	228	350	forward 3	chromo	'chromo' (CHR)romatin Organization	1.20E-17
347	LG:334752.12:2001MAR30	124	1431	forward 1	xan_ur_permease	MOfifier) domain	8.10E-88
348	LG:425641.11:2001MAR30	439	1719	forward 1	aa_permeases	Permease family	4.70E-06
351	LI:1072888.10:2001MAY17	1	1047	forward 1	sugar_tr	Amino acid permease	3.00E-04
352	LI:2048255.1:2001MAY17	145	1938	forward 1	SNF	Sugar (and other) transporter	1.10E-204
354	LI:410188.4:2001MAY17	616	1386	forward 1	ion_trans	Sodium:neurotransmitter symporter family	5.60E-33
354	LI:410188.4:2001MAY17	3761	4456	forward 2	ion_trans	Ion transport protein	5.30E-25
359	LG:1398822.1:2001JUN22	91	741	forward 1	MIP	Major intrinsic protein	2.40E-118
366	LG:226475.15:2001JUN22	60	314	forward 3	PDZ	PDZ domain (Also known as DHR or GLGF)	6.90E-23
366	LG:226475.15:2001JUN22	812	1228	forward 2	PDZ	PDZ domain (Also known as DHR or GLGF)	1.80E-04
369	LG:1087811.6:2001MAR30	193	567	forward 1	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-trans isomerase	1.90E-07
369	LG:1087811.6:2001MAR30	141	683	forward 3	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-trans isomerase	3.80E-07
370	LG:208877.7:2001MAR30	595	918	forward 1	NTR	NTR/C345C module	1.60E-04
372	LG:331078.21:2001MAR30	1239	1952	forward 3	trypsin	Trypsin	4.80E-83
373	LG:334345.5:2001MAR30	2	397	forward 2	trypsin	Trypsin	2.70E-06
374	LG:345279.19:2001MAR30	924	1394	forward 3	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-trans isomerase	4.40E-55
376	LG:001294.11:2001MAR30	2962	3105	forward 1	GRIP	trans isomerase	4.00E-21
376	LG:001294.11:2001MAR30	991	1356	forward 1	Ran_BPI	GRIP domain	1.00E-81
377	LG:230895.5:2001MAR30	73	627	forward 1	Glycos_transf_2	RanBPI domain. Glycosyl transferase	5.60E-37

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
377	LG:230895.5:2001MAR30	1012	1137	forward 1	Ricin_B_lectin	GXW lectin repeat	5.60E-10
379	LI:1072276.1:2001MAY17	172	681	forward 1	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-trans isomerase	2.70E-103
380	LI:1072654.40:2001MAY17	493	762	forward 1	Calpain_III	Calpain large subunit, domain III	2.50E-08
380	LI:1072654.40:2001MAY17	4	462	forward 1	Peptidase_C2	Calpain family cysteine protease	1.30E-21
381	LI:123815.12:2001MAY17	302	1078	forward 2	Peptidase_C2	Calpain family cysteine protease	1.30E-70
382	LI:198705.6:2001MAY17	308	787	forward 2	Calpain_III	Calpain large subunit, domain III	5.50E-75
386	LI:207915.45:2001MAY17	17	541	forward 2	Reprolysin	Reprolysin (M12B) family zinc metalloprotease	6.80E-13
383	LI:237520.26:2001MAY17	135	611	forward 3	Peptidase_S26	Signal peptidase 1	3.50E-62
389	LI:243892.46:2001MAY17	857	1504	forward 2	trypsin	Trypsin	4.70E-101
390	LI:400590.4:2001MAY17	238	702	forward 1	MATH	MATH domain	9.30E-23
392	LI:2052211.9:2001MAY17	657	815	forward 3	tsp_1	Thrombospondin type 1 domain	5.60E-04
393	LI:407291.5:2001MAY17	135	1292	forward 3	serpin	Serpin (serine protease inhibitor)	3.20E-98
396	LG:1093982.21:2001JUN22	42	485	forward 3	pro_isomerase	Cyclophilin type peptidyl-prolyl cis-trans isomerase	2.00E-07
397	LG:1383133.102:2001JUN22	150	734	forward 3	trypsin	Trypsin	1.50E-23
398	LG:199121.19:2001JUN22	1282	1512	forward 1	disintegrin	Disintegrin	2.70E-21
398	LG:199121.19:2001JUN22	318	668	forward 3	Pep_M12B_propep	Reprolysin family propeptide	8.00E-57
398	LG:199121.19:2001JUN22	714	1298	forward 3	Reprolysin	Reprolysin (M12B) family zinc metalloprotease	4.50E-107
399	LG:482411.11:2001JUN22	51	320	forward 3	CARD	Caspase recruitment domain	2.10E-30
399	LG:482411.11:2001JUN22	972	1229	forward 3	ICE_p10	ICE-like protease (caspase) p10	6.20E-51
399	LG:482411.11:2001JUN22	504	899	forward 3	ICE_p20	ICE-like protease (caspase) p20	5.30E-85
400	LG:991986.23:2001JUN22	323	418	forward 2	UCH-1	Ubiquitin carboxyl-terminal hydrolases family 2	4.60E-12
404	LG:104970.6:2001MAR30	696	857	forward 3	R3H	R3H domain	8.70E-09
405	LG:1078420.1:2001MAR30	588	827	forward 3	Transposase_1	Transposase	1.40E-20
411	LI:347709.101:2001MAY17	326	991	forward 2	Fibrillarin	Fibrillarin	1.70E-105
411	LI:347709.101:2001MAY17	310	888	forward 1	Fibrillarin	Fibrillarin	7.60E-10
412	LI:480238.8:2001MAY17	368	658	forward 2	NTP_transf_2	Nucleotidyltransferase domain	5.30E-12
417	LG:7689014.1:2001JUN22	478	723	forward 1	Transposase_1	Transposase	1.10E-18

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TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
422	LG:292275.1:2001MAR30	1138	1416	forward 1	cadherin	Cadherin domain	3.10E-22
423	LG:407582.21:2001MAR30	12	281	forward 3	fn3	Fibronectin type III domain	8.00E-21
424	LI:2051428.9:2001MAY17	2160	2429	forward 3	cadherin	Cadherin domain	1.00E-23
429	LG:1135060.33:2001MAR30	129	353	forward 3	lg	Immunoglobulin domain	9.90E-09
431	LG:1400811.225:2001MAR30	138	389	forward 3	lg	Immunoglobulin domain	2.20E-08
432	LG:1401132.92:2001MAR30	121	345	forward 1	lg	Immunoglobulin domain	9.20E-11
435	LG:1503254.1:2001MAR30	142	366	forward 1	lg	Immunoglobulin domain	1.40E-11
437	LG:238631.16:2001MAR30	100	453	forward 1	KE2	KE2 family protein	3.80E-38
441	LI:1073108.49:2001MAY17	121	345	forward 1	lg	Immunoglobulin domain	4.40E-10
448	LI:392902.48:2001MAY17	950	1219	forward 2	bromodomain	Bromodomain	2.30E-42
448	LI:392902.48:2001MAY17	163	420	forward 1	bromodomain	Bromodomain	1.10E-37
453	LG:1225513.19:2001JUN22	126	350	forward 3	lg	Immunoglobulin domain	4.20E-09
458	LG:7696542.11:2001JUN22	116	340	forward 2	lg	Immunoglobulin domain	1.10E-08
459	LG:7696552.2:2001JUN22	149	373	forward 2	lg	Immunoglobulin domain	6.80E-08
460	LG:7696586.3:2001JUN22	136	366	forward 1	lg	Immunoglobulin domain	4.00E-08
461	LI:1072102.34:2001MAY17	2	1114	forward 2	p450	Cytochrome P450	7.10E-10
462	LI:2119925.1:2001MAY17	1316	1975	forward 2	FAD_binding	FAD binding domain	1.80E-122
462	LI:2119925.1:2001MAY17	731	1177	forward 2	flavodoxin	Flavodoxin	6.40E-56
462	LI:2119925.1:2001MAY17	2069	2311	forward 2	NAD_binding	Oxidoreductase NAD-binding domain	7.50E-07
464	LI:2193503.1:2001MAY17	139	387	forward 1	COX5A	Cytochrome c oxidase subunit Va	2.20E-13
466	LI:455378.1:2001MAY17	163	477	forward 1	thioredoxin	Thioredoxin	5.00E-18
467	LI:480845.50:2001MAY17	350	769	forward 2	COX4	Cytochrome c oxidase subunit IV	2.40E-27
467	LI:480845.50:2001MAY17	283	699	forward 1	COX4	Cytochrome c oxidase subunit IV	1.50E-04
468	LI:2205863.1:2001MAY17	114	347	forward 3	heme_1	Heme/Steroid binding domain	2.50E-41
474	LI:2031121.1:2001MAY17	634	747	forward 1	EGF	EGF-like domain	3.80E-06
478	LI:237999.48:2001MAY17	383	1828	forward 2	Glyco_hydro_18	Glycosyl hydrolases family 18	2.10E-77
479	LI:244935.47:2001MAY17	2571	3221	forward 3	COLFI	Fibrillar collagen C-terminal domain	2.20E-159
479	LI:244935.47:2001MAY17	1221	1400	forward 3	Collagen	Collagen triple helix repeat (20 copies)	9.10E-15
479	LI:244935.47:2001MAY17	1768	1947	forward 1	Collagen	Collagen triple helix repeat (20 copies)	1.30E-14
480	LI:257664.143:2001MAY17	36	995	forward 3	G-alpha	G-protein alpha subunit	6.10E-23
482	LI:346724.22:2001MAY17	559	690	forward 1	LEM	LEM domain	1.00E-24
483	LI:815333.1:2001MAY17	2416	2526	forward 1	EGF	EGF-like domain	1.30E-08

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
483	LI:815333.1:2001MAY17	660	767	forward 3	EGF	EGF-like domain	7.40E-07
483	LI:815333.1:2001MAY17	983	1084	forward 2	EGF	EGF-like domain	1.40E-04
483	LI:815333.1:2001MAY17	1250	1381	forward 2	TB	TB domain	1.20E-17
483	LI:815333.1:2001MAY17	825	950	forward 3	TB	TB domain	1.50E-17
483	LI:815333.1:2001MAY17	2224	2355	forward 1	TB	TB domain	3.20E-17
484	LI:889399.7:2001MAY17	135	974	forward 3	abhydrolase	alpha/beta hydrolase fold	5.70E-11
487	LG:081189.8:2001JUN22	1151	1264	forward 2	EGF	EGF-like domain	3.80E-06
487	LG:081189.8:2001JUN22	196	303	forward 1	EGF	EGF-like domain	1.80E-05
487	LG:081189.8:2001JUN22	607	738	forward 1	TB	TB domain	2.70E-11
489	LG:900035.56:2001JUN22	4061	4717	forward 2	COLFI	Fibrillar collagen C-terminal domain	9.50E-168
489	LG:900035.56:2001JUN22	2687	2866	forward 2	Collagen	Collagen triple helix repeat (20 copies)	3.90E-17
489	LG:900035.56:2001JUN22	1486	1665	forward 1	Collagen	Collagen triple helix repeat (20 copies)	9.10E-10
489	LG:900035.56:2001JUN22	204	386	forward 3	wvc	von Willebrand factor type C domain	2.50E-05
490	LG:008513.80:2001MAR30	570	1511	forward 3	filament	Intermediate filament protein	3.00E-176
492	LG:145361.1:2001MAR30	170	256	forward 2	efhand	EF hand	1.90E-04
493	LG:1500258.1:2001MAR30	164	250	forward 2	efhand	EF hand	5.30E-07
494	LG:1501754.5:2001MAR30	597	914	forward 3	CH	Calponin homology (CH) domain	2.20E-43
494	LG:1501754.5:2001MAR30	1989	2303	forward 3	spectrin	Spectrin repeat	3.00E-32
495	LG:1502796.1:2001MAR30	120	527	forward 3	cofilin_ADF	Cofilin/tropomyosin-type actin-binding protein	3.10E-54
496	LG:348973.11:2001MAR30	927	1244	forward 3	CH	Calponin homology (CH) domain	3.10E-42
496	LG:348973.11:2001MAR30	6952	7281	forward 1	PH	PH domain	7.30E-14
496	LG:348973.11:2001MAR30	5059	5373	forward 1	spectrin	Spectrin repeat	7.90E-24
496	LG:348973.11:2001MAR30	1674	1988	forward 3	spectrin	Spectrin repeat	2.40E-23
497	LG:362757.1:2001MAR30	136	519	forward 1	cofilin_ADF	Cofilin/tropomyosin-type actin-binding protein	3.50E-47
501	LI:245487.16:2001MAY17	2834	2932	forward 2	ank	Ankyrin repeat	2.00E-09
503	LI:333453.9:2001MAY17	309	590	forward 3	crystall	Beta/Gamma crystallin	3.30E-25
504	LI:412658.111:2001MAY17	1421	1507	forward 2	efhand	EF hand	2.70E-05
504	LI:412658.111:2001MAY17	536	853	forward 2	spectrin	Spectrin repeat	2.80E-32
505	LI:720054.1:2001MAY17	310	786	forward 1	myosin_head	Myosin head (motor domain)	2.20E-06
506	LI:765245.9:2001MAY17	535	612	forward 1	calponin	Calponin family repeat	2.30E-12



TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
506	LI:765245.9:2001MAY17	121	423	forward 1	CH	Calponin homology (CH) domain	1.50E-14
507	LI:814445.58:2001MAY17	857	1564	forward 2	filament	Intermediate filament protein	5.00E-43
507	LI:814445.58:2001MAY17	691	1476	forward 1	filament	Intermediate filament protein	8.20E-22
509	LI:311318.6:2001MAY17	4370	4699	forward 2	PH	PH domain	9.00E-16
509	LI:311318.6:2001MAY17	2903	3220	forward 2	spectrin	Spectrin repeat	1.40E-30
510	LI:401605.12:2001MAY17	93	1826	forward 3	myosin_head	Myosin head (motor domain)	1.60E-39
510	LI:401605.12:2001MAY17	385	2031	forward 1	myosin_head	Myosin head (motor domain)	7.30E-35
511	LG:1088618.90:2001JUN22	566	886	forward 2	CH	Calponin homology (CH) domain	7.50E-45
511	LG:1088618.90:2001JUN22	1325	1642	forward 2	spectrin	Spectrin repeat	3.20E-29
511	LG:1088618.90:2001JUN22	1989	2300	forward 3	spectrin	Spectrin repeat	1.80E-13
512	LG:1446318.6:2001JUN22	7	222	forward 1	FHA	FHA domain	2.20E-14
513	LG:229284.37:2001JUN22	2	406	forward 2	TTL	Tubulin-tyrosine ligase family	1.50E-05
515	LG:7697194.7:2001JUN22	58	1197	forward 1	actin	Actin	1.20E-42
515	LG:7697194.7:2001JUN22	1397	2494	forward 2	actin	Actin	3.60E-04
517	LG:248005.17:2001JUN22	4117	4263	forward 1	DAG_PE-bind	Phorbol esters/diacylglycerol binding domain (C1 domain)	1.60E-07
517	LG:248005.17:2001JUN22	2224	2286	forward 1	IQ	IQ calmodulin-binding motif	1.30E-04
517	LG:248005.17:2001JUN22	661	2043	forward 1	myosin_head	Myosin head (motor domain)	3.20E-08
517	LG:248005.17:2001JUN22	4357	4806	forward 1	RhoGAP	RhoGAP domain	2.60E-49
519	LG:1510893.1:2001MAR30	262	855	forward 1	kinesin	Kinesin motor domain	8.50E-52
520	LG:297070.1:2001MAR30	700	1179	forward 1	Branch	Core-2/I-Branching enzyme	6.80E-08
521	LG:363612.2:2001MAR30	107	943	forward 2	Syntaxin	Syntaxin	1.00E-181
525	LI:1010121.1:2001MAY17	517	639	forward 1	Idl_recept_a	Low-density lipoprotein receptor domain class A	7.40E-08
525	LI:1010121.1:2001MAY17	652	1128	forward 1	MAM	MAM domain	3.10E-27
528	LI:2118902.5:2001MAY17	1539	2792	forward 3	Adap_comp_sub	Adaptor complexes medium subunit family	1.30E-202
528	LI:2118902.5:2001MAY17	2456	3127	forward 2	Adap_comp_sub	Adaptor complexes medium subunit family	6.30E-08
530	LI:337830.1:2001MAY17	448	828	forward 1	C1q	C1q domain	2.20E-47
532	LI:253580.4:2001MAY17	255	848	forward 3	EMP24_GP25L	emp24/gp25/p24 family	2.10E-46
533	LG:330850.3:2001JUN22	1592	1888	forward 2	Bcl-2	Apoptosis regulator proteins, Bcl-2	4.70E-55

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
533	LG:330850.3:2001JUN22	1322	1402	forward 2	BH4	Bcl-2 homology region 4	3.30E-13
534	LG:464722.13:2001JUN22	4	621	forward 1	DDOST_48kD	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48kD	2.00E-14
537	LG:1096385.3:2001MAR30	135	425	forward 3	60s_ribosomal	60s Acidic ribosomal protein	1.30E-06
538	LG:1101445.1:2001MAR30	306	464	forward 3	Ribosomal_L30	Ribosomal protein L30p/L7e	6.80E-26
540	LG:1440118.1:2001MAR30	80	466	forward 2	Ribosomal_S9	Ribosomal protein S9/S16	5.50E-74
541	LG:1443997.1:2001MAR30	2	502	forward 2	Ribosomal_L3	Ribosomal protein L3	1.80E-62
542	LG:1497707.1:2001MAR30	92	322	forward 2	Ribosomal_L21e	Ribosomal protein L21e	1.60E-24
543	LG:1501729.1:2001MAR30	139	426	forward 1	Ribosomal_S10	Ribosomal protein S10p/S20e	7.10E-55
544	LG:1502186.1:2001MAR30	53	427	forward 2	Ribosomal_S12	Ribosomal protein S12	4.20E-56
546	LG:255713.1:2001MAR30	118	396	forward 1	Ribosomal_L31e	Ribosomal protein L31e	2.30E-14
548	LG:449413.3:2001MAR30	90	494	forward 3	Ribosomal_S12	Ribosomal protein S12	1.80E-78
549	LG:997599.1:2001MAR30	47	574	forward 2	Ribosomal_L10e	Ribosomal protein L10	1.10E-134
551	LI:1045207.1:2001MAY17	285	569	forward 3	Ribosomal_L32e	Ribosomal protein L32	8.00E-20
553	LI:1045207.1:2001MAY17	9	155	forward 3	Ribosomal_S14	Ribosomal protein S14p/S29e	2.40E-05
554	LI:1142855.1:2001MAY17	391	681	forward 1	60s_ribosomal	60s Acidic ribosomal protein	1.30E-06
555	LI:2188689.1:2001MAY17	640	870	forward 1	Ribosomal_L21e	Ribosomal protein L21e	3.70E-16
557	LI:2193411.1:2001MAY17	91	456	forward 1	Ribosomal_L114	Ribosomal protein L114p/L23e	2.60E-54
557	LI:2198795.4:2001MAY17	38	271	forward 2	Ribosomal_L31e	Ribosomal protein L31e	1.90E-07
560	LI:757871.10:2001MAY17	161	454	forward 2	Ribosomal_S10	Ribosomal protein S10p/S20e	9.50E-04
561	LG:1096385.2:2001JUN22	382	630	forward 1	60s_ribosomal	60s Acidic ribosomal protein	6.80E-06
568	LG:7694341.2:2001JUN22	71	421	forward 2	histone	Core histone H2A/H2B/H3/H4	4.80E-53
573	LG:1330214.34:2001MAR30	215	511	forward 2	mito_carr	Mitochondrial carrier protein	2.70E-34
575	LG:1449837.4:2001MAR30	222	2279	forward 3	trRNA-synt_1	trRNA synthetases class 1 (L, M and V)	1.10E-184
576	LG:1452330.5:2001MAR30	1518	1745	forward 3	GTF2l	GTF2l-like repeat	7.90E-52
576	LG:1452330.5:2001MAR30	959	1186	forward 2	GTF2l	GTF2l-like repeat	1.30E-48
577	LG:1510248.1:2001MAR30	59	232	forward 2	LIM	LIM domain	2.70E-15
577	LG:1510248.1:2001MAR30	379	543	forward 1	LIM	LIM domain	1.70E-13
579	LG:279978.17:2001MAR30	137	1372	forward 2	AMP-binding	AMP-binding enzyme	5.40E-93
580	LG:414732.1:2001MAR30	77	532	forward 2	Glyco_hydro_2_N	Glycosyl hydrolases family 2, sugar binding domain	2.70E-10
581	LG:1132208.1:2001MAR30	75	824	forward 3	adh_short	short chain dehydrogenase	1.20E-08

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
588	LI:270318.18:2001MAY17	952	1254	forward 1	mito_carr	Mitochondrial carrier protein	6.00E-22
596	LG:336953.5:2001JUN22	2350	2496	forward 1	BPL_C	Biotin protein ligase C terminal domain	5.50E-11
596	LG:336953.5:2001JUN22	1744	2175	forward 1	BPL_LipA_LipB	Biotin/lipocate A/B protein ligase family	1.30E-36
603	LG:091743.1:2001MAR30	571	729	forward 1	metalthio	Metalthionein	7.50E-06
604	LG:1397656.6:2001MAR30	1374	1745	forward 3	SPRY	SPRY domain	9.00E-38
605	LG:1500866.5:2001MAR30	1046	1132	forward 2	efhand	EF hand	2.90E-05
605	LG:1500866.5:2001MAR30	130	261	forward 1	S_100	S-100/CaBP type calcium binding domain	5.70E-18
607	LG:233288.31:2001MAR30	814	951	forward 1	myb_DNA-binding	Myb-like DNA-binding domain	2.10E-11
608	LG:269269.24:2001MAR30	1055	1156	forward 2	SAPA	Saposin A-type domain	4.70E-20
609	LG:331581.5:2001MAR30	506	748	forward 2	FHA	FHA domain	1.10E-23
610	LG:481433.4:2001MAR30	528	650	forward 3	Armadillo_seg	Armadillo/beta-catenin-like repeat	1.20E-13
610	LG:481433.4:2001MAR30	75	344	forward 3	IBB	Importin beta binding domain	6.40E-38
612	LG:475420.1:2001MAR30	553	1584	forward 1	IRBP	Interphotoreceptor retinoid-binding	1.40E-263
612	LG:475420.1:2001MAR30	3242	4195	forward 2	IRBP	Interphotoreceptor retinoid-binding	1.50E-63
613	LI:1073084.60:2001MAY17	2560	2913	forward 1	ferritin	Ferritin	1.30E-34
613	LI:1073084.60:2001MAY17	818	1108	forward 2	HSP20	Hsp20/alpha crystallin family	8.30E-10
619	LI:235487.10:2001MAY17	1154	1393	forward 2	PDZ	PDZ domain (Also known as DHR or GLGF).	1.50E-09
620	LI:476342.4:2001MAY17	159	299	forward 3	Gamma-thionin	Gamma-thionins family	4.60E-20
622	LI:765589.1:2001MAY17	276	662	forward 3	DUF279	Eukaryotic protein of unknown function, DUF279	1.80E-46
623	LI:902535.3:2001MAY17	18	440	forward 3	globin	Globin	1.30E-53
626	LG:1382838.272:2001JUN22	1428	1868	forward 3	ferritin	Ferritin	2.10E-91
632	LG:1051541.1:2001MAR30	490	837	forward 1	Gag_MA	Matrix protein (MA), p15	3.50E-10
633	LG:1090140.1:2001MAR30	1	201	forward 1	NIF	NIJ interacting factor	6.10E-05
634	LG:1094595.2:2001MAR30	2067	2471	forward 3	DUF232	Purative transcriptional regulator	1.90E-53
635	LG:1500340.1:2001MAR30	23	361	forward 2	DAD	DAD family	2.50E-74
637	LG:1511710.6:2001MAR30	980	1069	forward 2	WW	WW domain	7.50E-10
639	LG:234855.6:2001MAR30	539	1021	forward 2	FtsJ	FtsJ-like methyltransferase	1.10E-40
640	LG:242157.8:2001MAR30	658	852	forward 1	bZIP	bZIP transcription factor	8.50E-08
642	LG:412684.17:2001MAR30	326	628	forward 2	K_tetra	K+ channel tetramerisation domain	1.70E-13

TABLE 3

SEQ ID NO:	Template ID	Start	Stop	Frame	Pfam Hit	Pfam Description	E-value
643	LG:474937.20:2001MAR30	48	212	forward 3	SH3	SH3 domain	2.50E-24
645	LG:1503673.1:2001MAR30	6	974	forward 3	perilipin	Perilipin family	4.00E-30
650	LI:1011706.2:2001MAY17	164	1468	forward 2	TMS_TDE	TMS membrane protein/tumour differentially expressed protein (TDE)	5.50E-223
652	LI:2049713.6:2001MAY17	117	437	forward 3	cofilin_ADF	Cofilin/tropomyosin-type actin-binding protein	4.50E-06
655	LI:903668.7:2001MAY17	997	1065	forward 1	zf-C2H2	Zinc finger, C2H2 type	3.00E-06
656	LI:903956.35:2001MAY17	403	768	forward 1	PID	Phosphotyrosine interaction domain (PTB/PID)	1.80E-39
657	LI:055784.15:2001MAY17	3974	4501	forward 2	RasGAP	GTPase-activator protein for Ras-like GTPase	2.90E-102
658	LI:2195792.2:2001MAY17	86	646	forward 2	ras	Ras family	4.80E-56
659	LI:2207923.8:2001MAY17	490	687	forward 1	DnaJ	DnaJ domain	2.90E-09
659	LI:2207923.8:2001MAY17	23	376	forward 2	ras	Ras family	2.50E-09
660	LI:232953.31:2001MAY17	387	1226	forward 3	GTP_CDC	Cell division protein	1.30E-146
663	LG:1121446.8:2001JUN22	25	507	forward 1	Anti_proliferat	BTG1 family	1.50E-100
665	LG:370271.9:2001JUN22	87	209	forward 3	Thymosin	Thymosin beta-4 family	1.00E-13
667	LG:7683385.1:2001JUN22	61	183	forward 1	Thymosin	Thymosin beta-4 family	1.80E-24

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
4	LG:1097673.1:2001MAR30	1	1106	forward 1	TM	Non-Cytosolic
4	LG:1097673.1:2001MAR30	1107	1129	forward 1	TM	Transmembrane
4	LG:1097673.1:2001MAR30	1130	1369	forward 1	TM	Cytosolic
4	LG:1097673.1:2001MAR30	1370	1392	forward 1	TM	Transmembrane
4	LG:1097673.1:2001MAR30	1393	2366	forward 1	TM	Non-Cytosolic
4	LG:1097673.1:2001MAR30	1	1071	forward 2	TM	Non-Cytosolic
4	LG:1097673.1:2001MAR30	1072	1094	forward 2	TM	Transmembrane
4	LG:1097673.1:2001MAR30	1095	1105	forward 2	TM	Cytosolic
4	LG:1097673.1:2001MAR30	1106	1128	forward 2	TM	Transmembrane
4	LG:1097673.1:2001MAR30	1129	2366	forward 2	TM	Non-Cytosolic
4	LG:1097673.1:2001MAR30	1	1107	forward 3	TM	Non-Cytosolic
4	LG:1097673.1:2001MAR30	1108	1130	forward 3	TM	Transmembrane
4	LG:1097673.1:2001MAR30	1131	1369	forward 3	TM	Cytosolic
4	LG:1097673.1:2001MAR30	1370	1392	forward 3	TM	Transmembrane
4	LG:1097673.1:2001MAR30	1393	2365	forward 3	TM	Non-Cytosolic
6	LG:1397110.7:2001MAR30	1	75	forward 1	TM	Cytosolic
6	LG:1397110.7:2001MAR30	76	98	forward 1	TM	Transmembrane
6	LG:1397110.7:2001MAR30	99	150	forward 1	TM	Non-Cytosolic
6	LG:1397110.7:2001MAR30	151	173	forward 1	TM	Transmembrane
6	LG:1397110.7:2001MAR30	174	193	forward 1	TM	Cytosolic
6	LG:1397110.7:2001MAR30	194	216	forward 1	TM	Transmembrane
6	LG:1397110.7:2001MAR30	217	264	forward 1	TM	Non-Cytosolic
6	LG:1397110.7:2001MAR30	265	282	forward 1	TM	Transmembrane
6	LG:1397110.7:2001MAR30	283	411	forward 1	TM	Cytosolic
6	LG:1397110.7:2001MAR30	412	434	forward 1	TM	Transmembrane
6	LG:1397110.7:2001MAR30	435	487	forward 1	TM	Non-Cytosolic
6	LG:1397110.7:2001MAR30	488	510	forward 1	TM	Transmembrane
6	LG:1397110.7:2001MAR30	511	619	forward 1	TM	Cytosolic
8	LG:230734.53:2001MAR30	1	14	forward 1	TM	Non-Cytosolic
8	LG:230734.53:2001MAR30	15	34	forward 1	TM	Transmembrane
8	LG:230734.53:2001MAR30	35	270	forward 1	TM	Cytosolic
8	LG:230734.53:2001MAR30	1	9	forward 2	TM	Non-Cytosolic
8	LG:230734.53:2001MAR30	10	29	forward 2	TM	Transmembrane
8	LG:230734.53:2001MAR30	30	49	forward 2	TM	Cytosolic
8	LG:230734.53:2001MAR30	50	72	forward 2	TM	Transmembrane
8	LG:230734.53:2001MAR30	73	180	forward 2	TM	Non-Cytosolic
8	LG:230734.53:2001MAR30	181	203	forward 2	TM	Transmembrane
8	LG:230734.53:2001MAR30	204	270	forward 2	TM	Cytosolic
8	LG:230734.53:2001MAR30	1	6	forward 3	TM	Cytosolic
8	LG:230734.53:2001MAR30	7	26	forward 3	TM	Transmembrane
8	LG:230734.53:2001MAR30	27	269	forward 3	TM	Non-Cytosolic
9	LG:240154.9:2001MAR30	1	181	forward 3	TM	Cytosolic
9	LG:240154.9:2001MAR30	182	204	forward 3	TM	Transmembrane
9	LG:240154.9:2001MAR30	205	218	forward 3	TM	Non-Cytosolic
9	LG:240154.9:2001MAR30	219	236	forward 3	TM	Transmembrane
9	LG:240154.9:2001MAR30	237	369	forward 3	TM	Cytosolic
9	LG:240154.9:2001MAR30	370	392	forward 3	TM	Transmembrane
9	LG:240154.9:2001MAR30	393	411	forward 3	TM	Non-Cytosolic
9	LG:240154.9:2001MAR30	412	431	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
9	LG:240154.9:2001MAR30	432	483	forward 3	TM	Cytosolic
9	LG:240154.9:2001MAR30	484	503	forward 3	TM	Transmembrane
9	LG:240154.9:2001MAR30	504	517	forward 3	TM	Non-Cytosolic
9	LG:240154.9:2001MAR30	518	540	forward 3	TM	Transmembrane
9	LG:240154.9:2001MAR30	541	605	forward 3	TM	Cytosolic
11	LG:257151.4:2001MAR30	1	52	forward 1	TM	Cytosolic
11	LG:257151.4:2001MAR30	53	75	forward 1	TM	Transmembrane
11	LG:257151.4:2001MAR30	76	94	forward 1	TM	Non-Cytosolic
11	LG:257151.4:2001MAR30	95	117	forward 1	TM	Transmembrane
11	LG:257151.4:2001MAR30	118	137	forward 1	TM	Cytosolic
11	LG:257151.4:2001MAR30	138	160	forward 1	TM	Transmembrane
11	LG:257151.4:2001MAR30	161	416	forward 1	TM	Non-Cytosolic
11	LG:257151.4:2001MAR30	417	439	forward 1	TM	Transmembrane
11	LG:257151.4:2001MAR30	440	533	forward 1	TM	Cytosolic
11	LG:257151.4:2001MAR30	534	556	forward 1	TM	Transmembrane
11	LG:257151.4:2001MAR30	557	575	forward 1	TM	Non-Cytosolic
11	LG:257151.4:2001MAR30	576	598	forward 1	TM	Transmembrane
11	LG:257151.4:2001MAR30	599	670	forward 1	TM	Cytosolic
11	LG:257151.4:2001MAR30	671	693	forward 1	TM	Transmembrane
11	LG:257151.4:2001MAR30	694	694	forward 1	TM	Non-Cytosolic
11	LG:257151.4:2001MAR30	1	57	forward 2	TM	Non-Cytosolic
11	LG:257151.4:2001MAR30	58	80	forward 2	TM	Transmembrane
11	LG:257151.4:2001MAR30	81	105	forward 2	TM	Cytosolic
11	LG:257151.4:2001MAR30	106	127	forward 2	TM	Transmembrane
11	LG:257151.4:2001MAR30	128	694	forward 2	TM	Non-Cytosolic
11	LG:257151.4:2001MAR30	1	418	forward 3	TM	Non-Cytosolic
11	LG:257151.4:2001MAR30	419	441	forward 3	TM	Transmembrane
11	LG:257151.4:2001MAR30	442	693	forward 3	TM	Cytosolic
12	LG:334053.8:2001MAR30	1	10	forward 3	TM	Cytosolic
12	LG:334053.8:2001MAR30	11	33	forward 3	TM	Transmembrane
12	LG:334053.8:2001MAR30	34	573	forward 3	TM	Non-Cytosolic
14	LG:401748.16:2001MAR30	1	163	forward 1	TM	Cytosolic
14	LG:401748.16:2001MAR30	164	186	forward 1	TM	Transmembrane
14	LG:401748.16:2001MAR30	187	412	forward 1	TM	Non-Cytosolic
14	LG:401748.16:2001MAR30	1	168	forward 2	TM	Non-Cytosolic
14	LG:401748.16:2001MAR30	169	191	forward 2	TM	Transmembrane
14	LG:401748.16:2001MAR30	192	210	forward 2	TM	Cytosolic
14	LG:401748.16:2001MAR30	211	228	forward 2	TM	Transmembrane
14	LG:401748.16:2001MAR30	229	412	forward 2	TM	Non-Cytosolic
15	LG:476084.1:2001MAR30	1	964	forward 1	TM	Non-Cytosolic
15	LG:476084.1:2001MAR30	965	987	forward 1	TM	Transmembrane
15	LG:476084.1:2001MAR30	988	1128	forward 1	TM	Cytosolic
15	LG:476084.1:2001MAR30	1129	1146	forward 1	TM	Transmembrane
15	LG:476084.1:2001MAR30	1147	1269	forward 1	TM	Non-Cytosolic
15	LG:476084.1:2001MAR30	1	1051	forward 2	TM	Non-Cytosolic
15	LG:476084.1:2001MAR30	1052	1074	forward 2	TM	Transmembrane
15	LG:476084.1:2001MAR30	1075	1128	forward 2	TM	Cytosolic
15	LG:476084.1:2001MAR30	1129	1151	forward 2	TM	Transmembrane
15	LG:476084.1:2001MAR30	1152	1269	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
16	LG:068514.1:2001MAR30	1	428	forward 2	TM	Non-Cytosolic
16	LG:068514.1:2001MAR30	429	451	forward 2	TM	Transmembrane
16	LG:068514.1:2001MAR30	452	482	forward 2	TM	Cytosolic
16	LG:068514.1:2001MAR30	483	505	forward 2	TM	Transmembrane
16	LG:068514.1:2001MAR30	506	514	forward 2	TM	Non-Cytosolic
16	LG:068514.1:2001MAR30	515	537	forward 2	TM	Transmembrane
16	LG:068514.1:2001MAR30	538	548	forward 2	TM	Cytosolic
16	LG:068514.1:2001MAR30	549	571	forward 2	TM	Transmembrane
16	LG:068514.1:2001MAR30	572	590	forward 2	TM	Non-Cytosolic
16	LG:068514.1:2001MAR30	591	613	forward 2	TM	Transmembrane
16	LG:068514.1:2001MAR30	614	708	forward 2	TM	Cytosolic
17	LI:010505.1:2001MAY17	1	182	forward 1	TM	Cytosolic
17	LI:010505.1:2001MAY17	183	205	forward 1	TM	Transmembrane
17	LI:010505.1:2001MAY17	206	240	forward 1	TM	Non-Cytosolic
21	LI:1071608.1:2001MAY17	1	124	forward 1	TM	Cytosolic
21	LI:1071608.1:2001MAY17	125	144	forward 1	TM	Transmembrane
21	LI:1071608.1:2001MAY17	145	228	forward 1	TM	Non-Cytosolic
23	LI:1173294.9:2001MAY17	1	63	forward 1	TM	Cytosolic
23	LI:1173294.9:2001MAY17	64	83	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	84	102	forward 1	TM	Non-Cytosolic
23	LI:1173294.9:2001MAY17	103	125	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	126	221	forward 1	TM	Cytosolic
23	LI:1173294.9:2001MAY17	222	244	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	245	258	forward 1	TM	Non-Cytosolic
23	LI:1173294.9:2001MAY17	259	281	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	282	483	forward 1	TM	Cytosolic
23	LI:1173294.9:2001MAY17	484	506	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	507	562	forward 1	TM	Non-Cytosolic
23	LI:1173294.9:2001MAY17	563	585	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	586	632	forward 1	TM	Cytosolic
23	LI:1173294.9:2001MAY17	633	655	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	656	1033	forward 1	TM	Non-Cytosolic
23	LI:1173294.9:2001MAY17	1034	1056	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	1057	1067	forward 1	TM	Cytosolic
23	LI:1173294.9:2001MAY17	1068	1090	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	1091	1113	forward 1	TM	Non-Cytosolic
23	LI:1173294.9:2001MAY17	1114	1131	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	1132	1385	forward 1	TM	Cytosolic
23	LI:1173294.9:2001MAY17	1386	1408	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	1409	1438	forward 1	TM	Non-Cytosolic
23	LI:1173294.9:2001MAY17	1439	1461	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	1462	1473	forward 1	TM	Cytosolic
23	LI:1173294.9:2001MAY17	1474	1496	forward 1	TM	Transmembrane
23	LI:1173294.9:2001MAY17	1497	1527	forward 1	TM	Non-Cytosolic
23	LI:1173294.9:2001MAY17	1	102	forward 2	TM	Cytosolic
23	LI:1173294.9:2001MAY17	103	125	forward 2	TM	Transmembrane
23	LI:1173294.9:2001MAY17	126	198	forward 2	TM	Non-Cytosolic
23	LI:1173294.9:2001MAY17	199	218	forward 2	TM	Transmembrane
23	LI:1173294.9:2001MAY17	219	222	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
23	U:1173294.9:2001MAY17	223	240	forward 2	TM	Transmembrane
23	U:1173294.9:2001MAY17	241	328	forward 2	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	329	351	forward 2	TM	Transmembrane
23	U:1173294.9:2001MAY17	352	560	forward 2	TM	Cytosolic
23	U:1173294.9:2001MAY17	561	583	forward 2	TM	Transmembrane
23	U:1173294.9:2001MAY17	584	625	forward 2	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	626	648	forward 2	TM	Transmembrane
23	U:1173294.9:2001MAY17	649	1028	forward 2	TM	Cytosolic
23	U:1173294.9:2001MAY17	1029	1051	forward 2	TM	Transmembrane
23	U:1173294.9:2001MAY17	1052	1212	forward 2	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	1213	1232	forward 2	TM	Transmembrane
23	U:1173294.9:2001MAY17	1233	1244	forward 2	TM	Cytosolic
23	U:1173294.9:2001MAY17	1245	1267	forward 2	TM	Transmembrane
23	U:1173294.9:2001MAY17	1268	1311	forward 2	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	1312	1334	forward 2	TM	Transmembrane
23	U:1173294.9:2001MAY17	1335	1454	forward 2	TM	Cytosolic
23	U:1173294.9:2001MAY17	1455	1477	forward 2	TM	Transmembrane
23	U:1173294.9:2001MAY17	1478	1480	forward 2	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	1481	1503	forward 2	TM	Transmembrane
23	U:1173294.9:2001MAY17	1504	1527	forward 2	TM	Cytosolic
23	U:1173294.9:2001MAY17	1	214	forward 3	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	215	237	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	238	497	forward 3	TM	Cytosolic
23	U:1173294.9:2001MAY17	498	520	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	521	543	forward 3	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	544	566	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	567	567	forward 3	TM	Cytosolic
23	U:1173294.9:2001MAY17	568	585	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	586	632	forward 3	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	633	652	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	653	996	forward 3	TM	Cytosolic
23	U:1173294.9:2001MAY17	997	1014	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	1015	1028	forward 3	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	1029	1051	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	1052	1212	forward 3	TM	Cytosolic
23	U:1173294.9:2001MAY17	1213	1233	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	1234	1252	forward 3	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	1253	1270	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	1271	1468	forward 3	TM	Cytosolic
23	U:1173294.9:2001MAY17	1469	1491	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	1492	1500	forward 3	TM	Non-Cytosolic
23	U:1173294.9:2001MAY17	1501	1523	forward 3	TM	Transmembrane
23	U:1173294.9:2001MAY17	1524	1527	forward 3	TM	Cytosolic
28	U:240143.12:2001MAY17	1	378	forward 2	TM	Non-Cytosolic
28	U:240143.12:2001MAY17	379	401	forward 2	TM	Transmembrane
28	U:240143.12:2001MAY17	402	407	forward 2	TM	Cytosolic
28	U:240143.12:2001MAY17	408	430	forward 2	TM	Transmembrane
28	U:240143.12:2001MAY17	431	794	forward 2	TM	Non-Cytosolic
29	U:250855.6:2001MAY17	1	12	forward 1	TM	Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
29	LI:250855.6:2001MAY17	13	35	forward 1	TM	Transmembrane
29	LI:250855.6:2001MAY17	36	229	forward 1	TM	Non-Cytosolic
29	LI:250855.6:2001MAY17	1	202	forward 2	TM	Cytosolic
29	LI:250855.6:2001MAY17	203	222	forward 2	TM	Transmembrane
29	LI:250855.6:2001MAY17	223	229	forward 2	TM	Non-Cytosolic
29	LI:250855.6:2001MAY17	1	171	forward 3	TM	Cytosolic
29	LI:250855.6:2001MAY17	172	194	forward 3	TM	Transmembrane
29	LI:250855.6:2001MAY17	195	203	forward 3	TM	Non-Cytosolic
29	LI:250855.6:2001MAY17	204	226	forward 3	TM	Transmembrane
29	LI:250855.6:2001MAY17	227	228	forward 3	TM	Cytosolic
30	LI:293078.2:2001MAY17	1	263	forward 3	TM	Non-Cytosolic
30	LI:293078.2:2001MAY17	264	286	forward 3	TM	Transmembrane
30	LI:293078.2:2001MAY17	287	316	forward 3	TM	Cytosolic
30	LI:293078.2:2001MAY17	317	336	forward 3	TM	Transmembrane
30	LI:293078.2:2001MAY17	337	636	forward 3	TM	Non-Cytosolic
32	LI:409990.1:2001MAY17	1	621	forward 1	TM	Non-Cytosolic
32	LI:409990.1:2001MAY17	622	644	forward 1	TM	Transmembrane
32	LI:409990.1:2001MAY17	645	689	forward 1	TM	Cytosolic
32	LI:409990.1:2001MAY17	690	712	forward 1	TM	Transmembrane
32	LI:409990.1:2001MAY17	713	1236	forward 1	TM	Non-Cytosolic
32	LI:409990.1:2001MAY17	1	21	forward 2	TM	Cytosolic
32	LI:409990.1:2001MAY17	22	44	forward 2	TM	Transmembrane
32	LI:409990.1:2001MAY17	45	1236	forward 2	TM	Non-Cytosolic
32	LI:409990.1:2001MAY17	1	78	forward 3	TM	Cytosolic
32	LI:409990.1:2001MAY17	79	101	forward 3	TM	Transmembrane
32	LI:409990.1:2001MAY17	102	633	forward 3	TM	Non-Cytosolic
32	LI:409990.1:2001MAY17	634	656	forward 3	TM	Transmembrane
32	LI:409990.1:2001MAY17	657	690	forward 3	TM	Cytosolic
32	LI:409990.1:2001MAY17	691	713	forward 3	TM	Transmembrane
32	LI:409990.1:2001MAY17	714	1235	forward 3	TM	Non-Cytosolic
33	LI:474832.7:2001MAY17	1	452	forward 1	TM	Non-Cytosolic
33	LI:474832.7:2001MAY17	453	475	forward 1	TM	Transmembrane
33	LI:474832.7:2001MAY17	476	681	forward 1	TM	Cytosolic
33	LI:474832.7:2001MAY17	682	704	forward 1	TM	Transmembrane
33	LI:474832.7:2001MAY17	705	732	forward 1	TM	Non-Cytosolic
33	LI:474832.7:2001MAY17	733	755	forward 1	TM	Transmembrane
33	LI:474832.7:2001MAY17	756	887	forward 1	TM	Cytosolic
33	LI:474832.7:2001MAY17	888	910	forward 1	TM	Transmembrane
33	LI:474832.7:2001MAY17	911	1008	forward 1	TM	Non-Cytosolic
33	LI:474832.7:2001MAY17	1009	1028	forward 1	TM	Transmembrane
33	LI:474832.7:2001MAY17	1029	1219	forward 1	TM	Cytosolic
33	LI:474832.7:2001MAY17	1220	1242	forward 1	TM	Transmembrane
33	LI:474832.7:2001MAY17	1243	1251	forward 1	TM	Non-Cytosolic
33	LI:474832.7:2001MAY17	1252	1271	forward 1	TM	Transmembrane
33	LI:474832.7:2001MAY17	1272	1299	forward 1	TM	Cytosolic
33	LI:474832.7:2001MAY17	1	904	forward 2	TM	Non-Cytosolic
33	LI:474832.7:2001MAY17	905	927	forward 2	TM	Transmembrane
33	LI:474832.7:2001MAY17	928	966	forward 2	TM	Cytosolic
33	LI:474832.7:2001MAY17	967	986	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
33	U:474832.7:2001MAY17	987	1005	forward 2	TM	Non-Cytosolic
33	U:474832.7:2001MAY17	1006	1028	forward 2	TM	Transmembrane
33	U:474832.7:2001MAY17	1029	1048	forward 2	TM	Cytosolic
33	U:474832.7:2001MAY17	1049	1071	forward 2	TM	Transmembrane
33	U:474832.7:2001MAY17	1072	1135	forward 2	TM	Non-Cytosolic
33	U:474832.7:2001MAY17	1136	1158	forward 2	TM	Transmembrane
33	U:474832.7:2001MAY17	1159	1221	forward 2	TM	Cytosolic
33	U:474832.7:2001MAY17	1222	1244	forward 2	TM	Transmembrane
33	U:474832.7:2001MAY17	1245	1263	forward 2	TM	Non-Cytosolic
33	U:474832.7:2001MAY17	1264	1286	forward 2	TM	Transmembrane
33	U:474832.7:2001MAY17	1287	1298	forward 2	TM	Cytosolic
33	U:474832.7:2001MAY17	1	37	forward 3	TM	Non-Cytosolic
33	U:474832.7:2001MAY17	38	60	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	61	135	forward 3	TM	Cytosolic
33	U:474832.7:2001MAY17	136	158	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	159	198	forward 3	TM	Non-Cytosolic
33	U:474832.7:2001MAY17	199	221	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	222	734	forward 3	TM	Cytosolic
33	U:474832.7:2001MAY17	735	757	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	758	766	forward 3	TM	Non-Cytosolic
33	U:474832.7:2001MAY17	767	786	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	787	797	forward 3	TM	Cytosolic
33	U:474832.7:2001MAY17	798	817	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	818	863	forward 3	TM	Non-Cytosolic
33	U:474832.7:2001MAY17	864	886	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	887	892	forward 3	TM	Cytosolic
33	U:474832.7:2001MAY17	893	915	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	916	965	forward 3	TM	Non-Cytosolic
33	U:474832.7:2001MAY17	966	988	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	989	1048	forward 3	TM	Cytosolic
33	U:474832.7:2001MAY17	1049	1071	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	1072	1249	forward 3	TM	Non-Cytosolic
33	U:474832.7:2001MAY17	1250	1272	forward 3	TM	Transmembrane
33	U:474832.7:2001MAY17	1273	1298	forward 3	TM	Cytosolic
34	U:814696.11:2001MAY17	184	270	forward 1	SP	
35	U:818488.31:2001MAY17	1	141	forward 1	TM	Cytosolic
35	U:818488.31:2001MAY17	142	164	forward 1	TM	Transmembrane
35	U:818488.31:2001MAY17	165	671	forward 1	TM	Non-Cytosolic
36	U:2049834.12:2001MAY17	1	506	forward 2	TM	Non-Cytosolic
36	U:2049834.12:2001MAY17	507	529	forward 2	TM	Transmembrane
36	U:2049834.12:2001MAY17	530	549	forward 2	TM	Cytosolic
36	U:2049834.12:2001MAY17	550	572	forward 2	TM	Transmembrane
36	U:2049834.12:2001MAY17	573	1108	forward 2	TM	Non-Cytosolic
37	U:338956.8:2001MAY17	1	20	forward 3	TM	Cytosolic
37	U:338956.8:2001MAY17	21	43	forward 3	TM	Transmembrane
37	U:338956.8:2001MAY17	44	510	forward 3	TM	Non-Cytosolic
38	U:1175083.15:2001MAY17	1	303	forward 1	TM	Non-Cytosolic
38	U:1175083.15:2001MAY17	304	326	forward 1	TM	Transmembrane
38	U:1175083.15:2001MAY17	327	354	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
39	LI:1189311.14:2001MAY17	1	153	forward 3	TM	Cytosolic
39	LI:1189311.14:2001MAY17	154	176	forward 3	TM	Transmembrane
39	LI:1189311.14:2001MAY17	177	195	forward 3	TM	Non-Cytosolic
39	LI:1189311.14:2001MAY17	196	215	forward 3	TM	Transmembrane
39	LI:1189311.14:2001MAY17	216	234	forward 3	TM	Cytosolic
39	LI:1189311.14:2001MAY17	235	257	forward 3	TM	Transmembrane
39	LI:1189311.14:2001MAY17	258	800	forward 3	TM	Non-Cytosolic
40	LI:330984.6:2001MAY17	1	11	forward 1	TM	Cytosolic
40	LI:330984.6:2001MAY17	12	31	forward 1	TM	Transmembrane
40	LI:330984.6:2001MAY17	32	1025	forward 1	TM	Non-Cytosolic
40	LI:330984.6:2001MAY17	1	537	forward 2	TM	Non-Cytosolic
40	LI:330984.6:2001MAY17	538	560	forward 2	TM	Transmembrane
40	LI:330984.6:2001MAY17	561	750	forward 2	TM	Cytosolic
40	LI:330984.6:2001MAY17	751	769	forward 2	TM	Transmembrane
40	LI:330984.6:2001MAY17	770	814	forward 2	TM	Non-Cytosolic
40	LI:330984.6:2001MAY17	815	837	forward 2	TM	Transmembrane
40	LI:330984.6:2001MAY17	838	951	forward 2	TM	Cytosolic
40	LI:330984.6:2001MAY17	952	974	forward 2	TM	Transmembrane
40	LI:330984.6:2001MAY17	975	1024	forward 2	TM	Non-Cytosolic
40	LI:330984.6:2001MAY17	1	528	forward 3	TM	Non-Cytosolic
40	LI:330984.6:2001MAY17	529	551	forward 3	TM	Transmembrane
40	LI:330984.6:2001MAY17	552	585	forward 3	TM	Cytosolic
40	LI:330984.6:2001MAY17	586	608	forward 3	TM	Transmembrane
40	LI:330984.6:2001MAY17	609	627	forward 3	TM	Non-Cytosolic
40	LI:330984.6:2001MAY17	628	650	forward 3	TM	Transmembrane
40	LI:330984.6:2001MAY17	651	654	forward 3	TM	Cytosolic
40	LI:330984.6:2001MAY17	655	672	forward 3	TM	Transmembrane
40	LI:330984.6:2001MAY17	673	697	forward 3	TM	Non-Cytosolic
40	LI:330984.6:2001MAY17	698	718	forward 3	TM	Transmembrane
40	LI:330984.6:2001MAY17	719	751	forward 3	TM	Cytosolic
40	LI:330984.6:2001MAY17	752	774	forward 3	TM	Transmembrane
40	LI:330984.6:2001MAY17	775	777	forward 3	TM	Non-Cytosolic
40	LI:330984.6:2001MAY17	778	797	forward 3	TM	Transmembrane
40	LI:330984.6:2001MAY17	798	816	forward 3	TM	Cytosolic
40	LI:330984.6:2001MAY17	817	836	forward 3	TM	Transmembrane
40	LI:330984.6:2001MAY17	837	1024	forward 3	TM	Non-Cytosolic
42	LG:1138554.48:2001JUN22	1	165	forward 1	TM	Non-Cytosolic
42	LG:1138554.48:2001JUN22	166	188	forward 1	TM	Transmembrane
42	LG:1138554.48:2001JUN22	189	210	forward 1	TM	Cytosolic
42	LG:1138554.48:2001JUN22	1	51	forward 2	TM	Non-Cytosolic
42	LG:1138554.48:2001JUN22	52	71	forward 2	TM	Transmembrane
42	LG:1138554.48:2001JUN22	72	91	forward 2	TM	Cytosolic
42	LG:1138554.48:2001JUN22	92	114	forward 2	TM	Transmembrane
42	LG:1138554.48:2001JUN22	115	128	forward 2	TM	Non-Cytosolic
42	LG:1138554.48:2001JUN22	129	151	forward 2	TM	Transmembrane
42	LG:1138554.48:2001JUN22	152	210	forward 2	TM	Cytosolic
45	LG:437008.4:2001JUN22	1	232	forward 1	TM	Non-Cytosolic
45	LG:437008.4:2001JUN22	233	255	forward 1	TM	Transmembrane
45	LG:437008.4:2001JUN22	256	275	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
45	LG:437008.4:2001JUN22	276	298	forward 1	TM	Transmembrane
45	LG:437008.4:2001JUN22	299	317	forward 1	TM	Non-Cytosolic
45	LG:437008.4:2001JUN22	318	340	forward 1	TM	Transmembrane
45	LG:437008.4:2001JUN22	341	413	forward 1	TM	Cytosolic
45	LG:437008.4:2001JUN22	414	436	forward 1	TM	Transmembrane
45	LG:437008.4:2001JUN22	437	450	forward 1	TM	Non-Cytosolic
45	LG:437008.4:2001JUN22	1	278	forward 3	TM	Non-Cytosolic
45	LG:437008.4:2001JUN22	279	301	forward 3	TM	Transmembrane
45	LG:437008.4:2001JUN22	302	313	forward 3	TM	Cytosolic
45	LG:437008.4:2001JUN22	314	336	forward 3	TM	Transmembrane
45	LG:437008.4:2001JUN22	337	350	forward 3	TM	Non-Cytosolic
45	LG:437008.4:2001JUN22	351	373	forward 3	TM	Transmembrane
45	LG:437008.4:2001JUN22	374	450	forward 3	TM	Cytosolic
48	LG:068514.3:2001JUN22	1	428	forward 2	TM	Non-Cytosolic
48	LG:068514.3:2001JUN22	429	451	forward 2	TM	Transmembrane
48	LG:068514.3:2001JUN22	452	482	forward 2	TM	Cytosolic
48	LG:068514.3:2001JUN22	483	505	forward 2	TM	Transmembrane
48	LG:068514.3:2001JUN22	506	514	forward 2	TM	Non-Cytosolic
48	LG:068514.3:2001JUN22	515	537	forward 2	TM	Transmembrane
48	LG:068514.3:2001JUN22	538	548	forward 2	TM	Cytosolic
48	LG:068514.3:2001JUN22	549	571	forward 2	TM	Transmembrane
48	LG:068514.3:2001JUN22	572	590	forward 2	TM	Non-Cytosolic
48	LG:068514.3:2001JUN22	591	613	forward 2	TM	Transmembrane
48	LG:068514.3:2001JUN22	614	684	forward 2	TM	Cytosolic
51	LG:242968.4:2001MAR30	1	892	forward 1	TM	Non-Cytosolic
51	LG:242968.4:2001MAR30	893	912	forward 1	TM	Transmembrane
51	LG:242968.4:2001MAR30	913	1139	forward 1	TM	Cytosolic
51	LG:242968.4:2001MAR30	1140	1162	forward 1	TM	Transmembrane
51	LG:242968.4:2001MAR30	1163	2192	forward 1	TM	Non-Cytosolic
51	LG:242968.4:2001MAR30	1	676	forward 2	TM	Non-Cytosolic
51	LG:242968.4:2001MAR30	677	699	forward 2	TM	Transmembrane
51	LG:242968.4:2001MAR30	700	888	forward 2	TM	Cytosolic
51	LG:242968.4:2001MAR30	889	911	forward 2	TM	Transmembrane
51	LG:242968.4:2001MAR30	912	2192	forward 2	TM	Non-Cytosolic
51	LG:242968.4:2001MAR30	1	833	forward 3	TM	Non-Cytosolic
51	LG:242968.4:2001MAR30	834	856	forward 3	TM	Transmembrane
51	LG:242968.4:2001MAR30	857	888	forward 3	TM	Cytosolic
51	LG:242968.4:2001MAR30	889	911	forward 3	TM	Transmembrane
51	LG:242968.4:2001MAR30	912	2191	forward 3	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	1	751	forward 1	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	752	774	forward 1	TM	Transmembrane
52	LG:344741.17:2001MAR30	775	812	forward 1	TM	Cytosolic
52	LG:344741.17:2001MAR30	813	835	forward 1	TM	Transmembrane
52	LG:344741.17:2001MAR30	836	865	forward 1	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	866	888	forward 1	TM	Transmembrane
52	LG:344741.17:2001MAR30	889	973	forward 1	TM	Cytosolic
52	LG:344741.17:2001MAR30	974	996	forward 1	TM	Transmembrane
52	LG:344741.17:2001MAR30	997	1005	forward 1	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	1006	1025	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
52	LG:344741.17:2001MAR30	1026	1224	forward 1	TM	Cytosolic
52	LG:344741.17:2001MAR30	1225	1247	forward 1	TM	Transmembrane
52	LG:344741.17:2001MAR30	1248	1815	forward 1	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	1816	1838	forward 1	TM	Transmembrane
52	LG:344741.17:2001MAR30	1839	1896	forward 1	TM	Cytosolic
52	LG:344741.17:2001MAR30	1897	1919	forward 1	TM	Transmembrane
52	LG:344741.17:2001MAR30	1920	1938	forward 1	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	1939	1961	forward 1	TM	Transmembrane
52	LG:344741.17:2001MAR30	1962	2025	forward 1	TM	Cytosolic
52	LG:344741.17:2001MAR30	1	828	forward 2	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	829	851	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	852	871	forward 2	TM	Cytosolic
52	LG:344741.17:2001MAR30	872	886	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	887	905	forward 2	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	906	928	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	929	988	forward 2	TM	Cytosolic
52	LG:344741.17:2001MAR30	989	1011	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	1012	1585	forward 2	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	1586	1608	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	1609	1628	forward 2	TM	Cytosolic
52	LG:344741.17:2001MAR30	1629	1651	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	1652	1871	forward 2	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	1872	1894	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	1895	1895	forward 2	TM	Cytosolic
52	LG:344741.17:2001MAR30	1896	1918	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	1919	1932	forward 2	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	1933	1955	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	1956	1966	forward 2	TM	Cytosolic
52	LG:344741.17:2001MAR30	1967	1989	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	1990	1992	forward 2	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	1993	2015	forward 2	TM	Transmembrane
52	LG:344741.17:2001MAR30	2016	2024	forward 2	TM	Cytosolic
52	LG:344741.17:2001MAR30	1	780	forward 3	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	781	799	forward 3	TM	Transmembrane
52	LG:344741.17:2001MAR30	800	811	forward 3	TM	Cytosolic
52	LG:344741.17:2001MAR30	812	834	forward 3	TM	Transmembrane
52	LG:344741.17:2001MAR30	835	872	forward 3	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	873	887	forward 3	TM	Transmembrane
52	LG:344741.17:2001MAR30	888	971	forward 3	TM	Cytosolic
52	LG:344741.17:2001MAR30	972	994	forward 3	TM	Transmembrane
52	LG:344741.17:2001MAR30	995	1271	forward 3	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	1272	1294	forward 3	TM	Transmembrane
52	LG:344741.17:2001MAR30	1295	1457	forward 3	TM	Cytosolic
52	LG:344741.17:2001MAR30	1458	1480	forward 3	TM	Transmembrane
52	LG:344741.17:2001MAR30	1481	1494	forward 3	TM	Non-Cytosolic
52	LG:344741.17:2001MAR30	1495	1517	forward 3	TM	Transmembrane
52	LG:344741.17:2001MAR30	1518	1815	forward 3	TM	Cytosolic
52	LG:344741.17:2001MAR30	1816	1838	forward 3	TM	Transmembrane
52	LG:344741.17:2001MAR30	1839	1888	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
52	LG:344741.17:2001MAR30	1889	1911	forward 3	TM	Transmembrane
52	LG:344741.17:2001MAR30	1912	1964	forward 3	TM	Cytosolic
52	LG:344741.17:2001MAR30	1965	1987	forward 3	TM	Transmembrane
52	LG:344741.17:2001MAR30	1988	2024	forward 3	TM	Non-Cytosolic
54	LG:481492.6:2001MAR30	1	206	forward 1	TM	Non-Cytosolic
54	LG:481492.6:2001MAR30	207	226	forward 1	TM	Transmembrane
54	LG:481492.6:2001MAR30	227	246	forward 1	TM	Cytosolic
54	LG:481492.6:2001MAR30	247	269	forward 1	TM	Transmembrane
54	LG:481492.6:2001MAR30	270	384	forward 1	TM	Non-Cytosolic
55	LI:035870.26:2001MAY17	1	6	forward 1	TM	Cytosolic
55	LI:035870.26:2001MAY17	7	26	forward 1	TM	Transmembrane
55	LI:035870.26:2001MAY17	27	29	forward 1	TM	Non-Cytosolic
55	LI:035870.26:2001MAY17	30	52	forward 1	TM	Transmembrane
55	LI:035870.26:2001MAY17	53	58	forward 1	TM	Cytosolic
55	LI:035870.26:2001MAY17	59	81	forward 1	TM	Transmembrane
55	LI:035870.26:2001MAY17	82	1175	forward 1	TM	Non-Cytosolic
55	LI:035870.26:2001MAY17	1	11	forward 2	TM	Cytosolic
55	LI:035870.26:2001MAY17	12	34	forward 2	TM	Transmembrane
55	LI:035870.26:2001MAY17	35	38	forward 2	TM	Non-Cytosolic
55	LI:035870.26:2001MAY17	39	56	forward 2	TM	Transmembrane
55	LI:035870.26:2001MAY17	57	62	forward 2	TM	Cytosolic
55	LI:035870.26:2001MAY17	63	85	forward 2	TM	Transmembrane
55	LI:035870.26:2001MAY17	86	1175	forward 2	TM	Non-Cytosolic
55	LI:035870.26:2001MAY17	1	4	forward 3	TM	Non-Cytosolic
55	LI:035870.26:2001MAY17	5	22	forward 3	TM	Transmembrane
55	LI:035870.26:2001MAY17	23	28	forward 3	TM	Cytosolic
55	LI:035870.26:2001MAY17	29	51	forward 3	TM	Transmembrane
55	LI:035870.26:2001MAY17	52	1174	forward 3	TM	Non-Cytosolic
56	LI:2121852.1:2001MAY17	1	58	forward 1	TM	Cytosolic
56	LI:2121852.1:2001MAY17	59	81	forward 1	TM	Transmembrane
56	LI:2121852.1:2001MAY17	82	95	forward 1	TM	Non-Cytosolic
56	LI:2121852.1:2001MAY17	96	115	forward 1	TM	Transmembrane
56	LI:2121852.1:2001MAY17	116	204	forward 1	TM	Cytosolic
56	LI:2121852.1:2001MAY17	1	3	forward 3	TM	Non-Cytosolic
56	LI:2121852.1:2001MAY17	4	26	forward 3	TM	Transmembrane
56	LI:2121852.1:2001MAY17	27	38	forward 3	TM	Cytosolic
56	LI:2121852.1:2001MAY17	39	61	forward 3	TM	Transmembrane
56	LI:2121852.1:2001MAY17	62	107	forward 3	TM	Non-Cytosolic
56	LI:2121852.1:2001MAY17	108	130	forward 3	TM	Transmembrane
56	LI:2121852.1:2001MAY17	131	150	forward 3	TM	Cytosolic
56	LI:2121852.1:2001MAY17	151	173	forward 3	TM	Transmembrane
56	LI:2121852.1:2001MAY17	174	204	forward 3	TM	Non-Cytosolic
58	LI:2167150.1:2001MAY17	1	129	forward 3	TM	Cytosolic
58	LI:2167150.1:2001MAY17	130	152	forward 3	TM	Transmembrane
58	LI:2167150.1:2001MAY17	153	166	forward 3	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1	1080	forward 1	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1081	1103	forward 1	TM	Transmembrane
59	LI:230062.10:2001MAY17	1104	1200	forward 1	TM	Cytosolic
59	LI:230062.10:2001MAY17	1201	1220	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
59	LI:230062.10:2001MAY17	1221	1553	forward 1	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1554	1576	forward 1	TM	Transmembrane
59	LI:230062.10:2001MAY17	1577	1790	forward 1	TM	Cytosolic
59	LI:230062.10:2001MAY17	1791	1813	forward 1	TM	Transmembrane
59	LI:230062.10:2001MAY17	1814	1827	forward 1	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1828	1847	forward 1	TM	Transmembrane
59	LI:230062.10:2001MAY17	1848	1859	forward 1	TM	Cytosolic
59	LI:230062.10:2001MAY17	1860	1878	forward 1	TM	Transmembrane
59	LI:230062.10:2001MAY17	1879	1940	forward 1	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1941	1963	forward 1	TM	Transmembrane
59	LI:230062.10:2001MAY17	1964	2080	forward 1	TM	Cytosolic
59	LI:230062.10:2001MAY17	2081	2103	forward 1	TM	Transmembrane
59	LI:230062.10:2001MAY17	2104	2170	forward 1	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	2171	2190	forward 1	TM	Transmembrane
59	LI:230062.10:2001MAY17	2191	2216	forward 1	TM	Cytosolic
59	LI:230062.10:2001MAY17	1	622	forward 2	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	623	645	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	646	719	forward 2	TM	Cytosolic
59	LI:230062.10:2001MAY17	720	742	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	743	791	forward 2	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	792	814	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	815	1004	forward 2	TM	Cytosolic
59	LI:230062.10:2001MAY17	1005	1027	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	1028	1046	forward 2	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1047	1069	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	1070	1199	forward 2	TM	Cytosolic
59	LI:230062.10:2001MAY17	1200	1219	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	1220	1238	forward 2	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1239	1261	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	1262	1267	forward 2	TM	Cytosolic
59	LI:230062.10:2001MAY17	1268	1285	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	1286	1312	forward 2	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1313	1335	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	1336	1489	forward 2	TM	Cytosolic
59	LI:230062.10:2001MAY17	1490	1512	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	1513	1553	forward 2	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1554	1573	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	1574	1806	forward 2	TM	Cytosolic
59	LI:230062.10:2001MAY17	1807	1829	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	1830	1848	forward 2	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1849	1871	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	1872	2063	forward 2	TM	Cytosolic
59	LI:230062.10:2001MAY17	2064	2086	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	2087	2095	forward 2	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	2096	2118	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	2119	2165	forward 2	TM	Cytosolic
59	LI:230062.10:2001MAY17	2166	2188	forward 2	TM	Transmembrane
59	LI:230062.10:2001MAY17	2189	2216	forward 2	TM	Non-Cytosolic
59	LI:230062.10:2001MAY17	1	619	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
59	U:230062.10:2001MAY17	620	642	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	643	718	forward 3	TM	Cytosolic
59	U:230062.10:2001MAY17	719	741	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	742	1010	forward 3	TM	Non-Cytosolic
59	U:230062.10:2001MAY17	1011	1033	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1034	1060	forward 3	TM	Cytosolic
59	U:230062.10:2001MAY17	1061	1083	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1084	1253	forward 3	TM	Non-Cytosolic
59	U:230062.10:2001MAY17	1254	1276	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1277	1341	forward 3	TM	Cytosolic
59	U:230062.10:2001MAY17	1342	1359	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1360	1368	forward 3	TM	Non-Cytosolic
59	U:230062.10:2001MAY17	1369	1391	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1392	1399	forward 3	TM	Cytosolic
59	U:230062.10:2001MAY17	1400	1422	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1423	1436	forward 3	TM	Non-Cytosolic
59	U:230062.10:2001MAY17	1437	1459	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1460	1465	forward 3	TM	Cytosolic
59	U:230062.10:2001MAY17	1466	1488	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1489	1695	forward 3	TM	Non-Cytosolic
59	U:230062.10:2001MAY17	1696	1718	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1719	1805	forward 3	TM	Cytosolic
59	U:230062.10:2001MAY17	1806	1828	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1829	1863	forward 3	TM	Non-Cytosolic
59	U:230062.10:2001MAY17	1864	1883	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	1884	2179	forward 3	TM	Cytosolic
59	U:230062.10:2001MAY17	2180	2202	forward 3	TM	Transmembrane
59	U:230062.10:2001MAY17	2203	2215	forward 3	TM	Non-Cytosolic
62	U:401269.13:2001MAY17	1	306	forward 1	TM	Non-Cytosolic
62	U:401269.13:2001MAY17	307	326	forward 1	TM	Transmembrane
62	U:401269.13:2001MAY17	327	345	forward 1	TM	Cytosolic
62	U:401269.13:2001MAY17	346	368	forward 1	TM	Transmembrane
62	U:401269.13:2001MAY17	369	1415	forward 1	TM	Non-Cytosolic
62	U:401269.13:2001MAY17	1	4	forward 2	TM	Cytosolic
62	U:401269.13:2001MAY17	5	24	forward 2	TM	Transmembrane
62	U:401269.13:2001MAY17	25	33	forward 2	TM	Non-Cytosolic
62	U:401269.13:2001MAY17	34	51	forward 2	TM	Transmembrane
62	U:401269.13:2001MAY17	52	62	forward 2	TM	Cytosolic
62	U:401269.13:2001MAY17	63	82	forward 2	TM	Transmembrane
62	U:401269.13:2001MAY17	83	85	forward 2	TM	Non-Cytosolic
62	U:401269.13:2001MAY17	86	103	forward 2	TM	Transmembrane
62	U:401269.13:2001MAY17	104	246	forward 2	TM	Cytosolic
62	U:401269.13:2001MAY17	247	269	forward 2	TM	Transmembrane
62	U:401269.13:2001MAY17	270	304	forward 2	TM	Non-Cytosolic
62	U:401269.13:2001MAY17	305	327	forward 2	TM	Transmembrane
62	U:401269.13:2001MAY17	328	347	forward 2	TM	Cytosolic
62	U:401269.13:2001MAY17	348	370	forward 2	TM	Transmembrane
62	U:401269.13:2001MAY17	371	411	forward 2	TM	Non-Cytosolic
62	U:401269.13:2001MAY17	412	434	forward 2	TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
62	LI:401269.13:2001MAY17	435	870	forward 2	TM	Cytosolic
62	LI:401269.13:2001MAY17	871	890	forward 2	TM	Transmembrane
62	LI:401269.13:2001MAY17	891	1415	forward 2	TM	Non-Cytosolic
62	LI:401269.13:2001MAY17	1	345	forward 3	TM	Non-Cytosolic
62	LI:401269.13:2001MAY17	346	365	forward 3	TM	Transmembrane
62	LI:401269.13:2001MAY17	366	371	forward 3	TM	Cytosolic
62	LI:401269.13:2001MAY17	372	394	forward 3	TM	Transmembrane
62	LI:401269.13:2001MAY17	395	421	forward 3	TM	Non-Cytosolic
62	LI:401269.13:2001MAY17	422	444	forward 3	TM	Transmembrane
62	LI:401269.13:2001MAY17	445	725	forward 3	TM	Cytosolic
62	LI:401269.13:2001MAY17	726	748	forward 3	TM	Transmembrane
62	LI:401269.13:2001MAY17	749	872	forward 3	TM	Non-Cytosolic
62	LI:401269.13:2001MAY17	873	895	forward 3	TM	Transmembrane
62	LI:401269.13:2001MAY17	896	943	forward 3	TM	Cytosolic
62	LI:401269.13:2001MAY17	944	966	forward 3	TM	Transmembrane
62	LI:401269.13:2001MAY17	967	1415	forward 3	TM	Non-Cytosolic
63	LI:481492.3:2001MAY17	1	241	forward 2	TM	Non-Cytosolic
63	LI:481492.3:2001MAY17	242	261	forward 2	TM	Transmembrane
63	LI:481492.3:2001MAY17	262	281	forward 2	TM	Cytosolic
63	LI:481492.3:2001MAY17	282	304	forward 2	TM	Transmembrane
63	LI:481492.3:2001MAY17	305	419	forward 2	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	1	306	forward 1	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	307	326	forward 1	TM	Transmembrane
66	LG:142131.16:2001JUN22	327	345	forward 1	TM	Cytosolic
66	LG:142131.16:2001JUN22	346	368	forward 1	TM	Transmembrane
66	LG:142131.16:2001JUN22	369	1268	forward 1	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	1	4	forward 2	TM	Cytosolic
66	LG:142131.16:2001JUN22	5	24	forward 2	TM	Transmembrane
66	LG:142131.16:2001JUN22	25	33	forward 2	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	34	51	forward 2	TM	Transmembrane
66	LG:142131.16:2001JUN22	52	62	forward 2	TM	Cytosolic
66	LG:142131.16:2001JUN22	63	82	forward 2	TM	Transmembrane
66	LG:142131.16:2001JUN22	83	85	forward 2	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	86	103	forward 2	TM	Transmembrane
66	LG:142131.16:2001JUN22	104	246	forward 2	TM	Cytosolic
66	LG:142131.16:2001JUN22	247	269	forward 2	TM	Transmembrane
66	LG:142131.16:2001JUN22	270	304	forward 2	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	305	327	forward 2	TM	Transmembrane
66	LG:142131.16:2001JUN22	328	347	forward 2	TM	Cytosolic
66	LG:142131.16:2001JUN22	348	370	forward 2	TM	Transmembrane
66	LG:142131.16:2001JUN22	371	411	forward 2	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	412	434	forward 2	TM	Transmembrane
66	LG:142131.16:2001JUN22	435	870	forward 2	TM	Cytosolic
66	LG:142131.16:2001JUN22	871	890	forward 2	TM	Transmembrane
66	LG:142131.16:2001JUN22	891	1267	forward 2	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	1	345	forward 3	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	346	365	forward 3	TM	Transmembrane
66	LG:142131.16:2001JUN22	366	371	forward 3	TM	Cytosolic
66	LG:142131.16:2001JUN22	372	394	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
66	LG:142131.16:2001JUN22	395	421	forward 3	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	422	444	forward 3	TM	Transmembrane
66	LG:142131.16:2001JUN22	445	725	forward 3	TM	Cytosolic
66	LG:142131.16:2001JUN22	726	748	forward 3	TM	Transmembrane
66	LG:142131.16:2001JUN22	749	872	forward 3	TM	Non-Cytosolic
66	LG:142131.16:2001JUN22	873	895	forward 3	TM	Transmembrane
66	LG:142131.16:2001JUN22	896	943	forward 3	TM	Cytosolic
66	LG:142131.16:2001JUN22	944	966	forward 3	TM	Transmembrane
66	LG:142131.16:2001JUN22	967	1267	forward 3	TM	Non-Cytosolic
67	LG:407723.12:2001JUN22	1	354	forward 2	TM	Non-Cytosolic
67	LG:407723.12:2001JUN22	355	377	forward 2	TM	Transmembrane
67	LG:407723.12:2001JUN22	378	747	forward 2	TM	Cytosolic
67	LG:407723.12:2001JUN22	748	770	forward 2	TM	Transmembrane
67	LG:407723.12:2001JUN22	771	898	forward 2	TM	Non-Cytosolic
67	LG:407723.12:2001JUN22	1	617	forward 3	TM	Non-Cytosolic
67	LG:407723.12:2001JUN22	618	640	forward 3	TM	Transmembrane
67	LG:407723.12:2001JUN22	641	739	forward 3	TM	Cytosolic
67	LG:407723.12:2001JUN22	740	762	forward 3	TM	Transmembrane
67	LG:407723.12:2001JUN22	763	897	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1	1080	forward 1	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1081	1103	forward 1	TM	Transmembrane
70	LG:230062.16:2001JUN22	1104	1200	forward 1	TM	Cytosolic
70	LG:230062.16:2001JUN22	1201	1220	forward 1	TM	Transmembrane
70	LG:230062.16:2001JUN22	1221	1693	forward 1	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1694	1716	forward 1	TM	Transmembrane
70	LG:230062.16:2001JUN22	1717	1806	forward 1	TM	Cytosolic
70	LG:230062.16:2001JUN22	1807	1829	forward 1	TM	Transmembrane
70	LG:230062.16:2001JUN22	1830	1848	forward 1	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1849	1871	forward 1	TM	Transmembrane
70	LG:230062.16:2001JUN22	1872	2063	forward 1	TM	Cytosolic
70	LG:230062.16:2001JUN22	2064	2086	forward 1	TM	Transmembrane
70	LG:230062.16:2001JUN22	2087	2095	forward 1	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	2096	2118	forward 1	TM	Transmembrane
70	LG:230062.16:2001JUN22	2119	2165	forward 1	TM	Cytosolic
70	LG:230062.16:2001JUN22	2166	2188	forward 1	TM	Transmembrane
70	LG:230062.16:2001JUN22	2189	2216	forward 1	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1	401	forward 2	TM	Cytosolic
70	LG:230062.16:2001JUN22	402	424	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	425	454	forward 2	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	455	477	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	478	626	forward 2	TM	Cytosolic
70	LG:230062.16:2001JUN22	627	646	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	647	693	forward 2	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	694	713	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	714	719	forward 2	TM	Cytosolic
70	LG:230062.16:2001JUN22	720	742	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	743	791	forward 2	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	792	814	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	815	1004	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
70	LG:230062.16:2001JUN22	1005	1027	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	1028	1046	forward 2	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1047	1069	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	1070	1199	forward 2	TM	Cytosolic
70	LG:230062.16:2001JUN22	1200	1219	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	1220	1238	forward 2	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1239	1261	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	1262	1267	forward 2	TM	Cytosolic
70	LG:230062.16:2001JUN22	1268	1285	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	1286	1312	forward 2	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1313	1335	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	1336	1347	forward 2	TM	Cytosolic
70	LG:230062.16:2001JUN22	1348	1370	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	1371	1695	forward 2	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1696	1718	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	1719	1805	forward 2	TM	Cytosolic
70	LG:230062.16:2001JUN22	1806	1828	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	1829	1863	forward 2	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1864	1883	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	1884	2179	forward 2	TM	Cytosolic
70	LG:230062.16:2001JUN22	2180	2202	forward 2	TM	Transmembrane
70	LG:230062.16:2001JUN22	2203	2215	forward 2	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1	619	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	620	642	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	643	718	forward 3	TM	Cytosolic
70	LG:230062.16:2001JUN22	719	741	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	742	834	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	835	857	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	858	1010	forward 3	TM	Cytosolic
70	LG:230062.16:2001JUN22	1011	1033	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1034	1055	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1056	1078	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1079	1209	forward 3	TM	Cytosolic
70	LG:230062.16:2001JUN22	1210	1232	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1233	1253	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1254	1276	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1277	1341	forward 3	TM	Cytosolic
70	LG:230062.16:2001JUN22	1342	1359	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1360	1368	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1369	1391	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1392	1399	forward 3	TM	Cytosolic
70	LG:230062.16:2001JUN22	1400	1422	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1423	1436	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1437	1459	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1460	1465	forward 3	TM	Cytosolic
70	LG:230062.16:2001JUN22	1466	1488	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1489	1552	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1553	1575	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1576	1789	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
70	LG:230062.16:2001JUN22	1790	1812	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1813	1826	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1827	1846	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1847	1858	forward 3	TM	Cytosolic
70	LG:230062.16:2001JUN22	1859	1877	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1878	1939	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	1940	1962	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	1963	2079	forward 3	TM	Cytosolic
70	LG:230062.16:2001JUN22	2080	2102	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	2103	2169	forward 3	TM	Non-Cytosolic
70	LG:230062.16:2001JUN22	2170	2189	forward 3	TM	Transmembrane
70	LG:230062.16:2001JUN22	2190	2215	forward 3	TM	Cytosolic
72	LG:044276.1:2001JUN22	1	94	forward 1	TM	Cytosolic
72	LG:044276.1:2001JUN22	95	117	forward 1	TM	Transmembrane
72	LG:044276.1:2001JUN22	118	345	forward 1	TM	Non-Cytosolic
74	LG:242968.17:2001JUN22	1	892	forward 1	TM	Non-Cytosolic
74	LG:242968.17:2001JUN22	893	912	forward 1	TM	Transmembrane
74	LG:242968.17:2001JUN22	913	1139	forward 1	TM	Cytosolic
74	LG:242968.17:2001JUN22	1140	1162	forward 1	TM	Transmembrane
74	LG:242968.17:2001JUN22	1163	1695	forward 1	TM	Non-Cytosolic
74	LG:242968.17:2001JUN22	1	676	forward 2	TM	Non-Cytosolic
74	LG:242968.17:2001JUN22	677	699	forward 2	TM	Transmembrane
74	LG:242968.17:2001JUN22	700	888	forward 2	TM	Cytosolic
74	LG:242968.17:2001JUN22	889	911	forward 2	TM	Transmembrane
74	LG:242968.17:2001JUN22	912	1694	forward 2	TM	Non-Cytosolic
74	LG:242968.17:2001JUN22	1	833	forward 3	TM	Non-Cytosolic
74	LG:242968.17:2001JUN22	834	856	forward 3	TM	Transmembrane
74	LG:242968.17:2001JUN22	857	888	forward 3	TM	Cytosolic
74	LG:242968.17:2001JUN22	889	911	forward 3	TM	Transmembrane
74	LG:242968.17:2001JUN22	912	1694	forward 3	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	1	9	forward 1	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	10	32	forward 1	TM	Transmembrane
76	LG:1385255.10:2001MAR30	33	44	forward 1	TM	Cytosolic
76	LG:1385255.10:2001MAR30	45	67	forward 1	TM	Transmembrane
76	LG:1385255.10:2001MAR30	68	1098	forward 1	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	1099	1121	forward 1	TM	Transmembrane
76	LG:1385255.10:2001MAR30	1122	1337	forward 1	TM	Cytosolic
76	LG:1385255.10:2001MAR30	1338	1357	forward 1	TM	Transmembrane
76	LG:1385255.10:2001MAR30	1358	1376	forward 1	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	1377	1399	forward 1	TM	Transmembrane
76	LG:1385255.10:2001MAR30	1400	1708	forward 1	TM	Cytosolic
76	LG:1385255.10:2001MAR30	1709	1731	forward 1	TM	Transmembrane
76	LG:1385255.10:2001MAR30	1732	1745	forward 1	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	1746	1765	forward 1	TM	Transmembrane
76	LG:1385255.10:2001MAR30	1766	1771	forward 1	TM	Cytosolic
76	LG:1385255.10:2001MAR30	1772	1794	forward 1	TM	Transmembrane
76	LG:1385255.10:2001MAR30	1795	2553	forward 1	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	1	1	forward 2	TM	Cytosolic
76	LG:1385255.10:2001MAR30	2	24	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
76	LG:1385255.10:2001MAR30	25	1869	forward 2	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	1870	1892	forward 2	TM	Transmembrane
76	LG:1385255.10:2001MAR30	1893	2010	forward 2	TM	Cytosolic
76	LG:1385255.10:2001MAR30	2011	2033	forward 2	TM	Transmembrane
76	LG:1385255.10:2001MAR30	2034	2436	forward 2	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	2437	2459	forward 2	TM	Transmembrane
76	LG:1385255.10:2001MAR30	2460	2505	forward 2	TM	Cytosolic
76	LG:1385255.10:2001MAR30	2506	2528	forward 2	TM	Transmembrane
76	LG:1385255.10:2001MAR30	2529	2552	forward 2	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	1	6	forward 3	TM	Cytosolic
76	LG:1385255.10:2001MAR30	7	24	forward 3	TM	Transmembrane
76	LG:1385255.10:2001MAR30	25	203	forward 3	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	204	223	forward 3	TM	Transmembrane
76	LG:1385255.10:2001MAR30	224	601	forward 3	TM	Cytosolic
76	LG:1385255.10:2001MAR30	602	624	forward 3	TM	Transmembrane
76	LG:1385255.10:2001MAR30	625	1695	forward 3	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	1696	1718	forward 3	TM	Transmembrane
76	LG:1385255.10:2001MAR30	1719	1730	forward 3	TM	Cytosolic
76	LG:1385255.10:2001MAR30	1731	1753	forward 3	TM	Transmembrane
76	LG:1385255.10:2001MAR30	1754	1869	forward 3	TM	Non-Cytosolic
76	LG:1385255.10:2001MAR30	1870	1892	forward 3	TM	Transmembrane
76	LG:1385255.10:2001MAR30	1893	2010	forward 3	TM	Cytosolic
76	LG:1385255.10:2001MAR30	2011	2030	forward 3	TM	Transmembrane
76	LG:1385255.10:2001MAR30	2031	2552	forward 3	TM	Non-Cytosolic
77	LG:1397492.21:2001MAR30	1	461	forward 3	TM	Non-Cytosolic
77	LG:1397492.21:2001MAR30	462	484	forward 3	TM	Transmembrane
77	LG:1397492.21:2001MAR30	485	736	forward 3	TM	Cytosolic
78	LG:1512330.2:2001MAR30	1	168	forward 1	TM	Non-Cytosolic
78	LG:1512330.2:2001MAR30	169	188	forward 1	TM	Transmembrane
78	LG:1512330.2:2001MAR30	189	219	forward 1	TM	Cytosolic
78	LG:1512330.2:2001MAR30	220	242	forward 1	TM	Transmembrane
78	LG:1512330.2:2001MAR30	243	244	forward 1	TM	Non-Cytosolic
79	LG:300009.1:2001MAR30	1	238	forward 1	TM	Cytosolic
79	LG:300009.1:2001MAR30	239	261	forward 1	TM	Transmembrane
79	LG:300009.1:2001MAR30	262	288	forward 1	TM	Non-Cytosolic
79	LG:300009.1:2001MAR30	289	311	forward 1	TM	Transmembrane
79	LG:300009.1:2001MAR30	312	323	forward 1	TM	Cytosolic
79	LG:300009.1:2001MAR30	324	342	forward 1	TM	Transmembrane
79	LG:300009.1:2001MAR30	343	359	forward 1	TM	Non-Cytosolic
79	LG:300009.1:2001MAR30	1	331	forward 3	TM	Non-Cytosolic
79	LG:300009.1:2001MAR30	332	354	forward 3	TM	Transmembrane
79	LG:300009.1:2001MAR30	355	358	forward 3	TM	Cytosolic
80	LG:333886.2:2001MAR30	1	106	forward 2	TM	Cytosolic
80	LG:333886.2:2001MAR30	107	129	forward 2	TM	Transmembrane
80	LG:333886.2:2001MAR30	130	1084	forward 2	TM	Non-Cytosolic
80	LG:333886.2:2001MAR30	1085	1107	forward 2	TM	Transmembrane
80	LG:333886.2:2001MAR30	1108	1321	forward 2	TM	Cytosolic
80	LG:333886.2:2001MAR30	1322	1344	forward 2	TM	Transmembrane
80	LG:333886.2:2001MAR30	1345	1358	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO.:	Template ID	Start	Stop	Frame	Domain Type	Topology
80	LG:333886.2:2001MAR30	1359	1381	forward 2	TM	Transmembrane
80	LG:333886.2:2001MAR30	1382	1518	forward 2	TM	Cytosolic
80	LG:333886.2:2001MAR30	1519	1541	forward 2	TM	Transmembrane
80	LG:333886.2:2001MAR30	1542	1625	forward 2	TM	Non-Cytosolic
80	LG:333886.2:2001MAR30	1626	1644	forward 2	TM	Transmembrane
80	LG:333886.2:2001MAR30	1645	1656	forward 2	TM	Cytosolic
80	LG:333886.2:2001MAR30	1657	1675	forward 2	TM	Transmembrane
80	LG:333886.2:2001MAR30	1676	1676	forward 2	TM	Non-Cytosolic
80	LG:333886.2:2001MAR30	1	115	forward 3	TM	Cytosolic
80	LG:333886.2:2001MAR30	116	138	forward 3	TM	Transmembrane
80	LG:333886.2:2001MAR30	139	1241	forward 3	TM	Non-Cytosolic
80	LG:333886.2:2001MAR30	1242	1264	forward 3	TM	Transmembrane
80	LG:333886.2:2001MAR30	1265	1327	forward 3	TM	Cytosolic
80	LG:333886.2:2001MAR30	1328	1350	forward 3	TM	Transmembrane
80	LG:333886.2:2001MAR30	1351	1364	forward 3	TM	Non-Cytosolic
80	LG:333886.2:2001MAR30	1365	1387	forward 3	TM	Transmembrane
80	LG:333886.2:2001MAR30	1388	1516	forward 3	TM	Cytosolic
80	LG:333886.2:2001MAR30	1517	1539	forward 3	TM	Transmembrane
80	LG:333886.2:2001MAR30	1540	1623	forward 3	TM	Non-Cytosolic
80	LG:333886.2:2001MAR30	1624	1646	forward 3	TM	Transmembrane
80	LG:333886.2:2001MAR30	1647	1675	forward 3	TM	Cytosolic
81	LG:349438.18:2001MAR30	1	1368	forward 1	TM	Non-Cytosolic
81	LG:349438.18:2001MAR30	1369	1391	forward 1	TM	Transmembrane
81	LG:349438.18:2001MAR30	1392	1403	forward 1	TM	Cytosolic
81	LG:349438.18:2001MAR30	1404	1426	forward 1	TM	Transmembrane
81	LG:349438.18:2001MAR30	1427	1492	forward 1	TM	Non-Cytosolic
81	LG:349438.18:2001MAR30	1493	1515	forward 1	TM	Transmembrane
81	LG:349438.18:2001MAR30	1516	1538	forward 1	TM	Cytosolic
81	LG:349438.18:2001MAR30	1539	1561	forward 1	TM	Transmembrane
81	LG:349438.18:2001MAR30	1562	2156	forward 1	TM	Non-Cytosolic
81	LG:349438.18:2001MAR30	1	1922	forward 2	TM	Non-Cytosolic
81	LG:349438.18:2001MAR30	1923	1945	forward 2	TM	Transmembrane
81	LG:349438.18:2001MAR30	1946	1957	forward 2	TM	Cytosolic
81	LG:349438.18:2001MAR30	1958	1977	forward 2	TM	Transmembrane
81	LG:349438.18:2001MAR30	1978	2092	forward 2	TM	Non-Cytosolic
81	LG:349438.18:2001MAR30	2093	2115	forward 2	TM	Transmembrane
81	LG:349438.18:2001MAR30	2116	2155	forward 2	TM	Cytosolic
81	LG:349438.18:2001MAR30	1	1330	forward 3	TM	Non-Cytosolic
81	LG:349438.18:2001MAR30	1331	1353	forward 3	TM	Transmembrane
81	LG:349438.18:2001MAR30	1354	1409	forward 3	TM	Cytosolic
81	LG:349438.18:2001MAR30	1410	1432	forward 3	TM	Transmembrane
81	LG:349438.18:2001MAR30	1433	1491	forward 3	TM	Non-Cytosolic
81	LG:349438.18:2001MAR30	1492	1514	forward 3	TM	Transmembrane
81	LG:349438.18:2001MAR30	1515	1716	forward 3	TM	Cytosolic
81	LG:349438.18:2001MAR30	1717	1739	forward 3	TM	Transmembrane
81	LG:349438.18:2001MAR30	1740	2155	forward 3	TM	Non-Cytosolic
83	LG:250170.3:2001MAR30	1	560	forward 2	TM	Non-Cytosolic
83	LG:250170.3:2001MAR30	561	583	forward 2	TM	Transmembrane
83	LG:250170.3:2001MAR30	584	783	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
84	LG:1383159.5:2001MAR30	1	241	forward 2	TM	Cytosolic
84	LG:1383159.5:2001MAR30	242	264	forward 2	TM	Transmembrane
84	LG:1383159.5:2001MAR30	265	267	forward 2	TM	Non-Cytosolic
84	LG:1383159.5:2001MAR30	268	290	forward 2	TM	Transmembrane
84	LG:1383159.5:2001MAR30	291	299	forward 2	TM	Cytosolic
84	LG:1383159.5:2001MAR30	1	195	forward 3	TM	Cytosolic
84	LG:1383159.5:2001MAR30	196	218	forward 3	TM	Transmembrane
84	LG:1383159.5:2001MAR30	219	261	forward 3	TM	Non-Cytosolic
84	LG:1383159.5:2001MAR30	262	284	forward 3	TM	Transmembrane
84	LG:1383159.5:2001MAR30	285	299	forward 3	TM	Cytosolic
85	LI:044888.1:2001MAY17	1	204	forward 1	TM	Non-Cytosolic
85	LI:044888.1:2001MAY17	205	227	forward 1	TM	Transmembrane
85	LI:044888.1:2001MAY17	228	273	forward 1	TM	Cytosolic
85	LI:044888.1:2001MAY17	274	296	forward 1	TM	Transmembrane
85	LI:044888.1:2001MAY17	297	571	forward 1	TM	Non-Cytosolic
85	LI:044888.1:2001MAY17	1	12	forward 3	TM	Cytosolic
85	LI:044888.1:2001MAY17	13	35	forward 3	TM	Transmembrane
85	LI:044888.1:2001MAY17	36	239	forward 3	TM	Non-Cytosolic
85	LI:044888.1:2001MAY17	240	262	forward 3	TM	Transmembrane
85	LI:044888.1:2001MAY17	263	309	forward 3	TM	Cytosolic
85	LI:044888.1:2001MAY17	310	332	forward 3	TM	Transmembrane
85	LI:044888.1:2001MAY17	333	570	forward 3	TM	Non-Cytosolic
86	LI:101277.1:2001MAY17	1	64	forward 1	TM	Non-Cytosolic
86	LI:101277.1:2001MAY17	65	87	forward 1	TM	Transmembrane
86	LI:101277.1:2001MAY17	88	98	forward 1	TM	Cytosolic
86	LI:101277.1:2001MAY17	99	121	forward 1	TM	Transmembrane
86	LI:101277.1:2001MAY17	122	135	forward 1	TM	Non-Cytosolic
86	LI:101277.1:2001MAY17	136	155	forward 1	TM	Transmembrane
86	LI:101277.1:2001MAY17	156	175	forward 1	TM	Cytosolic
86	LI:101277.1:2001MAY17	176	198	forward 1	TM	Transmembrane
86	LI:101277.1:2001MAY17	199	222	forward 1	TM	Non-Cytosolic
86	LI:101277.1:2001MAY17	223	245	forward 1	TM	Transmembrane
86	LI:101277.1:2001MAY17	246	265	forward 1	TM	Cytosolic
86	LI:101277.1:2001MAY17	266	288	forward 1	TM	Transmembrane
86	LI:101277.1:2001MAY17	289	313	forward 1	TM	Non-Cytosolic
86	LI:101277.1:2001MAY17	314	336	forward 1	TM	Transmembrane
86	LI:101277.1:2001MAY17	337	491	forward 1	TM	Cytosolic
86	LI:101277.1:2001MAY17	1	94	forward 2	TM	Cytosolic
86	LI:101277.1:2001MAY17	95	117	forward 2	TM	Transmembrane
86	LI:101277.1:2001MAY17	118	192	forward 2	TM	Non-Cytosolic
86	LI:101277.1:2001MAY17	193	215	forward 2	TM	Transmembrane
86	LI:101277.1:2001MAY17	216	226	forward 2	TM	Cytosolic
86	LI:101277.1:2001MAY17	227	249	forward 2	TM	Transmembrane
86	LI:101277.1:2001MAY17	250	490	forward 2	TM	Non-Cytosolic
87	LI:1021852.6:2001MAY17	1	288	forward 1	TM	Non-Cytosolic
87	LI:1021852.6:2001MAY17	289	311	forward 1	TM	Transmembrane
87	LI:1021852.6:2001MAY17	312	368	forward 1	TM	Cytosolic
87	LI:1021852.6:2001MAY17	369	386	forward 1	TM	Transmembrane
87	LI:1021852.6:2001MAY17	387	468	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
87	U:1021852.6:2001MAY17	1	64	forward 2	TM	Cytosolic
87	U:1021852.6:2001MAY17	65	87	forward 2	TM	Transmembrane
87	U:1021852.6:2001MAY17	88	113	forward 2	TM	Non-Cytosolic
87	U:1021852.6:2001MAY17	114	136	forward 2	TM	Transmembrane
87	U:1021852.6:2001MAY17	137	171	forward 2	TM	Cytosolic
87	U:1021852.6:2001MAY17	172	194	forward 2	TM	Transmembrane
87	U:1021852.6:2001MAY17	195	272	forward 2	TM	Non-Cytosolic
87	U:1021852.6:2001MAY17	273	295	forward 2	TM	Transmembrane
87	U:1021852.6:2001MAY17	296	296	forward 2	TM	Cytosolic
87	U:1021852.6:2001MAY17	297	316	forward 2	TM	Transmembrane
87	U:1021852.6:2001MAY17	317	330	forward 2	TM	Non-Cytosolic
87	U:1021852.6:2001MAY17	331	348	forward 2	TM	Transmembrane
87	U:1021852.6:2001MAY17	349	368	forward 2	TM	Cytosolic
87	U:1021852.6:2001MAY17	369	391	forward 2	TM	Transmembrane
87	U:1021852.6:2001MAY17	392	405	forward 2	TM	Non-Cytosolic
87	U:1021852.6:2001MAY17	406	428	forward 2	TM	Transmembrane
87	U:1021852.6:2001MAY17	429	467	forward 2	TM	Cytosolic
87	U:1021852.6:2001MAY17	1	284	forward 3	TM	Non-Cytosolic
87	U:1021852.6:2001MAY17	285	307	forward 3	TM	Transmembrane
87	U:1021852.6:2001MAY17	308	368	forward 3	TM	Cytosolic
87	U:1021852.6:2001MAY17	369	391	forward 3	TM	Transmembrane
87	U:1021852.6:2001MAY17	392	394	forward 3	TM	Non-Cytosolic
87	U:1021852.6:2001MAY17	395	417	forward 3	TM	Transmembrane
87	U:1021852.6:2001MAY17	418	467	forward 3	TM	Cytosolic
89	U:1084017.20:2001MAY17	1	270	forward 3	TM	Non-Cytosolic
89	U:1084017.20:2001MAY17	271	293	forward 3	TM	Transmembrane
89	U:1084017.20:2001MAY17	294	411	forward 3	TM	Cytosolic
90	U:1183158.1:2001MAY17	1	20	forward 2	TM	Cytosolic
90	U:1183158.1:2001MAY17	21	40	forward 2	TM	Transmembrane
90	U:1183158.1:2001MAY17	41	59	forward 2	TM	Non-Cytosolic
90	U:1183158.1:2001MAY17	60	82	forward 2	TM	Transmembrane
90	U:1183158.1:2001MAY17	83	88	forward 2	TM	Cytosolic
90	U:1183158.1:2001MAY17	89	107	forward 2	TM	Transmembrane
90	U:1183158.1:2001MAY17	108	596	forward 2	TM	Non-Cytosolic
91	U:1188807.9:2001MAY17	1	178	forward 1	TM	Cytosolic
91	U:1188807.9:2001MAY17	179	201	forward 1	TM	Transmembrane
91	U:1188807.9:2001MAY17	202	763	forward 1	TM	Non-Cytosolic
91	U:1188807.9:2001MAY17	1	721	forward 2	TM	Non-Cytosolic
91	U:1188807.9:2001MAY17	722	744	forward 2	TM	Transmembrane
91	U:1188807.9:2001MAY17	745	762	forward 2	TM	Cytosolic
92	U:206576.15:2001MAY17	1	526	forward 1	TM	Non-Cytosolic
92	U:206576.15:2001MAY17	527	549	forward 1	TM	Transmembrane
92	U:206576.15:2001MAY17	550	561	forward 1	TM	Cytosolic
92	U:206576.15:2001MAY17	562	584	forward 1	TM	Transmembrane
92	U:206576.15:2001MAY17	585	826	forward 1	TM	Non-Cytosolic
92	U:206576.15:2001MAY17	827	849	forward 1	TM	Transmembrane
92	U:206576.15:2001MAY17	850	906	forward 1	TM	Cytosolic
92	U:206576.15:2001MAY17	907	924	forward 1	TM	Transmembrane
92	U:206576.15:2001MAY17	925	975	forward 1	TM	Non-Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
92	U:206576.15:2001MAY17	976	998	forward 1	TM	Transmembrane
92	U:206576.15:2001MAY17	999	1018	forward 1	TM	Cytosolic
92	U:206576.15:2001MAY17	1019	1041	forward 1	TM	Transmembrane
92	U:206576.15:2001MAY17	1042	1160	forward 1	TM	Non-Cytosolic
92	U:206576.15:2001MAY17	1	829	forward 2	TM	Non-Cytosolic
92	U:206576.15:2001MAY17	830	852	forward 2	TM	Transmembrane
92	U:206576.15:2001MAY17	853	906	forward 2	TM	Cytosolic
92	U:206576.15:2001MAY17	907	926	forward 2	TM	Transmembrane
92	U:206576.15:2001MAY17	927	938	forward 2	TM	Non-Cytosolic
92	U:206576.15:2001MAY17	939	961	forward 2	TM	Transmembrane
92	U:206576.15:2001MAY17	962	972	forward 2	TM	Cytosolic
92	U:206576.15:2001MAY17	973	995	forward 2	TM	Transmembrane
92	U:206576.15:2001MAY17	996	1096	forward 2	TM	Non-Cytosolic
92	U:206576.15:2001MAY17	1097	1119	forward 2	TM	Transmembrane
92	U:206576.15:2001MAY17	1120	1160	forward 2	TM	Cytosolic
92	U:206576.15:2001MAY17	1	980	forward 3	TM	Non-Cytosolic
92	U:206576.15:2001MAY17	981	1003	forward 3	TM	Transmembrane
92	U:206576.15:2001MAY17	1004	1160	forward 3	TM	Cytosolic
93	U:2120427.4:2001MAY17	1	40	forward 2	TM	Non-Cytosolic
93	U:2120427.4:2001MAY17	41	63	forward 2	TM	Transmembrane
93	U:2120427.4:2001MAY17	64	212	forward 2	TM	Cytosolic
93	U:2120427.4:2001MAY17	1	170	forward 3	TM	Cytosolic
93	U:2120427.4:2001MAY17	171	193	forward 3	TM	Transmembrane
93	U:2120427.4:2001MAY17	194	212	forward 3	TM	Non-Cytosolic
95	U:220797.7:2001MAY17	1	22	forward 3	TM	Non-Cytosolic
95	U:220797.7:2001MAY17	23	45	forward 3	TM	Transmembrane
95	U:220797.7:2001MAY17	46	57	forward 3	TM	Cytosolic
95	U:220797.7:2001MAY17	58	80	forward 3	TM	Transmembrane
95	U:220797.7:2001MAY17	81	89	forward 3	TM	Non-Cytosolic
95	U:220797.7:2001MAY17	90	112	forward 3	TM	Transmembrane
95	U:220797.7:2001MAY17	113	150	forward 3	TM	Cytosolic
96	U:237723.23:2001MAY17	1	340	forward 1	TM	Non-Cytosolic
96	U:237723.23:2001MAY17	341	363	forward 1	TM	Transmembrane
96	U:237723.23:2001MAY17	364	383	forward 1	TM	Cytosolic
96	U:237723.23:2001MAY17	384	401	forward 1	TM	Transmembrane
96	U:237723.23:2001MAY17	402	415	forward 1	TM	Non-Cytosolic
96	U:237723.23:2001MAY17	416	433	forward 1	TM	Transmembrane
96	U:237723.23:2001MAY17	434	473	forward 1	TM	Cytosolic
96	U:237723.23:2001MAY17	474	496	forward 1	TM	Transmembrane
96	U:237723.23:2001MAY17	497	500	forward 1	TM	Non-Cytosolic
96	U:237723.23:2001MAY17	501	523	forward 1	TM	Transmembrane
96	U:237723.23:2001MAY17	524	557	forward 1	TM	Cytosolic
96	U:237723.23:2001MAY17	558	580	forward 1	TM	Transmembrane
96	U:237723.23:2001MAY17	581	584	forward 1	TM	Non-Cytosolic
96	U:237723.23:2001MAY17	585	607	forward 1	TM	Transmembrane
96	U:237723.23:2001MAY17	608	638	forward 1	TM	Cytosolic
96	U:237723.23:2001MAY17	1	347	forward 2	TM	Non-Cytosolic
96	U:237723.23:2001MAY17	348	367	forward 2	TM	Transmembrane
96	U:237723.23:2001MAY17	368	414	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
96	U:237723.23:2001MAY17	415	432	forward 2	TM	Transmembrane
96	U:237723.23:2001MAY17	433	436	forward 2	TM	Non-Cytosolic
96	U:237723.23:2001MAY17	437	456	forward 2	TM	Transmembrane
96	U:237723.23:2001MAY17	457	510	forward 2	TM	Cytosolic
96	U:237723.23:2001MAY17	511	533	forward 2	TM	Transmembrane
96	U:237723.23:2001MAY17	534	552	forward 2	TM	Non-Cytosolic
96	U:237723.23:2001MAY17	553	575	forward 2	TM	Transmembrane
96	U:237723.23:2001MAY17	576	637	forward 2	TM	Cytosolic
96	U:237723.23:2001MAY17	1	216	forward 3	TM	Non-Cytosolic
96	U:237723.23:2001MAY17	217	239	forward 3	TM	Transmembrane
96	U:237723.23:2001MAY17	240	345	forward 3	TM	Cytosolic
96	U:237723.23:2001MAY17	346	368	forward 3	TM	Transmembrane
96	U:237723.23:2001MAY17	369	414	forward 3	TM	Non-Cytosolic
96	U:237723.23:2001MAY17	415	432	forward 3	TM	Transmembrane
96	U:237723.23:2001MAY17	433	518	forward 3	TM	Cytosolic
96	U:237723.23:2001MAY17	519	537	forward 3	TM	Transmembrane
96	U:237723.23:2001MAY17	538	587	forward 3	TM	Non-Cytosolic
96	U:237723.23:2001MAY17	588	607	forward 3	TM	Transmembrane
96	U:237723.23:2001MAY17	608	637	forward 3	TM	Cytosolic
97	U:817560.12:2001MAY17	1	347	forward 1	TM	Non-Cytosolic
97	U:817560.12:2001MAY17	348	365	forward 1	TM	Transmembrane
97	U:817560.12:2001MAY17	366	377	forward 1	TM	Cytosolic
97	U:817560.12:2001MAY17	378	400	forward 1	TM	Transmembrane
97	U:817560.12:2001MAY17	401	419	forward 1	TM	Non-Cytosolic
97	U:817560.12:2001MAY17	420	442	forward 1	TM	Transmembrane
97	U:817560.12:2001MAY17	443	474	forward 1	TM	Cytosolic
97	U:817560.12:2001MAY17	475	497	forward 1	TM	Transmembrane
97	U:817560.12:2001MAY17	498	525	forward 1	TM	Non-Cytosolic
97	U:817560.12:2001MAY17	526	548	forward 1	TM	Transmembrane
97	U:817560.12:2001MAY17	549	554	forward 1	TM	Cytosolic
97	U:817560.12:2001MAY17	555	577	forward 1	TM	Transmembrane
97	U:817560.12:2001MAY17	578	586	forward 1	TM	Non-Cytosolic
97	U:817560.12:2001MAY17	1	420	forward 2	TM	Non-Cytosolic
97	U:817560.12:2001MAY17	421	443	forward 2	TM	Transmembrane
97	U:817560.12:2001MAY17	444	455	forward 2	TM	Cytosolic
97	U:817560.12:2001MAY17	456	473	forward 2	TM	Transmembrane
97	U:817560.12:2001MAY17	474	476	forward 2	TM	Non-Cytosolic
97	U:817560.12:2001MAY17	477	499	forward 2	TM	Transmembrane
97	U:817560.12:2001MAY17	500	511	forward 2	TM	Cytosolic
97	U:817560.12:2001MAY17	512	534	forward 2	TM	Transmembrane
97	U:817560.12:2001MAY17	535	548	forward 2	TM	Non-Cytosolic
97	U:817560.12:2001MAY17	549	571	forward 2	TM	Transmembrane
97	U:817560.12:2001MAY17	572	586	forward 2	TM	Cytosolic
97	U:817560.12:2001MAY17	1	346	forward 3	TM	Non-Cytosolic
97	U:817560.12:2001MAY17	347	369	forward 3	TM	Transmembrane
97	U:817560.12:2001MAY17	370	381	forward 3	TM	Cytosolic
97	U:817560.12:2001MAY17	382	401	forward 3	TM	Transmembrane
97	U:817560.12:2001MAY17	402	420	forward 3	TM	Non-Cytosolic
97	U:817560.12:2001MAY17	421	443	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
97	LI:817560.12:2001MAY17	444	455	forward 3	TM	Cytosolic
97	LI:817560.12:2001MAY17	456	478	forward 3	TM	Transmembrane
97	LI:817560.12:2001MAY17	479	481	forward 3	TM	Non-Cytosolic
97	LI:817560.12:2001MAY17	482	504	forward 3	TM	Transmembrane
97	LI:817560.12:2001MAY17	505	586	forward 3	TM	Cytosolic
98	LI:140935.16:2001MAY17	1	353	forward 2	TM	Non-Cytosolic
98	LI:140935.16:2001MAY17	354	376	forward 2	TM	Transmembrane
98	LI:140935.16:2001MAY17	377	391	forward 2	TM	Cytosolic
99	LI:235333.5:2001MAY17	1	1269	forward 1	TM	Non-Cytosolic
99	LI:235333.5:2001MAY17	1270	1292	forward 1	TM	Transmembrane
99	LI:235333.5:2001MAY17	1293	1364	forward 1	TM	Cytosolic
99	LI:235333.5:2001MAY17	1	243	forward 3	TM	Cytosolic
99	LI:235333.5:2001MAY17	244	266	forward 3	TM	Transmembrane
99	LI:235333.5:2001MAY17	267	1363	forward 3	TM	Non-Cytosolic
102	LG:028634.1:2001JUN22	1	175	forward 1	TM	Cytosolic
102	LG:028634.1:2001JUN22	176	193	forward 1	TM	Transmembrane
102	LG:028634.1:2001JUN22	194	207	forward 1	TM	Non-Cytosolic
102	LG:028634.1:2001JUN22	208	230	forward 1	TM	Transmembrane
102	LG:028634.1:2001JUN22	231	234	forward 1	TM	Cytosolic
102	LG:028634.1:2001JUN22	235	257	forward 1	TM	Transmembrane
102	LG:028634.1:2001JUN22	258	596	forward 1	TM	Non-Cytosolic
102	LG:028634.1:2001JUN22	1	144	forward 2	TM	Non-Cytosolic
102	LG:028634.1:2001JUN22	145	167	forward 2	TM	Transmembrane
102	LG:028634.1:2001JUN22	168	179	forward 2	TM	Cytosolic
102	LG:028634.1:2001JUN22	180	202	forward 2	TM	Transmembrane
102	LG:028634.1:2001JUN22	203	214	forward 2	TM	Non-Cytosolic
102	LG:028634.1:2001JUN22	215	237	forward 2	TM	Transmembrane
102	LG:028634.1:2001JUN22	238	248	forward 2	TM	Cytosolic
102	LG:028634.1:2001JUN22	249	271	forward 2	TM	Transmembrane
102	LG:028634.1:2001JUN22	272	595	forward 2	TM	Non-Cytosolic
102	LG:028634.1:2001JUN22	1	71	forward 3	TM	Non-Cytosolic
102	LG:028634.1:2001JUN22	72	94	forward 3	TM	Transmembrane
102	LG:028634.1:2001JUN22	95	138	forward 3	TM	Cytosolic
102	LG:028634.1:2001JUN22	139	161	forward 3	TM	Transmembrane
102	LG:028634.1:2001JUN22	162	205	forward 3	TM	Non-Cytosolic
102	LG:028634.1:2001JUN22	206	228	forward 3	TM	Transmembrane
102	LG:028634.1:2001JUN22	229	258	forward 3	TM	Cytosolic
102	LG:028634.1:2001JUN22	259	281	forward 3	TM	Transmembrane
102	LG:028634.1:2001JUN22	282	595	forward 3	TM	Non-Cytosolic
103	LG:087230.3:2001JUN22	1	85	forward 3	TM	Cytosolic
103	LG:087230.3:2001JUN22	86	103	forward 3	TM	Transmembrane
103	LG:087230.3:2001JUN22	104	312	forward 3	TM	Non-Cytosolic
104	LG:1397520.8:2001JUN22	1	19	forward 2	TM	Cytosolic
104	LG:1397520.8:2001JUN22	20	39	forward 2	TM	Transmembrane
104	LG:1397520.8:2001JUN22	40	131	forward 2	TM	Non-Cytosolic
105	LG:213947.1:2001JUN22	1	137	forward 1	TM	Cytosolic
105	LG:213947.1:2001JUN22	138	160	forward 1	TM	Transmembrane
105	LG:213947.1:2001JUN22	161	196	forward 1	TM	Non-Cytosolic
105	LG:213947.1:2001JUN22	197	219	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
105	LG:213947.1:2001JUN22	220	225	forward 1	TM	Cytosolic
105	LG:213947.1:2001JUN22	226	248	forward 1	TM	Transmembrane
105	LG:213947.1:2001JUN22	249	283	forward 1	TM	Non-Cytosolic
105	LG:213947.1:2001JUN22	1	14	forward 2	TM	Non-Cytosolic
105	LG:213947.1:2001JUN22	15	37	forward 2	TM	Transmembrane
105	LG:213947.1:2001JUN22	38	207	forward 2	TM	Cytosolic
105	LG:213947.1:2001JUN22	208	230	forward 2	TM	Transmembrane
105	LG:213947.1:2001JUN22	231	239	forward 2	TM	Non-Cytosolic
105	LG:213947.1:2001JUN22	240	262	forward 2	TM	Transmembrane
105	LG:213947.1:2001JUN22	263	283	forward 2	TM	Cytosolic
107	LG:300009.1:2001JUN22	1	389	forward 1	TM	Non-Cytosolic
107	LG:300009.1:2001JUN22	390	412	forward 1	TM	Transmembrane
107	LG:300009.1:2001JUN22	413	416	forward 1	TM	Cytosolic
107	LG:300009.1:2001JUN22	1	295	forward 2	TM	Cytosolic
107	LG:300009.1:2001JUN22	296	318	forward 2	TM	Transmembrane
107	LG:300009.1:2001JUN22	319	345	forward 2	TM	Non-Cytosolic
107	LG:300009.1:2001JUN22	346	368	forward 2	TM	Transmembrane
107	LG:300009.1:2001JUN22	369	380	forward 2	TM	Cytosolic
107	LG:300009.1:2001JUN22	381	399	forward 2	TM	Transmembrane
107	LG:300009.1:2001JUN22	400	416	forward 2	TM	Non-Cytosolic
108	LG:411188.1:2001JUN22	1	499	forward 1	TM	Non-Cytosolic
108	LG:411188.1:2001JUN22	500	522	forward 1	TM	Transmembrane
108	LG:411188.1:2001JUN22	523	558	forward 1	TM	Cytosolic
108	LG:411188.1:2001JUN22	559	581	forward 1	TM	Transmembrane
108	LG:411188.1:2001JUN22	582	603	forward 1	TM	Non-Cytosolic
108	LG:411188.1:2001JUN22	604	626	forward 1	TM	Transmembrane
108	LG:411188.1:2001JUN22	627	632	forward 1	TM	Cytosolic
108	LG:411188.1:2001JUN22	633	655	forward 1	TM	Transmembrane
108	LG:411188.1:2001JUN22	656	955	forward 1	TM	Non-Cytosolic
108	LG:411188.1:2001JUN22	1	77	forward 2	TM	Non-Cytosolic
108	LG:411188.1:2001JUN22	78	100	forward 2	TM	Transmembrane
108	LG:411188.1:2001JUN22	101	441	forward 2	TM	Cytosolic
108	LG:411188.1:2001JUN22	442	464	forward 2	TM	Transmembrane
108	LG:411188.1:2001JUN22	465	502	forward 2	TM	Non-Cytosolic
108	LG:411188.1:2001JUN22	503	520	forward 2	TM	Transmembrane
108	LG:411188.1:2001JUN22	521	532	forward 2	TM	Cytosolic
108	LG:411188.1:2001JUN22	533	555	forward 2	TM	Transmembrane
108	LG:411188.1:2001JUN22	556	955	forward 2	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	1	941	forward 1	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	942	964	forward 1	TM	Transmembrane
109	LG:481295.21:2001JUN22	965	1022	forward 1	TM	Cytosolic
109	LG:481295.21:2001JUN22	1023	1042	forward 1	TM	Transmembrane
109	LG:481295.21:2001JUN22	1043	1046	forward 1	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	1047	1066	forward 1	TM	Transmembrane
109	LG:481295.21:2001JUN22	1067	1094	forward 1	TM	Cytosolic
109	LG:481295.21:2001JUN22	1095	1117	forward 1	TM	Transmembrane
109	LG:481295.21:2001JUN22	1118	1131	forward 1	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	1132	1154	forward 1	TM	Transmembrane
109	LG:481295.21:2001JUN22	1155	1417	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
109	LG:481295.21:2001JUN22	1418	1440	forward 1	TM	Transmembrane
109	LG:481295.21:2001JUN22	1441	1478	forward 1	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	1479	1501	forward 1	TM	Transmembrane
109	LG:481295.21:2001JUN22	1502	1659	forward 1	TM	Cytosolic
109	LG:481295.21:2001JUN22	1660	1677	forward 1	TM	Transmembrane
109	LG:481295.21:2001JUN22	1678	2257	forward 1	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	1	918	forward 2	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	919	941	forward 2	TM	Transmembrane
109	LG:481295.21:2001JUN22	942	945	forward 2	TM	Cytosolic
109	LG:481295.21:2001JUN22	946	968	forward 2	TM	Transmembrane
109	LG:481295.21:2001JUN22	969	1038	forward 2	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	1039	1061	forward 2	TM	Transmembrane
109	LG:481295.21:2001JUN22	1062	1080	forward 2	TM	Cytosolic
109	LG:481295.21:2001JUN22	1081	1103	forward 2	TM	Transmembrane
109	LG:481295.21:2001JUN22	1104	2000	forward 2	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	2001	2023	forward 2	TM	Transmembrane
109	LG:481295.21:2001JUN22	2024	2102	forward 2	TM	Cytosolic
109	LG:481295.21:2001JUN22	2103	2125	forward 2	TM	Transmembrane
109	LG:481295.21:2001JUN22	2126	2182	forward 2	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	2183	2202	forward 2	TM	Transmembrane
109	LG:481295.21:2001JUN22	2203	2257	forward 2	TM	Cytosolic
109	LG:481295.21:2001JUN22	1	938	forward 3	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	939	961	forward 3	TM	Transmembrane
109	LG:481295.21:2001JUN22	962	1082	forward 3	TM	Cytosolic
109	LG:481295.21:2001JUN22	1083	1105	forward 3	TM	Transmembrane
109	LG:481295.21:2001JUN22	1106	1418	forward 3	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	1419	1441	forward 3	TM	Transmembrane
109	LG:481295.21:2001JUN22	1442	1467	forward 3	TM	Cytosolic
109	LG:481295.21:2001JUN22	1468	1485	forward 3	TM	Transmembrane
109	LG:481295.21:2001JUN22	1486	2110	forward 3	TM	Non-Cytosolic
109	LG:481295.21:2001JUN22	2111	2133	forward 3	TM	Transmembrane
109	LG:481295.21:2001JUN22	2134	2257	forward 3	TM	Cytosolic
111	LG:7690928.6:2001JUN22	1	39	forward 3	TM	Non-Cytosolic
111	LG:7690928.6:2001JUN22	40	62	forward 3	TM	Transmembrane
111	LG:7690928.6:2001JUN22	63	228	forward 3	TM	Cytosolic
112	LG:990040.8:2001JUN22	1	1376	forward 1	TM	Non-Cytosolic
112	LG:990040.8:2001JUN22	1377	1399	forward 1	TM	Transmembrane
112	LG:990040.8:2001JUN22	1400	1549	forward 1	TM	Cytosolic
112	LG:990040.8:2001JUN22	1550	1569	forward 1	TM	Transmembrane
112	LG:990040.8:2001JUN22	1570	1583	forward 1	TM	Non-Cytosolic
112	LG:990040.8:2001JUN22	1584	1606	forward 1	TM	Transmembrane
112	LG:990040.8:2001JUN22	1607	1653	forward 1	TM	Cytosolic
112	LG:990040.8:2001JUN22	1	1096	forward 2	TM	Non-Cytosolic
112	LG:990040.8:2001JUN22	1097	1114	forward 2	TM	Transmembrane
112	LG:990040.8:2001JUN22	1115	1120	forward 2	TM	Cytosolic
112	LG:990040.8:2001JUN22	1121	1143	forward 2	TM	Transmembrane
112	LG:990040.8:2001JUN22	1144	1157	forward 2	TM	Non-Cytosolic
112	LG:990040.8:2001JUN22	1158	1175	forward 2	TM	Transmembrane
112	LG:990040.8:2001JUN22	1176	1286	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
112	LG:990040.8:2001JUN22	1287	1309	forward 2	TM	Transmembrane
112	LG:990040.8:2001JUN22	1310	1546	forward 2	TM	Non-Cytosolic
112	LG:990040.8:2001JUN22	1547	1569	forward 2	TM	Transmembrane
112	LG:990040.8:2001JUN22	1570	1652	forward 2	TM	Cytosolic
112	LG:990040.8:2001JUN22	1	117	forward 3	TM	Cytosolic
112	LG:990040.8:2001JUN22	118	140	forward 3	TM	Transmembrane
112	LG:990040.8:2001JUN22	141	1123	forward 3	TM	Non-Cytosolic
112	LG:990040.8:2001JUN22	1124	1146	forward 3	TM	Transmembrane
112	LG:990040.8:2001JUN22	1147	1265	forward 3	TM	Cytosolic
112	LG:990040.8:2001JUN22	1266	1288	forward 3	TM	Transmembrane
112	LG:990040.8:2001JUN22	1289	1652	forward 3	TM	Non-Cytosolic
113	LG:126510.8:2001JUN22	17	88	forward 2	SP	
113	LG:126510.8:2001JUN22	1	275	forward 3	TM	Cytosolic
113	LG:126510.8:2001JUN22	276	298	forward 3	TM	Transmembrane
113	LG:126510.8:2001JUN22	299	343	forward 3	TM	Non-Cytosolic
113	LG:126510.8:2001JUN22	344	366	forward 3	TM	Transmembrane
113	LG:126510.8:2001JUN22	367	386	forward 3	TM	Cytosolic
113	LG:126510.8:2001JUN22	387	409	forward 3	TM	Transmembrane
113	LG:126510.8:2001JUN22	410	412	forward 3	TM	Non-Cytosolic
113	LG:126510.8:2001JUN22	413	435	forward 3	TM	Transmembrane
113	LG:126510.8:2001JUN22	436	765	forward 3	TM	Cytosolic
114	LG:7692710.8:2001JUN22	1	409	forward 2	TM	Cytosolic
114	LG:7692710.8:2001JUN22	410	429	forward 2	TM	Transmembrane
114	LG:7692710.8:2001JUN22	430	452	forward 2	TM	Non-Cytosolic
114	LG:7692710.8:2001JUN22	453	475	forward 2	TM	Transmembrane
114	LG:7692710.8:2001JUN22	476	486	forward 2	TM	Cytosolic
114	LG:7692710.8:2001JUN22	487	509	forward 2	TM	Transmembrane
114	LG:7692710.8:2001JUN22	510	523	forward 2	TM	Non-Cytosolic
114	LG:7692710.8:2001JUN22	524	546	forward 2	TM	Transmembrane
114	LG:7692710.8:2001JUN22	547	566	forward 2	TM	Cytosolic
114	LG:7692710.8:2001JUN22	567	589	forward 2	TM	Transmembrane
114	LG:7692710.8:2001JUN22	590	622	forward 2	TM	Non-Cytosolic
114	LG:7692710.8:2001JUN22	623	645	forward 2	TM	Transmembrane
114	LG:7692710.8:2001JUN22	646	665	forward 2	TM	Cytosolic
114	LG:7692710.8:2001JUN22	666	688	forward 2	TM	Transmembrane
114	LG:7692710.8:2001JUN22	689	936	forward 2	TM	Non-Cytosolic
114	LG:7692710.8:2001JUN22	1	86	forward 3	TM	Cytosolic
114	LG:7692710.8:2001JUN22	87	104	forward 3	TM	Transmembrane
114	LG:7692710.8:2001JUN22	105	113	forward 3	TM	Non-Cytosolic
114	LG:7692710.8:2001JUN22	114	133	forward 3	TM	Transmembrane
114	LG:7692710.8:2001JUN22	134	321	forward 3	TM	Cytosolic
114	LG:7692710.8:2001JUN22	322	344	forward 3	TM	Transmembrane
114	LG:7692710.8:2001JUN22	345	935	forward 3	TM	Non-Cytosolic
115	LG:044888.1:2001JUN22	1	240	forward 1	TM	Non-Cytosolic
115	LG:044888.1:2001JUN22	241	263	forward 1	TM	Transmembrane
115	LG:044888.1:2001JUN22	264	310	forward 1	TM	Cytosolic
115	LG:044888.1:2001JUN22	311	333	forward 1	TM	Transmembrane
115	LG:044888.1:2001JUN22	334	571	forward 1	TM	Non-Cytosolic
115	LG:044888.1:2001JUN22	1	204	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
115	LG:044888.1:2001JUN22	205	227	forward 2	TM	Transmembrane
115	LG:044888.1:2001JUN22	228	273	forward 2	TM	Cytosolic
115	LG:044888.1:2001JUN22	274	296	forward 2	TM	Transmembrane
115	LG:044888.1:2001JUN22	297	571	forward 2	TM	Non-Cytosolic
115	LG:044888.1:2001JUN22	1	12	forward 3	TM	Cytosolic
115	LG:044888.1:2001JUN22	13	35	forward 3	TM	Transmembrane
115	LG:044888.1:2001JUN22	36	571	forward 3	TM	Non-Cytosolic
116	LG:1447083.2:2001JUN22	1	129	forward 1	TM	Non-Cytosolic
116	LG:1447083.2:2001JUN22	130	152	forward 1	TM	Transmembrane
116	LG:1447083.2:2001JUN22	153	158	forward 1	TM	Cytosolic
116	LG:1447083.2:2001JUN22	159	181	forward 1	TM	Transmembrane
116	LG:1447083.2:2001JUN22	182	954	forward 1	TM	Non-Cytosolic
117	LG:7672289.1:2001JUN22	1	11	forward 1	TM	Cytosolic
117	LG:7672289.1:2001JUN22	12	29	forward 1	TM	Transmembrane
117	LG:7672289.1:2001JUN22	30	141	forward 1	TM	Non-Cytosolic
119	LG:1096667.17:2001MAR30	1	179	forward 1	TM	Non-Cytosolic
119	LG:1096667.17:2001MAR30	180	202	forward 1	TM	Transmembrane
119	LG:1096667.17:2001MAR30	203	404	forward 1	TM	Cytosolic
119	LG:1096667.17:2001MAR30	405	427	forward 1	TM	Transmembrane
119	LG:1096667.17:2001MAR30	428	462	forward 1	TM	Non-Cytosolic
119	LG:1096667.17:2001MAR30	463	485	forward 1	TM	Transmembrane
119	LG:1096667.17:2001MAR30	486	505	forward 1	TM	Cytosolic
119	LG:1096667.17:2001MAR30	506	528	forward 1	TM	Transmembrane
119	LG:1096667.17:2001MAR30	529	941	forward 1	TM	Non-Cytosolic
119	LG:1096667.17:2001MAR30	1	414	forward 2	TM	Non-Cytosolic
119	LG:1096667.17:2001MAR30	415	437	forward 2	TM	Transmembrane
119	LG:1096667.17:2001MAR30	438	515	forward 2	TM	Cytosolic
119	LG:1096667.17:2001MAR30	516	538	forward 2	TM	Transmembrane
119	LG:1096667.17:2001MAR30	539	940	forward 2	TM	Non-Cytosolic
119	LG:1096667.17:2001MAR30	1	400	forward 3	TM	Non-Cytosolic
119	LG:1096667.17:2001MAR30	401	423	forward 3	TM	Transmembrane
119	LG:1096667.17:2001MAR30	424	427	forward 3	TM	Cytosolic
119	LG:1096667.17:2001MAR30	428	450	forward 3	TM	Transmembrane
119	LG:1096667.17:2001MAR30	451	464	forward 3	TM	Non-Cytosolic
119	LG:1096667.17:2001MAR30	465	487	forward 3	TM	Transmembrane
119	LG:1096667.17:2001MAR30	488	493	forward 3	TM	Cytosolic
119	LG:1096667.17:2001MAR30	494	511	forward 3	TM	Transmembrane
119	LG:1096667.17:2001MAR30	512	515	forward 3	TM	Non-Cytosolic
119	LG:1096667.17:2001MAR30	516	538	forward 3	TM	Transmembrane
119	LG:1096667.17:2001MAR30	539	619	forward 3	TM	Cytosolic
119	LG:1096667.17:2001MAR30	620	639	forward 3	TM	Transmembrane
119	LG:1096667.17:2001MAR30	640	653	forward 3	TM	Non-Cytosolic
119	LG:1096667.17:2001MAR30	654	676	forward 3	TM	Transmembrane
119	LG:1096667.17:2001MAR30	677	870	forward 3	TM	Cytosolic
119	LG:1096667.17:2001MAR30	871	893	forward 3	TM	Transmembrane
119	LG:1096667.17:2001MAR30	894	940	forward 3	TM	Non-Cytosolic
120	LG:1270681.12:2001MAR30	1	447	forward 3	TM	Non-Cytosolic
120	LG:1270681.12:2001MAR30	448	470	forward 3	TM	Transmembrane
120	LG:1270681.12:2001MAR30	471	501	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
120	LG:1270681.12:2001MAR30	502	521	forward 3	TM	Transmembrane
120	LG:1270681.12:2001MAR30	522	907	forward 3	TM	Non-Cytosolic
121	LG:1328242.1:2001MAR30	1	1084	forward 1	TM	Non-Cytosolic
121	LG:1328242.1:2001MAR30	1085	1107	forward 1	TM	Transmembrane
121	LG:1328242.1:2001MAR30	1108	1127	forward 1	TM	Cytosolic
121	LG:1328242.1:2001MAR30	1128	1150	forward 1	TM	Transmembrane
121	LG:1328242.1:2001MAR30	1151	1159	forward 1	TM	Non-Cytosolic
121	LG:1328242.1:2001MAR30	1	1069	forward 2	TM	Non-Cytosolic
121	LG:1328242.1:2001MAR30	1070	1092	forward 2	TM	Transmembrane
121	LG:1328242.1:2001MAR30	1093	1158	forward 2	TM	Cytosolic
121	LG:1328242.1:2001MAR30	1	1072	forward 3	TM	Non-Cytosolic
121	LG:1328242.1:2001MAR30	1073	1095	forward 3	TM	Transmembrane
121	LG:1328242.1:2001MAR30	1096	1158	forward 3	TM	Cytosolic
122	LG:1396586.4:2001MAR30	1	123	forward 2	TM	Non-Cytosolic
122	LG:1396586.4:2001MAR30	124	146	forward 2	TM	Transmembrane
122	LG:1396586.4:2001MAR30	147	158	forward 2	TM	Cytosolic
122	LG:1396586.4:2001MAR30	159	181	forward 2	TM	Transmembrane
122	LG:1396586.4:2001MAR30	182	252	forward 2	TM	Non-Cytosolic
122	LG:1396586.4:2001MAR30	253	275	forward 2	TM	Transmembrane
122	LG:1396586.4:2001MAR30	276	303	forward 2	TM	Cytosolic
122	LG:1396586.4:2001MAR30	1	67	forward 3	TM	Non-Cytosolic
122	LG:1396586.4:2001MAR30	68	90	forward 3	TM	Transmembrane
122	LG:1396586.4:2001MAR30	91	156	forward 3	TM	Cytosolic
122	LG:1396586.4:2001MAR30	157	179	forward 3	TM	Transmembrane
122	LG:1396586.4:2001MAR30	180	302	forward 3	TM	Non-Cytosolic
123	LG:1396919.6:2001MAR30	1	89	forward 1	TM	Cytosolic
125	LG:1450059.4:2001MAR30	1	94	forward 1	TM	Cytosolic
125	LG:1450059.4:2001MAR30	95	117	forward 1	TM	Transmembrane
125	LG:1450059.4:2001MAR30	118	621	forward 1	TM	Non-Cytosolic
125	LG:1450059.4:2001MAR30	622	644	forward 1	TM	Transmembrane
125	LG:1450059.4:2001MAR30	645	656	forward 1	TM	Cytosolic
125	LG:1450059.4:2001MAR30	657	675	forward 1	TM	Transmembrane
125	LG:1450059.4:2001MAR30	676	689	forward 1	TM	Non-Cytosolic
125	LG:1450059.4:2001MAR30	690	712	forward 1	TM	Transmembrane
125	LG:1450059.4:2001MAR30	713	815	forward 1	TM	Cytosolic
125	LG:1450059.4:2001MAR30	816	838	forward 1	TM	Transmembrane
125	LG:1450059.4:2001MAR30	839	932	forward 1	TM	Non-Cytosolic
125	LG:1450059.4:2001MAR30	933	955	forward 1	TM	Transmembrane
125	LG:1450059.4:2001MAR30	956	1134	forward 1	TM	Cytosolic
125	LG:1450059.4:2001MAR30	1	72	forward 2	TM	Cytosolic
125	LG:1450059.4:2001MAR30	73	95	forward 2	TM	Transmembrane
125	LG:1450059.4:2001MAR30	96	1134	forward 2	TM	Non-Cytosolic
125	LG:1450059.4:2001MAR30	1	86	forward 3	TM	Cytosolic
125	LG:1450059.4:2001MAR30	87	109	forward 3	TM	Transmembrane
125	LG:1450059.4:2001MAR30	110	546	forward 3	TM	Non-Cytosolic
125	LG:1450059.4:2001MAR30	547	569	forward 3	TM	Transmembrane
125	LG:1450059.4:2001MAR30	570	623	forward 3	TM	Cytosolic
125	LG:1450059.4:2001MAR30	624	646	forward 3	TM	Transmembrane
125	LG:1450059.4:2001MAR30	647	655	forward 3	TM	Non-Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
125	LG:1450059.4:2001MAR30	656	675	forward 3	TM	Transmembrane
125	LG:1450059.4:2001MAR30	676	681	forward 3	TM	Cytosolic
125	LG:1450059.4:2001MAR30	682	704	forward 3	TM	Transmembrane
125	LG:1450059.4:2001MAR30	705	1133	forward 3	TM	Non-Cytosolic
126	LG:1503615.8:2001MAR30	1	733	forward 1	TM	Non-Cytosolic
126	LG:1503615.8:2001MAR30	734	756	forward 1	TM	Transmembrane
126	LG:1503615.8:2001MAR30	757	783	forward 1	TM	Cytosolic
126	LG:1503615.8:2001MAR30	784	806	forward 1	TM	Transmembrane
126	LG:1503615.8:2001MAR30	807	815	forward 1	TM	Non-Cytosolic
126	LG:1503615.8:2001MAR30	816	838	forward 1	TM	Transmembrane
126	LG:1503615.8:2001MAR30	839	842	forward 1	TM	Cytosolic
126	LG:1503615.8:2001MAR30	1	690	forward 2	TM	Non-Cytosolic
126	LG:1503615.8:2001MAR30	691	713	forward 2	TM	Transmembrane
126	LG:1503615.8:2001MAR30	714	733	forward 2	TM	Cytosolic
126	LG:1503615.8:2001MAR30	734	756	forward 2	TM	Transmembrane
126	LG:1503615.8:2001MAR30	757	787	forward 2	TM	Non-Cytosolic
126	LG:1503615.8:2001MAR30	788	807	forward 2	TM	Transmembrane
126	LG:1503615.8:2001MAR30	808	842	forward 2	TM	Cytosolic
126	LG:1503615.8:2001MAR30	1	741	forward 3	TM	Non-Cytosolic
126	LG:1503615.8:2001MAR30	742	764	forward 3	TM	Transmembrane
126	LG:1503615.8:2001MAR30	765	784	forward 3	TM	Cytosolic
126	LG:1503615.8:2001MAR30	785	804	forward 3	TM	Transmembrane
126	LG:1503615.8:2001MAR30	805	841	forward 3	TM	Non-Cytosolic
127	LG:1507027.3:2001MAR30	1	37	forward 1	TM	Cytosolic
127	LG:1507027.3:2001MAR30	38	60	forward 1	TM	Transmembrane
127	LG:1507027.3:2001MAR30	61	593	forward 1	TM	Non-Cytosolic
128	LG:202892.1:2001MAR30	1	25	forward 1	TM	Non-Cytosolic
128	LG:202892.1:2001MAR30	26	48	forward 1	TM	Transmembrane
128	LG:202892.1:2001MAR30	49	54	forward 1	TM	Cytosolic
128	LG:202892.1:2001MAR30	55	77	forward 1	TM	Transmembrane
128	LG:202892.1:2001MAR30	78	341	forward 1	TM	Non-Cytosolic
128	LG:202892.1:2001MAR30	342	364	forward 1	TM	Transmembrane
128	LG:202892.1:2001MAR30	365	370	forward 1	TM	Cytosolic
128	LG:202892.1:2001MAR30	371	393	forward 1	TM	Transmembrane
128	LG:202892.1:2001MAR30	394	687	forward 1	TM	Non-Cytosolic
128	LG:202892.1:2001MAR30	1	38	forward 2	TM	Non-Cytosolic
128	LG:202892.1:2001MAR30	39	61	forward 2	TM	Transmembrane
128	LG:202892.1:2001MAR30	62	65	forward 2	TM	Cytosolic
128	LG:202892.1:2001MAR30	66	88	forward 2	TM	Transmembrane
128	LG:202892.1:2001MAR30	89	97	forward 2	TM	Non-Cytosolic
128	LG:202892.1:2001MAR30	98	120	forward 2	TM	Transmembrane
128	LG:202892.1:2001MAR30	121	294	forward 2	TM	Cytosolic
128	LG:202892.1:2001MAR30	295	312	forward 2	TM	Transmembrane
128	LG:202892.1:2001MAR30	313	350	forward 2	TM	Non-Cytosolic
128	LG:202892.1:2001MAR30	351	373	forward 2	TM	Transmembrane
128	LG:202892.1:2001MAR30	374	470	forward 2	TM	Cytosolic
128	LG:202892.1:2001MAR30	471	493	forward 2	TM	Transmembrane
128	LG:202892.1:2001MAR30	494	687	forward 2	TM	Non-Cytosolic
129	LG:220407.3:2001MAR30	1	394	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
129	LG:220407.3:2001MAR30	395	417	forward 1	TM	Transmembrane
129	LG:220407.3:2001MAR30	418	459	forward 1	TM	Cytosolic
129	LG:220407.3:2001MAR30	460	482	forward 1	TM	Transmembrane
129	LG:220407.3:2001MAR30	483	2184	forward 1	TM	Non-Cytosolic
129	LG:220407.3:2001MAR30	1	391	forward 2	TM	Non-Cytosolic
129	LG:220407.3:2001MAR30	392	414	forward 2	TM	Transmembrane
129	LG:220407.3:2001MAR30	415	444	forward 2	TM	Cytosolic
129	LG:220407.3:2001MAR30	445	467	forward 2	TM	Transmembrane
129	LG:220407.3:2001MAR30	468	1413	forward 2	TM	Non-Cytosolic
129	LG:220407.3:2001MAR30	1414	1436	forward 2	TM	Transmembrane
129	LG:220407.3:2001MAR30	1437	1557	forward 2	TM	Cytosolic
129	LG:220407.3:2001MAR30	1558	1580	forward 2	TM	Transmembrane
129	LG:220407.3:2001MAR30	1581	2183	forward 2	TM	Non-Cytosolic
129	LG:220407.3:2001MAR30	1	391	forward 3	TM	Non-Cytosolic
129	LG:220407.3:2001MAR30	392	414	forward 3	TM	Transmembrane
129	LG:220407.3:2001MAR30	415	458	forward 3	TM	Cytosolic
129	LG:220407.3:2001MAR30	459	481	forward 3	TM	Transmembrane
129	LG:220407.3:2001MAR30	482	2183	forward 3	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	1	548	forward 1	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	549	571	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	572	632	forward 1	TM	Cytosolic
130	LG:242234.11:2001MAR30	633	652	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	653	666	forward 1	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	667	689	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	690	723	forward 1	TM	Cytosolic
130	LG:242234.11:2001MAR30	724	746	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	747	765	forward 1	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	766	788	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	789	808	forward 1	TM	Cytosolic
130	LG:242234.11:2001MAR30	809	825	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	826	920	forward 1	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	921	943	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	944	963	forward 1	TM	Cytosolic
130	LG:242234.11:2001MAR30	964	986	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	987	990	forward 1	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	991	1008	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	1009	1028	forward 1	TM	Cytosolic
130	LG:242234.11:2001MAR30	1029	1051	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	1052	1094	forward 1	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	1095	1117	forward 1	TM	Transmembrane
130	LG:242234.11:2001MAR30	1118	1300	forward 1	TM	Cytosolic
130	LG:242234.11:2001MAR30	1	632	forward 2	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	633	652	forward 2	TM	Transmembrane
130	LG:242234.11:2001MAR30	653	751	forward 2	TM	Cytosolic
130	LG:242234.11:2001MAR30	752	774	forward 2	TM	Transmembrane
130	LG:242234.11:2001MAR30	775	920	forward 2	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	921	943	forward 2	TM	Transmembrane
130	LG:242234.11:2001MAR30	944	1027	forward 2	TM	Cytosolic
130	LG:242234.11:2001MAR30	1028	1050	forward 2	TM	Transmembrane

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
130	LG:242234.11:2001MAR30	1051	1096	forward 2	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	1097	1119	forward 2	TM	Transmembrane
130	LG:242234.11:2001MAR30	1120	1125	forward 2	TM	Cytosolic
130	LG:242234.11:2001MAR30	1126	1148	forward 2	TM	Transmembrane
130	LG:242234.11:2001MAR30	1149	1167	forward 2	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	1168	1190	forward 2	TM	Transmembrane
130	LG:242234.11:2001MAR30	1191	1300	forward 2	TM	Cytosolic
130	LG:242234.11:2001MAR30	1	557	forward 3	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	558	580	forward 3	TM	Transmembrane
130	LG:242234.11:2001MAR30	581	631	forward 3	TM	Cytosolic
130	LG:242234.11:2001MAR30	632	654	forward 3	TM	Transmembrane
130	LG:242234.11:2001MAR30	655	722	forward 3	TM	Non-Cytosolic
130	LG:242234.11:2001MAR30	723	745	forward 3	TM	Transmembrane
130	LG:242234.11:2001MAR30	746	751	forward 3	TM	Cytosolic
130	LG:242234.11:2001MAR30	752	774	forward 3	TM	Transmembrane
130	LG:242234.11:2001MAR30	775	1299	forward 3	TM	Non-Cytosolic
131	LG:245181.20:2001MAR30	1	724	forward 1	TM	Non-Cytosolic
131	LG:245181.20:2001MAR30	725	747	forward 1	TM	Transmembrane
131	LG:245181.20:2001MAR30	748	759	forward 1	TM	Cytosolic
131	LG:245181.20:2001MAR30	760	782	forward 1	TM	Transmembrane
131	LG:245181.20:2001MAR30	783	936	forward 1	TM	Non-Cytosolic
133	LG:333965.2:2001MAR30	1	9	forward 1	TM	Non-Cytosolic
133	LG:333965.2:2001MAR30	10	32	forward 1	TM	Transmembrane
133	LG:333965.2:2001MAR30	33	111	forward 1	TM	Cytosolic
133	LG:333965.2:2001MAR30	112	134	forward 1	TM	Transmembrane
133	LG:333965.2:2001MAR30	135	603	forward 1	TM	Non-Cytosolic
133	LG:333965.2:2001MAR30	1	12	forward 2	TM	Cytosolic
133	LG:333965.2:2001MAR30	13	35	forward 2	TM	Transmembrane
133	LG:333965.2:2001MAR30	36	49	forward 2	TM	Non-Cytosolic
133	LG:333965.2:2001MAR30	50	72	forward 2	TM	Transmembrane
133	LG:333965.2:2001MAR30	73	112	forward 2	TM	Cytosolic
133	LG:333965.2:2001MAR30	113	135	forward 2	TM	Transmembrane
133	LG:333965.2:2001MAR30	136	602	forward 2	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	1	590	forward 1	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	591	613	forward 1	TM	Transmembrane
134	LG:402431.16:2001MAR30	614	707	forward 1	TM	Cytosolic
134	LG:402431.16:2001MAR30	708	730	forward 1	TM	Transmembrane
134	LG:402431.16:2001MAR30	731	749	forward 1	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	750	772	forward 1	TM	Transmembrane
134	LG:402431.16:2001MAR30	773	1052	forward 1	TM	Cytosolic
134	LG:402431.16:2001MAR30	1053	1075	forward 1	TM	Transmembrane
134	LG:402431.16:2001MAR30	1076	1136	forward 1	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	1137	1159	forward 1	TM	Transmembrane
134	LG:402431.16:2001MAR30	1160	1170	forward 1	TM	Cytosolic
134	LG:402431.16:2001MAR30	1171	1193	forward 1	TM	Transmembrane
134	LG:402431.16:2001MAR30	1194	1224	forward 1	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	1225	1247	forward 1	TM	Transmembrane
134	LG:402431.16:2001MAR30	1248	1410	forward 1	TM	Cytosolic
134	LG:402431.16:2001MAR30	1411	1428	forward 1	TM	Transmembrane

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
134	LG:402431.16:2001MAR30	1429	1437	forward 1	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	1438	1460	forward 1	TM	Transmembrane
134	LG:402431.16:2001MAR30	1461	1509	forward 1	TM	Cytosolic
134	LG:402431.16:2001MAR30	1510	1529	forward 1	TM	Transmembrane
134	LG:402431.16:2001MAR30	1530	1542	forward 1	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	1	172	forward 2	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	173	192	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	193	204	forward 2	TM	Cytosolic
134	LG:402431.16:2001MAR30	205	227	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	228	751	forward 2	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	752	774	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	775	786	forward 2	TM	Cytosolic
134	LG:402431.16:2001MAR30	787	809	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	810	846	forward 2	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	847	866	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	867	886	forward 2	TM	Cytosolic
134	LG:402431.16:2001MAR30	887	909	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	910	948	forward 2	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	949	971	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	972	1148	forward 2	TM	Cytosolic
134	LG:402431.16:2001MAR30	1149	1171	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	1172	1204	forward 2	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	1205	1227	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	1228	1339	forward 2	TM	Cytosolic
134	LG:402431.16:2001MAR30	1340	1358	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	1359	1435	forward 2	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	1436	1458	forward 2	TM	Transmembrane
134	LG:402431.16:2001MAR30	1459	1541	forward 2	TM	Cytosolic
134	LG:402431.16:2001MAR30	1	42	forward 3	TM	Cytosolic
134	LG:402431.16:2001MAR30	43	65	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	66	74	forward 3	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	75	94	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	95	160	forward 3	TM	Cytosolic
134	LG:402431.16:2001MAR30	161	183	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	184	202	forward 3	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	203	225	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	226	582	forward 3	TM	Cytosolic
134	LG:402431.16:2001MAR30	583	605	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	606	661	forward 3	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	662	684	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	685	690	forward 3	TM	Cytosolic
134	LG:402431.16:2001MAR30	691	713	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	714	748	forward 3	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	749	771	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	772	777	forward 3	TM	Cytosolic
134	LG:402431.16:2001MAR30	778	800	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	801	932	forward 3	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	933	955	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	956	967	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
134	LG:402431.16:2001MAR30	968	990	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	991	1015	forward 3	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	1016	1038	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	1039	1050	forward 3	TM	Cytosolic
134	LG:402431.16:2001MAR30	1051	1073	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	1074	1133	forward 3	TM	Non-Cytosolic
134	LG:402431.16:2001MAR30	1134	1156	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	1157	1162	forward 3	TM	Cytosolic
134	LG:402431.16:2001MAR30	1163	1185	forward 3	TM	Transmembrane
134	LG:402431.16:2001MAR30	1186	1541	forward 3	TM	Non-Cytosolic
137	LG:413797.14:2001MAR30	1	681	forward 1	TM	Non-Cytosolic
137	LG:413797.14:2001MAR30	682	704	forward 1	TM	Transmembrane
137	LG:413797.14:2001MAR30	705	950	forward 1	TM	Cytosolic
137	LG:413797.14:2001MAR30	951	973	forward 1	TM	Transmembrane
137	LG:413797.14:2001MAR30	974	981	forward 1	TM	Non-Cytosolic
137	LG:413797.14:2001MAR30	1	621	forward 3	TM	Non-Cytosolic
137	LG:413797.14:2001MAR30	622	644	forward 3	TM	Transmembrane
137	LG:413797.14:2001MAR30	645	743	forward 3	TM	Cytosolic
137	LG:413797.14:2001MAR30	744	766	forward 3	TM	Transmembrane
137	LG:413797.14:2001MAR30	767	981	forward 3	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	1	223	forward 1	TM	Cytosolic
138	LG:420527.51:2001MAR30	224	246	forward 1	TM	Transmembrane
138	LG:420527.51:2001MAR30	247	287	forward 1	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	288	310	forward 1	TM	Transmembrane
138	LG:420527.51:2001MAR30	311	354	forward 1	TM	Cytosolic
138	LG:420527.51:2001MAR30	355	377	forward 1	TM	Transmembrane
138	LG:420527.51:2001MAR30	378	419	forward 1	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	420	442	forward 1	TM	Transmembrane
138	LG:420527.51:2001MAR30	443	501	forward 1	TM	Cytosolic
138	LG:420527.51:2001MAR30	502	524	forward 1	TM	Transmembrane
138	LG:420527.51:2001MAR30	525	566	forward 1	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	567	589	forward 1	TM	Transmembrane
138	LG:420527.51:2001MAR30	590	800	forward 1	TM	Cytosolic
138	LG:420527.51:2001MAR30	801	820	forward 1	TM	Transmembrane
138	LG:420527.51:2001MAR30	821	834	forward 1	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	835	854	forward 1	TM	Transmembrane
138	LG:420527.51:2001MAR30	855	860	forward 1	TM	Cytosolic
138	LG:420527.51:2001MAR30	861	883	forward 1	TM	Transmembrane
138	LG:420527.51:2001MAR30	884	897	forward 1	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	898	920	forward 1	TM	Transmembrane
138	LG:420527.51:2001MAR30	921	968	forward 1	TM	Cytosolic
138	LG:420527.51:2001MAR30	1	220	forward 2	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	221	243	forward 2	TM	Transmembrane
138	LG:420527.51:2001MAR30	244	275	forward 2	TM	Cytosolic
138	LG:420527.51:2001MAR30	276	298	forward 2	TM	Transmembrane
138	LG:420527.51:2001MAR30	299	500	forward 2	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	501	523	forward 2	TM	Transmembrane
138	LG:420527.51:2001MAR30	524	584	forward 2	TM	Cytosolic
138	LG:420527.51:2001MAR30	585	607	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
138	LG:420527.51:2001MAR30	608	668	forward 2	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	669	691	forward 2	TM	Transmembrane
138	LG:420527.51:2001MAR30	692	710	forward 2	TM	Cytosolic
138	LG:420527.51:2001MAR30	711	730	forward 2	TM	Transmembrane
138	LG:420527.51:2001MAR30	731	806	forward 2	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	807	829	forward 2	TM	Transmembrane
138	LG:420527.51:2001MAR30	830	849	forward 2	TM	Cytosolic
138	LG:420527.51:2001MAR30	850	869	forward 2	TM	Transmembrane
138	LG:420527.51:2001MAR30	870	888	forward 2	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	889	911	forward 2	TM	Transmembrane
138	LG:420527.51:2001MAR30	912	968	forward 2	TM	Cytosolic
138	LG:420527.51:2001MAR30	1	503	forward 3	TM	Non-Cytosolic
138	LG:420527.51:2001MAR30	504	526	forward 3	TM	Transmembrane
138	LG:420527.51:2001MAR30	527	967	forward 3	TM	Cytosolic
141	LG:418805.7:2001MAR30	1	1149	forward 1	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1150	1172	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	1173	1232	forward 1	TM	Cytosolic
141	LG:418805.7:2001MAR30	1233	1255	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	1256	1264	forward 1	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1265	1287	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	1288	1293	forward 1	TM	Cytosolic
141	LG:418805.7:2001MAR30	1294	1316	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	1317	1330	forward 1	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1331	1353	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	1354	1493	forward 1	TM	Cytosolic
141	LG:418805.7:2001MAR30	1494	1516	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	1517	1893	forward 1	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1894	1916	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	1917	1936	forward 1	TM	Cytosolic
141	LG:418805.7:2001MAR30	1937	1959	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	1960	1973	forward 1	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1974	1996	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	1997	2016	forward 1	TM	Cytosolic
141	LG:418805.7:2001MAR30	2017	2039	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	2040	2101	forward 1	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	2102	2124	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	2125	2293	forward 1	TM	Cytosolic
141	LG:418805.7:2001MAR30	2294	2316	forward 1	TM	Transmembrane
141	LG:418805.7:2001MAR30	2317	2745	forward 1	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1	1115	forward 2	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1116	1138	forward 2	TM	Transmembrane
141	LG:418805.7:2001MAR30	1139	1149	forward 2	TM	Cytosolic
141	LG:418805.7:2001MAR30	1150	1172	forward 2	TM	Transmembrane
141	LG:418805.7:2001MAR30	1173	1181	forward 2	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1182	1201	forward 2	TM	Transmembrane
141	LG:418805.7:2001MAR30	1202	1363	forward 2	TM	Cytosolic
141	LG:418805.7:2001MAR30	1364	1383	forward 2	TM	Transmembrane
141	LG:418805.7:2001MAR30	1384	1846	forward 2	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1847	1869	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
141	LG:418805.7:2001MAR30	1870	1902	forward 2	TM	Cytosolic
141	LG:418805.7:2001MAR30	1903	1925	forward 2	TM	Transmembrane
141	LG:418805.7:2001MAR30	1926	1974	forward 2	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1975	1997	forward 2	TM	Transmembrane
141	LG:418805.7:2001MAR30	1998	2095	forward 2	TM	Cytosolic
141	LG:418805.7:2001MAR30	2096	2118	forward 2	TM	Transmembrane
141	LG:418805.7:2001MAR30	2119	2744	forward 2	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1	520	forward 3	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	521	543	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	544	555	forward 3	TM	Cytosolic
141	LG:418805.7:2001MAR30	556	578	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	579	654	forward 3	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	655	674	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	675	1027	forward 3	TM	Cytosolic
141	LG:418805.7:2001MAR30	1028	1045	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	1046	1059	forward 3	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1060	1077	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	1078	1119	forward 3	TM	Cytosolic
141	LG:418805.7:2001MAR30	1120	1142	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	1143	1156	forward 3	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1157	1179	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	1180	1185	forward 3	TM	Cytosolic
141	LG:418805.7:2001MAR30	1186	1208	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	1209	1222	forward 3	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1223	1242	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	1243	1246	forward 3	TM	Cytosolic
141	LG:418805.7:2001MAR30	1247	1269	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	1270	1898	forward 3	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1899	1916	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	1917	1927	forward 3	TM	Cytosolic
141	LG:418805.7:2001MAR30	1928	1950	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	1951	1973	forward 3	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	1974	1996	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	1997	2127	forward 3	TM	Cytosolic
141	LG:418805.7:2001MAR30	2128	2150	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	2151	2164	forward 3	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	2165	2184	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	2185	2287	forward 3	TM	Cytosolic
141	LG:418805.7:2001MAR30	2288	2310	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	2311	2329	forward 3	TM	Non-Cytosolic
141	LG:418805.7:2001MAR30	2330	2352	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	2353	2363	forward 3	TM	Cytosolic
141	LG:418805.7:2001MAR30	2364	2386	forward 3	TM	Transmembrane
141	LG:418805.7:2001MAR30	2387	2744	forward 3	TM	Non-Cytosolic
143	LG:382911.1:2001MAR30	1	652	forward 1	TM	Non-Cytosolic
143	LG:382911.1:2001MAR30	653	675	forward 1	TM	Transmembrane
143	LG:382911.1:2001MAR30	676	859	forward 1	TM	Cytosolic
143	LG:382911.1:2001MAR30	860	882	forward 1	TM	Transmembrane
143	LG:382911.1:2001MAR30	883	896	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
143	LG:382911.1:2001MAR30	897	919	forward 1	TM	Transmembrane
143	LG:382911.1:2001MAR30	920	967	forward 1	TM	Cytosolic
143	LG:382911.1:2001MAR30	968	990	forward 1	TM	Transmembrane
143	LG:382911.1:2001MAR30	991	1096	forward 1	TM	Non-Cytosolic
143	LG:382911.1:2001MAR30	1097	1116	forward 1	TM	Transmembrane
143	LG:382911.1:2001MAR30	1117	1153	forward 1	TM	Cytosolic
143	LG:382911.1:2001MAR30	1154	1176	forward 1	TM	Transmembrane
143	LG:382911.1:2001MAR30	1177	2108	forward 1	TM	Non-Cytosolic
143	LG:382911.1:2001MAR30	1	864	forward 2	TM	Non-Cytosolic
143	LG:382911.1:2001MAR30	865	884	forward 2	TM	Transmembrane
143	LG:382911.1:2001MAR30	885	896	forward 2	TM	Cytosolic
143	LG:382911.1:2001MAR30	897	919	forward 2	TM	Transmembrane
143	LG:382911.1:2001MAR30	920	2108	forward 2	TM	Non-Cytosolic
143	LG:382911.1:2001MAR30	1	864	forward 3	TM	Non-Cytosolic
143	LG:382911.1:2001MAR30	865	887	forward 3	TM	Transmembrane
143	LG:382911.1:2001MAR30	888	1151	forward 3	TM	Cytosolic
143	LG:382911.1:2001MAR30	1152	1174	forward 3	TM	Transmembrane
143	LG:382911.1:2001MAR30	1175	1785	forward 3	TM	Non-Cytosolic
143	LG:382911.1:2001MAR30	1786	1803	forward 3	TM	Transmembrane
143	LG:382911.1:2001MAR30	1804	1815	forward 3	TM	Cytosolic
143	LG:382911.1:2001MAR30	1816	1834	forward 3	TM	Transmembrane
143	LG:382911.1:2001MAR30	1835	1843	forward 3	TM	Non-Cytosolic
143	LG:382911.1:2001MAR30	1844	1861	forward 3	TM	Transmembrane
143	LG:382911.1:2001MAR30	1862	2045	forward 3	TM	Cytosolic
143	LG:382911.1:2001MAR30	2046	2068	forward 3	TM	Transmembrane
143	LG:382911.1:2001MAR30	2069	2077	forward 3	TM	Non-Cytosolic
143	LG:382911.1:2001MAR30	2078	2100	forward 3	TM	Transmembrane
143	LG:382911.1:2001MAR30	2101	2108	forward 3	TM	Cytosolic
146	LI:1073062.138:2001MAY17	1	232	forward 1	TM	Cytosolic
146	LI:1073062.138:2001MAY17	233	255	forward 1	TM	Transmembrane
146	LI:1073062.138:2001MAY17	256	274	forward 1	TM	Non-Cytosolic
146	LI:1073062.138:2001MAY17	275	294	forward 1	TM	Transmembrane
146	LI:1073062.138:2001MAY17	295	372	forward 1	TM	Cytosolic
146	LI:1073062.138:2001MAY17	373	392	forward 1	TM	Transmembrane
146	LI:1073062.138:2001MAY17	393	411	forward 1	TM	Non-Cytosolic
146	LI:1073062.138:2001MAY17	412	434	forward 1	TM	Transmembrane
146	LI:1073062.138:2001MAY17	435	509	forward 1	TM	Cytosolic
146	LI:1073062.138:2001MAY17	1	231	forward 2	TM	Cytosolic
146	LI:1073062.138:2001MAY17	232	254	forward 2	TM	Transmembrane
146	LI:1073062.138:2001MAY17	255	273	forward 2	TM	Non-Cytosolic
146	LI:1073062.138:2001MAY17	274	296	forward 2	TM	Transmembrane
146	LI:1073062.138:2001MAY17	297	316	forward 2	TM	Cytosolic
146	LI:1073062.138:2001MAY17	317	339	forward 2	TM	Transmembrane
146	LI:1073062.138:2001MAY17	340	342	forward 2	TM	Non-Cytosolic
146	LI:1073062.138:2001MAY17	343	365	forward 2	TM	Transmembrane
146	LI:1073062.138:2001MAY17	366	376	forward 2	TM	Cytosolic
146	LI:1073062.138:2001MAY17	377	399	forward 2	TM	Transmembrane
146	LI:1073062.138:2001MAY17	400	413	forward 2	TM	Non-Cytosolic
146	LI:1073062.138:2001MAY17	414	436	forward 2	TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
146	U:1073062.138:2001MAY17	437	509	forward 2	TM	Cytosolic
146	U:1073062.138:2001MAY17	1	228	forward 3	TM	Cytosolic
146	U:1073062.138:2001MAY17	229	251	forward 3	TM	Transmembrane
146	U:1073062.138:2001MAY17	252	279	forward 3	TM	Non-Cytosolic
146	U:1073062.138:2001MAY17	280	302	forward 3	TM	Transmembrane
146	U:1073062.138:2001MAY17	303	321	forward 3	TM	Cytosolic
146	U:1073062.138:2001MAY17	322	344	forward 3	TM	Transmembrane
146	U:1073062.138:2001MAY17	345	371	forward 3	TM	Non-Cytosolic
146	U:1073062.138:2001MAY17	372	394	forward 3	TM	Transmembrane
146	U:1073062.138:2001MAY17	395	413	forward 3	TM	Cytosolic
146	U:1073062.138:2001MAY17	414	436	forward 3	TM	Transmembrane
146	U:1073062.138:2001MAY17	437	483	forward 3	TM	Non-Cytosolic
146	U:1073062.138:2001MAY17	484	506	forward 3	TM	Transmembrane
146	U:1073062.138:2001MAY17	507	508	forward 3	TM	Cytosolic
147	U:1084954.7:2001MAY17	1	278	forward 1	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	279	296	forward 1	TM	Transmembrane
147	U:1084954.7:2001MAY17	297	361	forward 1	TM	Cytosolic
147	U:1084954.7:2001MAY17	362	384	forward 1	TM	Transmembrane
147	U:1084954.7:2001MAY17	385	418	forward 1	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	419	441	forward 1	TM	Transmembrane
147	U:1084954.7:2001MAY17	442	459	forward 1	TM	Cytosolic
147	U:1084954.7:2001MAY17	460	482	forward 1	TM	Transmembrane
147	U:1084954.7:2001MAY17	483	517	forward 1	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	518	540	forward 1	TM	Transmembrane
147	U:1084954.7:2001MAY17	541	577	forward 1	TM	Cytosolic
147	U:1084954.7:2001MAY17	578	597	forward 1	TM	Transmembrane
147	U:1084954.7:2001MAY17	598	606	forward 1	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	607	629	forward 1	TM	Transmembrane
147	U:1084954.7:2001MAY17	630	633	forward 1	TM	Cytosolic
147	U:1084954.7:2001MAY17	1	399	forward 2	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	400	422	forward 2	TM	Transmembrane
147	U:1084954.7:2001MAY17	423	428	forward 2	TM	Cytosolic
147	U:1084954.7:2001MAY17	429	451	forward 2	TM	Transmembrane
147	U:1084954.7:2001MAY17	452	465	forward 2	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	466	488	forward 2	TM	Transmembrane
147	U:1084954.7:2001MAY17	489	507	forward 2	TM	Cytosolic
147	U:1084954.7:2001MAY17	508	527	forward 2	TM	Transmembrane
147	U:1084954.7:2001MAY17	528	536	forward 2	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	537	559	forward 2	TM	Transmembrane
147	U:1084954.7:2001MAY17	560	571	forward 2	TM	Cytosolic
147	U:1084954.7:2001MAY17	572	594	forward 2	TM	Transmembrane
147	U:1084954.7:2001MAY17	595	606	forward 2	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	607	629	forward 2	TM	Transmembrane
147	U:1084954.7:2001MAY17	630	633	forward 2	TM	Cytosolic
147	U:1084954.7:2001MAY17	1	410	forward 3	TM	Cytosolic
147	U:1084954.7:2001MAY17	411	442	forward 3	TM	Transmembrane
147	U:1084954.7:2001MAY17	443	461	forward 3	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	462	484	forward 3	TM	Transmembrane
147	U:1084954.7:2001MAY17	485	504	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
147	U:1084954.7:2001MAY17	505	524	forward 3	TM	Transmembrane
147	U:1084954.7:2001MAY17	525	543	forward 3	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	544	566	forward 3	TM	Transmembrane
147	U:1084954.7:2001MAY17	567	577	forward 3	TM	Cytosolic
147	U:1084954.7:2001MAY17	578	600	forward 3	TM	Transmembrane
147	U:1084954.7:2001MAY17	601	609	forward 3	TM	Non-Cytosolic
147	U:1084954.7:2001MAY17	610	629	forward 3	TM	Transmembrane
147	U:1084954.7:2001MAY17	630	632	forward 3	TM	Cytosolic
148	U:202892.5:2001MAY17	1	316	forward 1	TM	Non-Cytosolic
148	U:202892.5:2001MAY17	317	339	forward 1	TM	Transmembrane
148	U:202892.5:2001MAY17	340	436	forward 1	TM	Cytosolic
148	U:202892.5:2001MAY17	437	459	forward 1	TM	Transmembrane
148	U:202892.5:2001MAY17	460	653	forward 1	TM	Non-Cytosolic
148	U:202892.5:2001MAY17	1	306	forward 3	TM	Non-Cytosolic
148	U:202892.5:2001MAY17	307	329	forward 3	TM	Transmembrane
148	U:202892.5:2001MAY17	330	335	forward 3	TM	Cytosolic
148	U:202892.5:2001MAY17	336	358	forward 3	TM	Transmembrane
148	U:202892.5:2001MAY17	359	652	forward 3	TM	Non-Cytosolic
149	U:2030686.1:2001MAY17	1	68	forward 1	TM	Cytosolic
149	U:2030686.1:2001MAY17	69	91	forward 1	TM	Transmembrane
149	U:2030686.1:2001MAY17	92	149	forward 1	TM	Non-Cytosolic
149	U:2030686.1:2001MAY17	150	169	forward 1	TM	Transmembrane
149	U:2030686.1:2001MAY17	170	393	forward 1	TM	Cytosolic
149	U:2030686.1:2001MAY17	394	416	forward 1	TM	Transmembrane
149	U:2030686.1:2001MAY17	417	430	forward 1	TM	Non-Cytosolic
149	U:2030686.1:2001MAY17	1	198	forward 2	TM	Cytosolic
149	U:2030686.1:2001MAY17	199	221	forward 2	TM	Transmembrane
149	U:2030686.1:2001MAY17	222	262	forward 2	TM	Non-Cytosolic
149	U:2030686.1:2001MAY17	263	285	forward 2	TM	Transmembrane
149	U:2030686.1:2001MAY17	286	430	forward 2	TM	Cytosolic
149	U:2030686.1:2001MAY17	1	147	forward 3	TM	Cytosolic
149	U:2030686.1:2001MAY17	148	170	forward 3	TM	Transmembrane
149	U:2030686.1:2001MAY17	171	429	forward 3	TM	Non-Cytosolic
150	U:2043289.10:2001MAY17	1	9	forward 1	TM	Non-Cytosolic
150	U:2043289.10:2001MAY17	10	32	forward 1	TM	Transmembrane
150	U:2043289.10:2001MAY17	33	97	forward 1	TM	Cytosolic
150	U:2043289.10:2001MAY17	98	120	forward 1	TM	Transmembrane
150	U:2043289.10:2001MAY17	121	165	forward 1	TM	Non-Cytosolic
150	U:2043289.10:2001MAY17	166	188	forward 1	TM	Transmembrane
150	U:2043289.10:2001MAY17	189	205	forward 1	TM	Cytosolic
152	U:2118901.10:2001MAY17	1	74	forward 3	TM	Non-Cytosolic
152	U:2118901.10:2001MAY17	75	94	forward 3	TM	Transmembrane
152	U:2118901.10:2001MAY17	95	131	forward 3	TM	Cytosolic
152	U:2118901.10:2001MAY17	132	154	forward 3	TM	Transmembrane
152	U:2118901.10:2001MAY17	155	200	forward 3	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	1	19	forward 1	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	20	42	forward 1	TM	Transmembrane
157	U:238414.1:2001MAY17	43	62	forward 1	TM	Cytosolic
157	U:238414.1:2001MAY17	63	85	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
157	U:238414.1:2001MAY17	86	99	forward 1	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	100	119	forward 1	TM	Transmembrane
157	U:238414.1:2001MAY17	120	259	forward 1	TM	Cytosolic
157	U:238414.1:2001MAY17	260	282	forward 1	TM	Transmembrane
157	U:238414.1:2001MAY17	283	411	forward 1	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	412	429	forward 1	TM	Transmembrane
157	U:238414.1:2001MAY17	430	483	forward 1	TM	Cytosolic
157	U:238414.1:2001MAY17	484	506	forward 1	TM	Transmembrane
157	U:238414.1:2001MAY17	507	961	forward 1	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	962	984	forward 1	TM	Transmembrane
157	U:238414.1:2001MAY17	985	1021	forward 1	TM	Cytosolic
157	U:238414.1:2001MAY17	1022	1044	forward 1	TM	Transmembrane
157	U:238414.1:2001MAY17	1045	1378	forward 1	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	1	14	forward 2	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	15	37	forward 2	TM	Transmembrane
157	U:238414.1:2001MAY17	38	142	forward 2	TM	Cytosolic
157	U:238414.1:2001MAY17	143	165	forward 2	TM	Transmembrane
157	U:238414.1:2001MAY17	166	243	forward 2	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	244	266	forward 2	TM	Transmembrane
157	U:238414.1:2001MAY17	267	286	forward 2	TM	Cytosolic
157	U:238414.1:2001MAY17	287	304	forward 2	TM	Transmembrane
157	U:238414.1:2001MAY17	305	323	forward 2	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	324	346	forward 2	TM	Transmembrane
157	U:238414.1:2001MAY17	347	434	forward 2	TM	Cytosolic
157	U:238414.1:2001MAY17	435	457	forward 2	TM	Transmembrane
157	U:238414.1:2001MAY17	458	469	forward 2	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	470	492	forward 2	TM	Transmembrane
157	U:238414.1:2001MAY17	493	717	forward 2	TM	Cytosolic
157	U:238414.1:2001MAY17	718	740	forward 2	TM	Transmembrane
157	U:238414.1:2001MAY17	741	1377	forward 2	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	1	14	forward 3	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	15	37	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	38	57	forward 3	TM	Cytosolic
157	U:238414.1:2001MAY17	58	80	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	81	101	forward 3	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	102	124	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	125	259	forward 3	TM	Cytosolic
157	U:238414.1:2001MAY17	260	282	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	283	323	forward 3	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	324	346	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	347	409	forward 3	TM	Cytosolic
157	U:238414.1:2001MAY17	410	432	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	433	435	forward 3	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	436	458	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	459	716	forward 3	TM	Cytosolic
157	U:238414.1:2001MAY17	717	739	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	740	820	forward 3	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	821	843	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	844	855	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
157	U:238414.1:2001MAY17	856	875	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	876	878	forward 3	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	879	901	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	902	912	forward 3	TM	Cytosolic
157	U:238414.1:2001MAY17	913	935	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	936	1027	forward 3	TM	Non-Cytosolic
157	U:238414.1:2001MAY17	1028	1050	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	1051	1062	forward 3	TM	Cytosolic
157	U:238414.1:2001MAY17	1063	1085	forward 3	TM	Transmembrane
157	U:238414.1:2001MAY17	1086	1377	forward 3	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	1	294	forward 1	TM	Cytosolic
158	U:242234.6:2001MAY17	295	314	forward 1	TM	Transmembrane
158	U:242234.6:2001MAY17	315	328	forward 1	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	329	351	forward 1	TM	Transmembrane
158	U:242234.6:2001MAY17	352	385	forward 1	TM	Cytosolic
158	U:242234.6:2001MAY17	386	408	forward 1	TM	Transmembrane
158	U:242234.6:2001MAY17	409	427	forward 1	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	428	450	forward 1	TM	Transmembrane
158	U:242234.6:2001MAY17	451	470	forward 1	TM	Cytosolic
158	U:242234.6:2001MAY17	471	487	forward 1	TM	Transmembrane
158	U:242234.6:2001MAY17	488	582	forward 1	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	583	605	forward 1	TM	Transmembrane
158	U:242234.6:2001MAY17	606	625	forward 1	TM	Cytosolic
158	U:242234.6:2001MAY17	626	648	forward 1	TM	Transmembrane
158	U:242234.6:2001MAY17	649	652	forward 1	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	653	670	forward 1	TM	Transmembrane
158	U:242234.6:2001MAY17	671	690	forward 1	TM	Cytosolic
158	U:242234.6:2001MAY17	691	713	forward 1	TM	Transmembrane
158	U:242234.6:2001MAY17	714	756	forward 1	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	757	779	forward 1	TM	Transmembrane
158	U:242234.6:2001MAY17	780	962	forward 1	TM	Cytosolic
158	U:242234.6:2001MAY17	1	294	forward 2	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	295	314	forward 2	TM	Transmembrane
158	U:242234.6:2001MAY17	315	413	forward 2	TM	Cytosolic
158	U:242234.6:2001MAY17	414	436	forward 2	TM	Transmembrane
158	U:242234.6:2001MAY17	437	582	forward 2	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	583	605	forward 2	TM	Transmembrane
158	U:242234.6:2001MAY17	606	689	forward 2	TM	Cytosolic
158	U:242234.6:2001MAY17	690	712	forward 2	TM	Transmembrane
158	U:242234.6:2001MAY17	713	758	forward 2	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	759	781	forward 2	TM	Transmembrane
158	U:242234.6:2001MAY17	782	787	forward 2	TM	Cytosolic
158	U:242234.6:2001MAY17	788	810	forward 2	TM	Transmembrane
158	U:242234.6:2001MAY17	811	829	forward 2	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	830	852	forward 2	TM	Transmembrane
158	U:242234.6:2001MAY17	853	962	forward 2	TM	Cytosolic
158	U:242234.6:2001MAY17	1	88	forward 3	TM	Cytosolic
158	U:242234.6:2001MAY17	89	111	forward 3	TM	Transmembrane
158	U:242234.6:2001MAY17	112	219	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
158	U:242234.6:2001MAY17	220	242	forward 3	TM	Transmembrane
158	U:242234.6:2001MAY17	243	293	forward 3	TM	Cytosolic
158	U:242234.6:2001MAY17	294	316	forward 3	TM	Transmembrane
158	U:242234.6:2001MAY17	317	384	forward 3	TM	Non-Cytosolic
158	U:242234.6:2001MAY17	385	407	forward 3	TM	Transmembrane
158	U:242234.6:2001MAY17	408	413	forward 3	TM	Cytosolic
158	U:242234.6:2001MAY17	414	436	forward 3	TM	Transmembrane
158	U:242234.6:2001MAY17	437	961	forward 3	TM	Non-Cytosolic
159	U:245181.22:2001MAY17	1	848	forward 1	TM	Non-Cytosolic
159	U:245181.22:2001MAY17	849	871	forward 1	TM	Transmembrane
159	U:245181.22:2001MAY17	872	883	forward 1	TM	Cytosolic
159	U:245181.22:2001MAY17	884	906	forward 1	TM	Transmembrane
159	U:245181.22:2001MAY17	907	1062	forward 1	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	1	512	forward 1	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	513	535	forward 1	TM	Transmembrane
160	U:245474.13:2001MAY17	536	611	forward 1	TM	Cytosolic
160	U:245474.13:2001MAY17	612	634	forward 1	TM	Transmembrane
160	U:245474.13:2001MAY17	635	716	forward 1	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	717	739	forward 1	TM	Transmembrane
160	U:245474.13:2001MAY17	740	747	forward 1	TM	Cytosolic
160	U:245474.13:2001MAY17	748	770	forward 1	TM	Transmembrane
160	U:245474.13:2001MAY17	771	1236	forward 1	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	1237	1259	forward 1	TM	Transmembrane
160	U:245474.13:2001MAY17	1260	1369	forward 1	TM	Cytosolic
160	U:245474.13:2001MAY17	1370	1392	forward 1	TM	Transmembrane
160	U:245474.13:2001MAY17	1393	1565	forward 1	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	1	22	forward 2	TM	Cytosolic
160	U:245474.13:2001MAY17	23	45	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	46	580	forward 2	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	581	603	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	604	609	forward 2	TM	Cytosolic
160	U:245474.13:2001MAY17	610	632	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	633	719	forward 2	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	720	742	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	743	748	forward 2	TM	Cytosolic
160	U:245474.13:2001MAY17	749	771	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	772	870	forward 2	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	871	893	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	894	1036	forward 2	TM	Cytosolic
160	U:245474.13:2001MAY17	1037	1059	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	1060	1249	forward 2	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	1250	1272	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	1273	1283	forward 2	TM	Cytosolic
160	U:245474.13:2001MAY17	1284	1306	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	1307	1375	forward 2	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	1376	1398	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	1399	1495	forward 2	TM	Cytosolic
160	U:245474.13:2001MAY17	1496	1518	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	1519	1527	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
160	U:245474.13:2001MAY17	1528	1550	forward 2	TM	Transmembrane
160	U:245474.13:2001MAY17	1551	1565	forward 2	TM	Cytosolic
160	U:245474.13:2001MAY17	1	28	forward 3	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	29	51	forward 3	TM	Transmembrane
160	U:245474.13:2001MAY17	52	145	forward 3	TM	Cytosolic
160	U:245474.13:2001MAY17	146	168	forward 3	TM	Transmembrane
160	U:245474.13:2001MAY17	169	850	forward 3	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	851	873	forward 3	TM	Transmembrane
160	U:245474.13:2001MAY17	874	1189	forward 3	TM	Cytosolic
160	U:245474.13:2001MAY17	1190	1212	forward 3	TM	Transmembrane
160	U:245474.13:2001MAY17	1213	1231	forward 3	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	1232	1254	forward 3	TM	Transmembrane
160	U:245474.13:2001MAY17	1255	1452	forward 3	TM	Cytosolic
160	U:245474.13:2001MAY17	1453	1475	forward 3	TM	Transmembrane
160	U:245474.13:2001MAY17	1476	1489	forward 3	TM	Non-Cytosolic
160	U:245474.13:2001MAY17	1490	1512	forward 3	TM	Transmembrane
160	U:245474.13:2001MAY17	1513	1523	forward 3	TM	Cytosolic
160	U:245474.13:2001MAY17	1524	1546	forward 3	TM	Transmembrane
160	U:245474.13:2001MAY17	1547	1564	forward 3	TM	Non-Cytosolic
161	U:311661.1:2001MAY17	1	28	forward 1	TM	Non-Cytosolic
161	U:311661.1:2001MAY17	29	51	forward 1	TM	Transmembrane
161	U:311661.1:2001MAY17	52	138	forward 1	TM	Cytosolic
161	U:311661.1:2001MAY17	139	161	forward 1	TM	Transmembrane
161	U:311661.1:2001MAY17	162	170	forward 1	TM	Non-Cytosolic
161	U:311661.1:2001MAY17	171	190	forward 1	TM	Transmembrane
161	U:311661.1:2001MAY17	191	199	forward 1	TM	Cytosolic
161	U:311661.1:2001MAY17	1	28	forward 2	TM	Non-Cytosolic
161	U:311661.1:2001MAY17	29	51	forward 2	TM	Transmembrane
161	U:311661.1:2001MAY17	52	199	forward 2	TM	Cytosolic
163	U:337026.1:2001MAY17	1	238	forward 2	TM	Cytosolic
163	U:337026.1:2001MAY17	239	258	forward 2	TM	Transmembrane
163	U:337026.1:2001MAY17	259	267	forward 2	TM	Non-Cytosolic
163	U:337026.1:2001MAY17	268	290	forward 2	TM	Transmembrane
163	U:337026.1:2001MAY17	291	302	forward 2	TM	Cytosolic
163	U:337026.1:2001MAY17	303	325	forward 2	TM	Transmembrane
163	U:337026.1:2001MAY17	326	690	forward 2	TM	Non-Cytosolic
163	U:337026.1:2001MAY17	691	713	forward 2	TM	Transmembrane
163	U:337026.1:2001MAY17	714	899	forward 2	TM	Cytosolic
163	U:337026.1:2001MAY17	900	922	forward 2	TM	Transmembrane
163	U:337026.1:2001MAY17	923	932	forward 2	TM	Non-Cytosolic
163	U:337026.1:2001MAY17	1	244	forward 3	TM	Cytosolic
163	U:337026.1:2001MAY17	245	267	forward 3	TM	Transmembrane
163	U:337026.1:2001MAY17	268	300	forward 3	TM	Non-Cytosolic
163	U:337026.1:2001MAY17	301	323	forward 3	TM	Transmembrane
163	U:337026.1:2001MAY17	324	371	forward 3	TM	Cytosolic
163	U:337026.1:2001MAY17	372	391	forward 3	TM	Transmembrane
163	U:337026.1:2001MAY17	392	416	forward 3	TM	Non-Cytosolic
163	U:337026.1:2001MAY17	417	439	forward 3	TM	Transmembrane
163	U:337026.1:2001MAY17	440	451	forward 3	TM	Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
163	LI:337026.1:2001MAY17	452	469	forward 3	TM	Transmembrane
163	LI:337026.1:2001MAY17	470	931	forward 3	TM	Non-Cytosolic
164	LI:347977.10:2001MAY17	1	804	forward 2	TM	Non-Cytosolic
164	LI:347977.10:2001MAY17	805	827	forward 2	TM	Transmembrane
164	LI:347977.10:2001MAY17	828	942	forward 2	TM	Cytosolic
164	LI:347977.10:2001MAY17	1	122	forward 3	TM	Cytosolic
164	LI:347977.10:2001MAY17	123	145	forward 3	TM	Transmembrane
164	LI:347977.10:2001MAY17	146	942	forward 3	TM	Non-Cytosolic
166	LI:467422.1:2001MAY17	1	209	forward 3	TM	Non-Cytosolic
166	LI:467422.1:2001MAY17	210	232	forward 3	TM	Transmembrane
166	LI:467422.1:2001MAY17	233	244	forward 3	TM	Cytosolic
166	LI:467422.1:2001MAY17	245	267	forward 3	TM	Transmembrane
166	LI:467422.1:2001MAY17	268	276	forward 3	TM	Non-Cytosolic
166	LI:467422.1:2001MAY17	277	299	forward 3	TM	Transmembrane
166	LI:467422.1:2001MAY17	300	332	forward 3	TM	Cytosolic
166	LI:467422.1:2001MAY17	333	355	forward 3	TM	Transmembrane
166	LI:467422.1:2001MAY17	356	750	forward 3	TM	Non-Cytosolic
167	LI:474596.53:2001MAY17	1	1191	forward 1	TM	Non-Cytosolic
167	LI:474596.53:2001MAY17	1192	1214	forward 1	TM	Transmembrane
167	LI:474596.53:2001MAY17	1215	1234	forward 1	TM	Cytosolic
167	LI:474596.53:2001MAY17	1235	1257	forward 1	TM	Transmembrane
167	LI:474596.53:2001MAY17	1258	1375	forward 1	TM	Non-Cytosolic
167	LI:474596.53:2001MAY17	1	1198	forward 3	TM	Non-Cytosolic
167	LI:474596.53:2001MAY17	1199	1221	forward 3	TM	Transmembrane
167	LI:474596.53:2001MAY17	1222	1233	forward 3	TM	Cytosolic
167	LI:474596.53:2001MAY17	1234	1253	forward 3	TM	Transmembrane
167	LI:474596.53:2001MAY17	1254	1374	forward 3	TM	Non-Cytosolic
168	LI:481144.22:2001MAY17	1	19	forward 1	TM	Non-Cytosolic
168	LI:481144.22:2001MAY17	20	42	forward 1	TM	Transmembrane
168	LI:481144.22:2001MAY17	43	479	forward 1	TM	Cytosolic
168	LI:481144.22:2001MAY17	480	502	forward 1	TM	Transmembrane
168	LI:481144.22:2001MAY17	503	511	forward 1	TM	Non-Cytosolic
168	LI:481144.22:2001MAY17	512	534	forward 1	TM	Transmembrane
168	LI:481144.22:2001MAY17	535	661	forward 1	TM	Cytosolic
168	LI:481144.22:2001MAY17	662	684	forward 1	TM	Transmembrane
168	LI:481144.22:2001MAY17	685	782	forward 1	TM	Non-Cytosolic
168	LI:481144.22:2001MAY17	783	805	forward 1	TM	Transmembrane
168	LI:481144.22:2001MAY17	806	864	forward 1	TM	Cytosolic
168	LI:481144.22:2001MAY17	865	887	forward 1	TM	Transmembrane
168	LI:481144.22:2001MAY17	888	1274	forward 1	TM	Non-Cytosolic
168	LI:481144.22:2001MAY17	1275	1297	forward 1	TM	Transmembrane
168	LI:481144.22:2001MAY17	1298	1309	forward 1	TM	Cytosolic
168	LI:481144.22:2001MAY17	1310	1329	forward 1	TM	Transmembrane
168	LI:481144.22:2001MAY17	1330	1423	forward 1	TM	Non-Cytosolic
168	LI:481144.22:2001MAY17	1424	1446	forward 1	TM	Transmembrane
168	LI:481144.22:2001MAY17	1447	1499	forward 1	TM	Cytosolic
168	LI:481144.22:2001MAY17	1500	1514	forward 1	TM	Transmembrane
168	LI:481144.22:2001MAY17	1515	1523	forward 1	TM	Non-Cytosolic
168	LI:481144.22:2001MAY17	1524	1543	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
168	U:481144.22:2001MAY17	1544	1633	forward 1	TM	Cytosolic
168	U:481144.22:2001MAY17	1634	1656	forward 1	TM	Transmembrane
168	U:481144.22:2001MAY17	1657	1660	forward 1	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	1661	1678	forward 1	TM	Transmembrane
168	U:481144.22:2001MAY17	1679	1682	forward 1	TM	Cytosolic
168	U:481144.22:2001MAY17	1683	1705	forward 1	TM	Transmembrane
168	U:481144.22:2001MAY17	1706	1713	forward 1	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	1	448	forward 2	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	449	471	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	472	482	forward 2	TM	Cytosolic
168	U:481144.22:2001MAY17	483	505	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	506	839	forward 2	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	840	862	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	863	866	forward 2	TM	Cytosolic
168	U:481144.22:2001MAY17	867	889	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	890	913	forward 2	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	914	936	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	937	974	forward 2	TM	Cytosolic
168	U:481144.22:2001MAY17	975	997	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	998	1322	forward 2	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	1323	1345	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	1346	1374	forward 2	TM	Cytosolic
168	U:481144.22:2001MAY17	1375	1397	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	1398	1433	forward 2	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	1434	1456	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	1457	1632	forward 2	TM	Cytosolic
168	U:481144.22:2001MAY17	1633	1652	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	1653	1671	forward 2	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	1672	1694	forward 2	TM	Transmembrane
168	U:481144.22:2001MAY17	1695	1713	forward 2	TM	Cytosolic
168	U:481144.22:2001MAY17	1	655	forward 3	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	656	678	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	679	818	forward 3	TM	Cytosolic
168	U:481144.22:2001MAY17	819	836	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	837	855	forward 3	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	856	878	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	879	919	forward 3	TM	Cytosolic
168	U:481144.22:2001MAY17	920	937	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	938	968	forward 3	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	969	991	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	992	1086	forward 3	TM	Cytosolic
168	U:481144.22:2001MAY17	1087	1109	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	1110	1118	forward 3	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	1119	1141	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	1142	1171	forward 3	TM	Cytosolic
168	U:481144.22:2001MAY17	1172	1191	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	1192	1272	forward 3	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	1273	1295	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	1296	1307	forward 3	TM	Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
168	U:481144.22:2001MAY17	1308	1330	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	1331	1680	forward 3	TM	Non-Cytosolic
168	U:481144.22:2001MAY17	1681	1703	forward 3	TM	Transmembrane
168	U:481144.22:2001MAY17	1704	1713	forward 3	TM	Cytosolic
171	U:815194.23:2001MAY17	1	587	forward 1	TM	Non-Cytosolic
171	U:815194.23:2001MAY17	588	610	forward 1	TM	Transmembrane
171	U:815194.23:2001MAY17	611	656	forward 1	TM	Cytosolic
171	U:815194.23:2001MAY17	657	676	forward 1	TM	Transmembrane
171	U:815194.23:2001MAY17	677	1326	forward 1	TM	Non-Cytosolic
171	U:815194.23:2001MAY17	1	1124	forward 2	TM	Non-Cytosolic
171	U:815194.23:2001MAY17	1125	1147	forward 2	TM	Transmembrane
171	U:815194.23:2001MAY17	1148	1153	forward 2	TM	Cytosolic
171	U:815194.23:2001MAY17	1154	1176	forward 2	TM	Transmembrane
171	U:815194.23:2001MAY17	1177	1225	forward 2	TM	Non-Cytosolic
171	U:815194.23:2001MAY17	1226	1248	forward 2	TM	Transmembrane
171	U:815194.23:2001MAY17	1249	1325	forward 2	TM	Cytosolic
171	U:815194.23:2001MAY17	1	1148	forward 3	TM	Non-Cytosolic
171	U:815194.23:2001MAY17	1149	1168	forward 3	TM	Transmembrane
171	U:815194.23:2001MAY17	1169	1210	forward 3	TM	Cytosolic
171	U:815194.23:2001MAY17	1211	1233	forward 3	TM	Transmembrane
171	U:815194.23:2001MAY17	1234	1279	forward 3	TM	Non-Cytosolic
171	U:815194.23:2001MAY17	1280	1302	forward 3	TM	Transmembrane
171	U:815194.23:2001MAY17	1303	1325	forward 3	TM	Cytosolic
172	U:817950.6:2001MAY17	1	445	forward 1	TM	Non-Cytosolic
172	U:817950.6:2001MAY17	446	468	forward 1	TM	Transmembrane
172	U:817950.6:2001MAY17	469	474	forward 1	TM	Cytosolic
172	U:817950.6:2001MAY17	475	497	forward 1	TM	Transmembrane
172	U:817950.6:2001MAY17	498	1019	forward 1	TM	Non-Cytosolic
172	U:817950.6:2001MAY17	1020	1042	forward 1	TM	Transmembrane
172	U:817950.6:2001MAY17	1043	1138	forward 1	TM	Cytosolic
172	U:817950.6:2001MAY17	1139	1161	forward 1	TM	Transmembrane
172	U:817950.6:2001MAY17	1162	1180	forward 1	TM	Non-Cytosolic
172	U:817950.6:2001MAY17	1181	1203	forward 1	TM	Transmembrane
172	U:817950.6:2001MAY17	1204	1209	forward 1	TM	Cytosolic
172	U:817950.6:2001MAY17	1210	1232	forward 1	TM	Transmembrane
172	U:817950.6:2001MAY17	1233	1300	forward 1	TM	Non-Cytosolic
172	U:817950.6:2001MAY17	1301	1323	forward 1	TM	Transmembrane
172	U:817950.6:2001MAY17	1324	1457	forward 1	TM	Cytosolic
172	U:817950.6:2001MAY17	1	55	forward 2	TM	Non-Cytosolic
172	U:817950.6:2001MAY17	56	78	forward 2	TM	Transmembrane
172	U:817950.6:2001MAY17	79	84	forward 2	TM	Cytosolic
172	U:817950.6:2001MAY17	85	107	forward 2	TM	Transmembrane
172	U:817950.6:2001MAY17	108	444	forward 2	TM	Non-Cytosolic
172	U:817950.6:2001MAY17	445	467	forward 2	TM	Transmembrane
172	U:817950.6:2001MAY17	468	471	forward 2	TM	Cytosolic
172	U:817950.6:2001MAY17	472	494	forward 2	TM	Transmembrane
172	U:817950.6:2001MAY17	495	1024	forward 2	TM	Non-Cytosolic
172	U:817950.6:2001MAY17	1025	1042	forward 2	TM	Transmembrane
172	U:817950.6:2001MAY17	1043	1177	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
172	U:817950.6:2001MAY17	1178	1200	forward 2	TM	Transmembrane
172	U:817950.6:2001MAY17	1201	1235	forward 2	TM	Non-Cytosolic
172	U:817950.6:2001MAY17	1236	1258	forward 2	TM	Transmembrane
172	U:817950.6:2001MAY17	1259	1456	forward 2	TM	Cytosolic
172	U:817950.6:2001MAY17	1	1300	forward 3	TM	Non-Cytosolic
172	U:817950.6:2001MAY17	1301	1323	forward 3	TM	Transmembrane
172	U:817950.6:2001MAY17	1324	1342	forward 3	TM	Cytosolic
172	U:817950.6:2001MAY17	1343	1365	forward 3	TM	Transmembrane
172	U:817950.6:2001MAY17	1366	1369	forward 3	TM	Non-Cytosolic
172	U:817950.6:2001MAY17	1370	1392	forward 3	TM	Transmembrane
172	U:817950.6:2001MAY17	1393	1404	forward 3	TM	Cytosolic
172	U:817950.6:2001MAY17	1405	1427	forward 3	TM	Transmembrane
172	U:817950.6:2001MAY17	1428	1456	forward 3	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1	151	forward 1	TM	Cytosolic
173	U:903485.6:2001MAY17	152	174	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	175	201	forward 1	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	202	224	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	225	243	forward 1	TM	Cytosolic
173	U:903485.6:2001MAY17	244	263	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	264	277	forward 1	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	278	300	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	301	446	forward 1	TM	Cytosolic
173	U:903485.6:2001MAY17	447	464	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	465	1283	forward 1	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1284	1306	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	1307	1386	forward 1	TM	Cytosolic
173	U:903485.6:2001MAY17	1387	1409	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	1410	1412	forward 1	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1413	1435	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	1436	1455	forward 1	TM	Cytosolic
173	U:903485.6:2001MAY17	1456	1478	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	1479	1507	forward 1	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1508	1530	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	1531	1661	forward 1	TM	Cytosolic
173	U:903485.6:2001MAY17	1662	1684	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	1685	1693	forward 1	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1694	1716	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	1717	1728	forward 1	TM	Cytosolic
173	U:903485.6:2001MAY17	1729	1751	forward 1	TM	Transmembrane
173	U:903485.6:2001MAY17	1752	2012	forward 1	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1	1411	forward 2	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1412	1431	forward 2	TM	Transmembrane
173	U:903485.6:2001MAY17	1432	1509	forward 2	TM	Cytosolic
173	U:903485.6:2001MAY17	1510	1532	forward 2	TM	Transmembrane
173	U:903485.6:2001MAY17	1533	1693	forward 2	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1694	1716	forward 2	TM	Transmembrane
173	U:903485.6:2001MAY17	1717	1727	forward 2	TM	Cytosolic
173	U:903485.6:2001MAY17	1728	1750	forward 2	TM	Transmembrane
173	U:903485.6:2001MAY17	1751	1759	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
173	U:903485.6:2001MAY17	1760	1778	forward 2	TM	Transmembrane
173	U:903485.6:2001MAY17	1779	1789	forward 2	TM	Cytosolic
173	U:903485.6:2001MAY17	1790	1812	forward 2	TM	Transmembrane
173	U:903485.6:2001MAY17	1813	1831	forward 2	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1832	1849	forward 2	TM	Transmembrane
173	U:903485.6:2001MAY17	1850	1869	forward 2	TM	Cytosolic
173	U:903485.6:2001MAY17	1870	1892	forward 2	TM	Transmembrane
173	U:903485.6:2001MAY17	1893	1944	forward 2	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1945	1962	forward 2	TM	Transmembrane
173	U:903485.6:2001MAY17	1963	1973	forward 2	TM	Cytosolic
173	U:903485.6:2001MAY17	1974	1996	forward 2	TM	Transmembrane
173	U:903485.6:2001MAY17	1997	2012	forward 2	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1	1408	forward 3	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1409	1431	forward 3	TM	Transmembrane
173	U:903485.6:2001MAY17	1432	1506	forward 3	TM	Cytosolic
173	U:903485.6:2001MAY17	1507	1529	forward 3	TM	Transmembrane
173	U:903485.6:2001MAY17	1530	1563	forward 3	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1564	1586	forward 3	TM	Transmembrane
173	U:903485.6:2001MAY17	1587	1606	forward 3	TM	Cytosolic
173	U:903485.6:2001MAY17	1607	1626	forward 3	TM	Transmembrane
173	U:903485.6:2001MAY17	1627	1693	forward 3	TM	Non-Cytosolic
173	U:903485.6:2001MAY17	1694	1713	forward 3	TM	Transmembrane
173	U:903485.6:2001MAY17	1714	1717	forward 3	TM	Cytosolic
173	U:903485.6:2001MAY17	1718	1740	forward 3	TM	Transmembrane
173	U:903485.6:2001MAY17	1741	2011	forward 3	TM	Non-Cytosolic
174	U:220407.8:2001MAY17	1	211	forward 1	TM	Non-Cytosolic
174	U:220407.8:2001MAY17	212	234	forward 1	TM	Transmembrane
174	U:220407.8:2001MAY17	235	276	forward 1	TM	Cytosolic
174	U:220407.8:2001MAY17	277	299	forward 1	TM	Transmembrane
174	U:220407.8:2001MAY17	300	1664	forward 1	TM	Non-Cytosolic
174	U:220407.8:2001MAY17	1665	1687	forward 1	TM	Transmembrane
174	U:220407.8:2001MAY17	1688	1698	forward 1	TM	Cytosolic
174	U:220407.8:2001MAY17	1699	1721	forward 1	TM	Transmembrane
174	U:220407.8:2001MAY17	1722	1996	forward 1	TM	Non-Cytosolic
174	U:220407.8:2001MAY17	1	208	forward 2	TM	Non-Cytosolic
174	U:220407.8:2001MAY17	209	231	forward 2	TM	Transmembrane
174	U:220407.8:2001MAY17	232	261	forward 2	TM	Cytosolic
174	U:220407.8:2001MAY17	262	284	forward 2	TM	Transmembrane
174	U:220407.8:2001MAY17	285	1230	forward 2	TM	Non-Cytosolic
174	U:220407.8:2001MAY17	1231	1253	forward 2	TM	Transmembrane
174	U:220407.8:2001MAY17	1254	1374	forward 2	TM	Cytosolic
174	U:220407.8:2001MAY17	1375	1397	forward 2	TM	Transmembrane
174	U:220407.8:2001MAY17	1398	1664	forward 2	TM	Non-Cytosolic
174	U:220407.8:2001MAY17	1665	1687	forward 2	TM	Transmembrane
174	U:220407.8:2001MAY17	1688	1693	forward 2	TM	Cytosolic
174	U:220407.8:2001MAY17	1694	1713	forward 2	TM	Transmembrane
174	U:220407.8:2001MAY17	1714	1996	forward 2	TM	Non-Cytosolic
174	U:220407.8:2001MAY17	1	208	forward 3	TM	Non-Cytosolic
174	U:220407.8:2001MAY17	209	231	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
174	U:220407.8:2001MAY17	232	275	forward 3	TM	Cytosolic
174	U:220407.8:2001MAY17	276	298	forward 3	TM	Transmembrane
174	U:220407.8:2001MAY17	299	1996	forward 3	TM	Non-Cytosolic
179	LG:113410.1:2001JUN22	1	176	forward 2	TM	Non-Cytosolic
179	LG:113410.1:2001JUN22	177	196	forward 2	TM	Transmembrane
179	LG:113410.1:2001JUN22	197	254	forward 2	TM	Cytosolic
181	LG:303607.15:2001JUN22	1	719	forward 1	TM	Non-Cytosolic
181	LG:303607.15:2001JUN22	720	742	forward 1	TM	Transmembrane
181	LG:303607.15:2001JUN22	743	762	forward 1	TM	Cytosolic
181	LG:303607.15:2001JUN22	763	785	forward 1	TM	Transmembrane
181	LG:303607.15:2001JUN22	786	788	forward 1	TM	Non-Cytosolic
181	LG:303607.15:2001JUN22	789	806	forward 1	TM	Transmembrane
181	LG:303607.15:2001JUN22	807	881	forward 1	TM	Cytosolic
181	LG:303607.15:2001JUN22	1	61	forward 2	TM	Non-Cytosolic
181	LG:303607.15:2001JUN22	62	84	forward 2	TM	Transmembrane
181	LG:303607.15:2001JUN22	85	104	forward 2	TM	Cytosolic
181	LG:303607.15:2001JUN22	105	124	forward 2	TM	Transmembrane
181	LG:303607.15:2001JUN22	125	133	forward 2	TM	Non-Cytosolic
181	LG:303607.15:2001JUN22	134	153	forward 2	TM	Transmembrane
181	LG:303607.15:2001JUN22	154	159	forward 2	TM	Cytosolic
181	LG:303607.15:2001JUN22	160	182	forward 2	TM	Transmembrane
181	LG:303607.15:2001JUN22	183	881	forward 2	TM	Non-Cytosolic
181	LG:303607.15:2001JUN22	1	159	forward 3	TM	Cytosolic
181	LG:303607.15:2001JUN22	160	182	forward 3	TM	Transmembrane
181	LG:303607.15:2001JUN22	183	495	forward 3	TM	Non-Cytosolic
181	LG:303607.15:2001JUN22	496	518	forward 3	TM	Transmembrane
181	LG:303607.15:2001JUN22	519	538	forward 3	TM	Cytosolic
181	LG:303607.15:2001JUN22	539	561	forward 3	TM	Transmembrane
181	LG:303607.15:2001JUN22	562	881	forward 3	TM	Non-Cytosolic
182	LG:411148.11:2001JUN22	1	483	forward 2	TM	Non-Cytosolic
182	LG:411148.11:2001JUN22	484	503	forward 2	TM	Transmembrane
182	LG:411148.11:2001JUN22	504	523	forward 2	TM	Cytosolic
182	LG:411148.11:2001JUN22	524	546	forward 2	TM	Transmembrane
182	LG:411148.11:2001JUN22	547	567	forward 2	TM	Non-Cytosolic
182	LG:411148.11:2001JUN22	1	485	forward 3	TM	Non-Cytosolic
182	LG:411148.11:2001JUN22	486	505	forward 3	TM	Transmembrane
182	LG:411148.11:2001JUN22	506	567	forward 3	TM	Cytosolic
186	LG:985139.2:2001JUN22	1	147	forward 1	TM	Cytosolic
186	LG:985139.2:2001JUN22	148	167	forward 1	TM	Transmembrane
186	LG:985139.2:2001JUN22	168	552	forward 1	TM	Non-Cytosolic
186	LG:985139.2:2001JUN22	1	147	forward 2	TM	Cytosolic
186	LG:985139.2:2001JUN22	148	170	forward 2	TM	Transmembrane
186	LG:985139.2:2001JUN22	171	552	forward 2	TM	Non-Cytosolic
186	LG:985139.2:2001JUN22	1	146	forward 3	TM	Cytosolic
186	LG:985139.2:2001JUN22	147	169	forward 3	TM	Transmembrane
186	LG:985139.2:2001JUN22	170	552	forward 3	TM	Non-Cytosolic
187	LG:149419.8:2001JUN22	1	132	forward 1	TM	Cytosolic
187	LG:149419.8:2001JUN22	133	155	forward 1	TM	Transmembrane
187	LG:149419.8:2001JUN22	156	164	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
187	LG:149419.8:2001JUN22	165	187	forward 1	TM	Transmembrane
187	LG:149419.8:2001JUN22	188	305	forward 1	TM	Cytosolic
187	LG:149419.8:2001JUN22	306	328	forward 1	TM	Transmembrane
187	LG:149419.8:2001JUN22	329	1177	forward 1	TM	Non-Cytosolic
187	LG:149419.8:2001JUN22	1178	1200	forward 1	TM	Transmembrane
187	LG:149419.8:2001JUN22	1201	1294	forward 1	TM	Cytosolic
187	LG:149419.8:2001JUN22	1	129	forward 2	TM	Non-Cytosolic
187	LG:149419.8:2001JUN22	130	147	forward 2	TM	Transmembrane
187	LG:149419.8:2001JUN22	148	159	forward 2	TM	Cytosolic
187	LG:149419.8:2001JUN22	160	182	forward 2	TM	Transmembrane
187	LG:149419.8:2001JUN22	183	1294	forward 2	TM	Non-Cytosolic
189	LG:256101.6:2001JUN22	1	289	forward 1	TM	Non-Cytosolic
189	LG:256101.6:2001JUN22	290	312	forward 1	TM	Transmembrane
189	LG:256101.6:2001JUN22	313	324	forward 1	TM	Cytosolic
189	LG:256101.6:2001JUN22	325	342	forward 1	TM	Transmembrane
189	LG:256101.6:2001JUN22	343	382	forward 1	TM	Non-Cytosolic
189	LG:256101.6:2001JUN22	1	273	forward 2	TM	Cytosolic
189	LG:256101.6:2001JUN22	274	296	forward 2	TM	Transmembrane
189	LG:256101.6:2001JUN22	297	334	forward 2	TM	Non-Cytosolic
189	LG:256101.6:2001JUN22	335	357	forward 2	TM	Transmembrane
189	LG:256101.6:2001JUN22	358	381	forward 2	TM	Cytosolic
190	LG:220407.3:2001JUN22	1	262	forward 1	TM	Cytosolic
190	LG:220407.3:2001JUN22	263	285	forward 1	TM	Transmembrane
190	LG:220407.3:2001JUN22	286	2184	forward 1	TM	Non-Cytosolic
190	LG:220407.3:2001JUN22	1	236	forward 3	TM	Non-Cytosolic
190	LG:220407.3:2001JUN22	237	259	forward 3	TM	Transmembrane
190	LG:220407.3:2001JUN22	260	270	forward 3	TM	Cytosolic
190	LG:220407.3:2001JUN22	271	293	forward 3	TM	Transmembrane
190	LG:220407.3:2001JUN22	294	2183	forward 3	TM	Non-Cytosolic
191	LG:331677.12:2001JUN22	1	1242	forward 1	TM	Non-Cytosolic
191	LG:331677.12:2001JUN22	1243	1265	forward 1	TM	Transmembrane
191	LG:331677.12:2001JUN22	1266	1266	forward 1	TM	Cytosolic
191	LG:331677.12:2001JUN22	1267	1289	forward 1	TM	Transmembrane
191	LG:331677.12:2001JUN22	1290	1556	forward 1	TM	Non-Cytosolic
191	LG:331677.12:2001JUN22	1	1242	forward 2	TM	Non-Cytosolic
191	LG:331677.12:2001JUN22	1243	1265	forward 2	TM	Transmembrane
191	LG:331677.12:2001JUN22	1266	1392	forward 2	TM	Cytosolic
191	LG:331677.12:2001JUN22	1393	1415	forward 2	TM	Transmembrane
191	LG:331677.12:2001JUN22	1416	1556	forward 2	TM	Non-Cytosolic
192	LG:367128.7:2001JUN22	1	286	forward 1	TM	Non-Cytosolic
192	LG:367128.7:2001JUN22	287	309	forward 1	TM	Transmembrane
192	LG:367128.7:2001JUN22	310	336	forward 1	TM	Cytosolic
192	LG:367128.7:2001JUN22	1	6	forward 3	TM	Cytosolic
192	LG:367128.7:2001JUN22	7	26	forward 3	TM	Transmembrane
192	LG:367128.7:2001JUN22	27	335	forward 3	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1	68	forward 1	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	69	91	forward 1	TM	Transmembrane
194	LG:985230.9:2001JUN22	92	95	forward 1	TM	Cytosolic
194	LG:985230.9:2001JUN22	96	118	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
194	LG:985230.9:2001JUN22	119	122	forward 1	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	123	140	forward 1	TM	Transmembrane
194	LG:985230.9:2001JUN22	141	152	forward 1	TM	Cytosolic
194	LG:985230.9:2001JUN22	153	175	forward 1	TM	Transmembrane
194	LG:985230.9:2001JUN22	176	1470	forward 1	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1	65	forward 2	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	66	88	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	89	100	forward 2	TM	Cytosolic
194	LG:985230.9:2001JUN22	101	123	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	124	789	forward 2	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	790	812	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	813	842	forward 2	TM	Cytosolic
194	LG:985230.9:2001JUN22	843	865	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	866	913	forward 2	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	914	936	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	937	1083	forward 2	TM	Cytosolic
194	LG:985230.9:2001JUN22	1084	1106	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	1107	1125	forward 2	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1126	1148	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	1149	1269	forward 2	TM	Cytosolic
194	LG:985230.9:2001JUN22	1270	1292	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	1293	1296	forward 2	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1297	1316	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	1317	1322	forward 2	TM	Cytosolic
194	LG:985230.9:2001JUN22	1323	1345	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	1346	1393	forward 2	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1394	1416	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	1417	1420	forward 2	TM	Cytosolic
194	LG:985230.9:2001JUN22	1421	1443	forward 2	TM	Transmembrane
194	LG:985230.9:2001JUN22	1444	1469	forward 2	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1	12	forward 3	TM	Cytosolic
194	LG:985230.9:2001JUN22	13	35	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	36	1047	forward 3	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1048	1067	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1068	1083	forward 3	TM	Cytosolic
194	LG:985230.9:2001JUN22	1084	1106	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1107	1127	forward 3	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1128	1150	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1151	1194	forward 3	TM	Cytosolic
194	LG:985230.9:2001JUN22	1195	1217	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1218	1226	forward 3	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1227	1246	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1247	1266	forward 3	TM	Cytosolic
194	LG:985230.9:2001JUN22	1267	1289	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1290	1298	forward 3	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1299	1318	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1319	1324	forward 3	TM	Cytosolic
194	LG:985230.9:2001JUN22	1325	1347	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1348	1350	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
194	LG:985230.9:2001JUN22	1351	1370	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1371	1390	forward 3	TM	Cytosolic
194	LG:985230.9:2001JUN22	1391	1408	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1409	1422	forward 3	TM	Non-Cytosolic
194	LG:985230.9:2001JUN22	1423	1445	forward 3	TM	Transmembrane
194	LG:985230.9:2001JUN22	1446	1469	forward 3	TM	Cytosolic
195	LG:005580.6:2001MAR30	1	429	forward 1	TM	Non-Cytosolic
195	LG:005580.6:2001MAR30	430	452	forward 1	TM	Transmembrane
195	LG:005580.6:2001MAR30	453	458	forward 1	TM	Cytosolic
195	LG:005580.6:2001MAR30	459	481	forward 1	TM	Transmembrane
195	LG:005580.6:2001MAR30	482	495	forward 1	TM	Non-Cytosolic
195	LG:005580.6:2001MAR30	496	513	forward 1	TM	Transmembrane
195	LG:005580.6:2001MAR30	514	558	forward 1	TM	Cytosolic
195	LG:005580.6:2001MAR30	1	391	forward 2	TM	Non-Cytosolic
195	LG:005580.6:2001MAR30	392	414	forward 2	TM	Transmembrane
195	LG:005580.6:2001MAR30	415	457	forward 2	TM	Cytosolic
195	LG:005580.6:2001MAR30	458	480	forward 2	TM	Transmembrane
195	LG:005580.6:2001MAR30	481	489	forward 2	TM	Non-Cytosolic
195	LG:005580.6:2001MAR30	490	512	forward 2	TM	Transmembrane
195	LG:005580.6:2001MAR30	513	558	forward 2	TM	Cytosolic
195	LG:005580.6:2001MAR30	1	391	forward 3	TM	Non-Cytosolic
195	LG:005580.6:2001MAR30	392	414	forward 3	TM	Transmembrane
195	LG:005580.6:2001MAR30	415	426	forward 3	TM	Cytosolic
195	LG:005580.6:2001MAR30	427	444	forward 3	TM	Transmembrane
195	LG:005580.6:2001MAR30	445	490	forward 3	TM	Non-Cytosolic
195	LG:005580.6:2001MAR30	491	513	forward 3	TM	Transmembrane
195	LG:005580.6:2001MAR30	514	558	forward 3	TM	Cytosolic
196	LG:100653.5:2001MAR30	1	384	forward 3	TM	Non-Cytosolic
196	LG:100653.5:2001MAR30	385	404	forward 3	TM	Transmembrane
196	LG:100653.5:2001MAR30	405	415	forward 3	TM	Cytosolic
196	LG:100653.5:2001MAR30	416	433	forward 3	TM	Transmembrane
196	LG:100653.5:2001MAR30	434	516	forward 3	TM	Non-Cytosolic
198	LG:117947.1:2001MAR30	1	364	forward 3	TM	Non-Cytosolic
198	LG:117947.1:2001MAR30	365	387	forward 3	TM	Transmembrane
198	LG:117947.1:2001MAR30	388	398	forward 3	TM	Cytosolic
198	LG:117947.1:2001MAR30	399	421	forward 3	TM	Transmembrane
198	LG:117947.1:2001MAR30	422	448	forward 3	TM	Non-Cytosolic
198	LG:117947.1:2001MAR30	449	471	forward 3	TM	Transmembrane
198	LG:117947.1:2001MAR30	472	483	forward 3	TM	Cytosolic
200	LG:1395721.9:2001MAR30	1	506	forward 1	TM	Non-Cytosolic
200	LG:1395721.9:2001MAR30	507	526	forward 1	TM	Transmembrane
200	LG:1395721.9:2001MAR30	527	537	forward 1	TM	Cytosolic
200	LG:1395721.9:2001MAR30	538	555	forward 1	TM	Transmembrane
200	LG:1395721.9:2001MAR30	556	727	forward 1	TM	Non-Cytosolic
201	LG:210508.1:2001MAR30	1	72	forward 1	TM	Cytosolic
201	LG:210508.1:2001MAR30	73	95	forward 1	TM	Transmembrane
201	LG:210508.1:2001MAR30	96	263	forward 1	TM	Non-Cytosolic
201	LG:210508.1:2001MAR30	264	286	forward 1	TM	Transmembrane
201	LG:210508.1:2001MAR30	287	310	forward 1	TM	Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
201	LG:210508.1:2001MAR30	311	333	forward 1	TM	Transmembrane
201	LG:210508.1:2001MAR30	334	355	forward 1	TM	Non-Cytosolic
201	LG:210508.1:2001MAR30	1	20	forward 2	TM	Cytosolic
201	LG:210508.1:2001MAR30	21	43	forward 2	TM	Transmembrane
201	LG:210508.1:2001MAR30	44	57	forward 2	TM	Non-Cytosolic
201	LG:210508.1:2001MAR30	58	80	forward 2	TM	Transmembrane
201	LG:210508.1:2001MAR30	81	354	forward 2	TM	Cytosolic
201	LG:210508.1:2001MAR30	1	246	forward 3	TM	Cytosolic
201	LG:210508.1:2001MAR30	247	269	forward 3	TM	Transmembrane
201	LG:210508.1:2001MAR30	270	313	forward 3	TM	Non-Cytosolic
201	LG:210508.1:2001MAR30	314	336	forward 3	TM	Transmembrane
201	LG:210508.1:2001MAR30	337	354	forward 3	TM	Cytosolic
202	LG:232313.46:2001MAR30	1	1016	forward 1	TM	Non-Cytosolic
202	LG:232313.46:2001MAR30	1017	1036	forward 1	TM	Transmembrane
202	LG:232313.46:2001MAR30	1037	1042	forward 1	TM	Cytosolic
202	LG:232313.46:2001MAR30	1043	1065	forward 1	TM	Transmembrane
202	LG:232313.46:2001MAR30	1066	1079	forward 1	TM	Non-Cytosolic
202	LG:232313.46:2001MAR30	1080	1102	forward 1	TM	Transmembrane
202	LG:232313.46:2001MAR30	1103	1146	forward 1	TM	Cytosolic
202	LG:232313.46:2001MAR30	1147	1169	forward 1	TM	Transmembrane
202	LG:232313.46:2001MAR30	1170	1181	forward 1	TM	Non-Cytosolic
202	LG:232313.46:2001MAR30	1	740	forward 3	TM	Non-Cytosolic
202	LG:232313.46:2001MAR30	741	763	forward 3	TM	Transmembrane
202	LG:232313.46:2001MAR30	764	888	forward 3	TM	Cytosolic
202	LG:232313.46:2001MAR30	889	911	forward 3	TM	Transmembrane
202	LG:232313.46:2001MAR30	912	1181	forward 3	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	1	618	forward 1	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	619	641	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	642	695	forward 1	TM	Cytosolic
203	LG:349746.22:2001MAR30	696	718	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	719	860	forward 1	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	861	883	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	884	939	forward 1	TM	Cytosolic
203	LG:349746.22:2001MAR30	940	962	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	963	971	forward 1	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	972	994	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	995	1024	forward 1	TM	Cytosolic
203	LG:349746.22:2001MAR30	1025	1047	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	1048	1061	forward 1	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	1062	1084	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	1085	1291	forward 1	TM	Cytosolic
203	LG:349746.22:2001MAR30	1292	1314	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	1315	1345	forward 1	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	1346	1368	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	1369	1576	forward 1	TM	Cytosolic
203	LG:349746.22:2001MAR30	1577	1599	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	1600	1656	forward 1	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	1657	1676	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	1677	1687	forward 1	TM	Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
203	LG:349746.22:2001MAR30	1688	1710	forward 1	TM	Transmembrane
203	LG:349746.22:2001MAR30	1711	2118	forward 1	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	1	827	forward 2	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	828	850	forward 2	TM	Transmembrane
203	LG:349746.22:2001MAR30	851	939	forward 2	TM	Cytosolic
203	LG:349746.22:2001MAR30	940	959	forward 2	TM	Transmembrane
203	LG:349746.22:2001MAR30	960	973	forward 2	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	974	996	forward 2	TM	Transmembrane
203	LG:349746.22:2001MAR30	997	1008	forward 2	TM	Cytosolic
203	LG:349746.22:2001MAR30	1009	1027	forward 2	TM	Transmembrane
203	LG:349746.22:2001MAR30	1028	1031	forward 2	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	1032	1049	forward 2	TM	Transmembrane
203	LG:349746.22:2001MAR30	1050	1061	forward 2	TM	Cytosolic
203	LG:349746.22:2001MAR30	1062	1084	forward 2	TM	Transmembrane
203	LG:349746.22:2001MAR30	1085	1766	forward 2	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	1767	1789	forward 2	TM	Transmembrane
203	LG:349746.22:2001MAR30	1790	1889	forward 2	TM	Cytosolic
203	LG:349746.22:2001MAR30	1890	1912	forward 2	TM	Transmembrane
203	LG:349746.22:2001MAR30	1913	2071	forward 2	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	2072	2094	forward 2	TM	Transmembrane
203	LG:349746.22:2001MAR30	2095	2118	forward 2	TM	Cytosolic
203	LG:349746.22:2001MAR30	1	616	forward 3	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	617	636	forward 3	TM	Transmembrane
203	LG:349746.22:2001MAR30	637	859	forward 3	TM	Cytosolic
203	LG:349746.22:2001MAR30	860	882	forward 3	TM	Transmembrane
203	LG:349746.22:2001MAR30	883	914	forward 3	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	915	937	forward 3	TM	Transmembrane
203	LG:349746.22:2001MAR30	938	960	forward 3	TM	Cytosolic
203	LG:349746.22:2001MAR30	961	983	forward 3	TM	Transmembrane
203	LG:349746.22:2001MAR30	984	1026	forward 3	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	1027	1049	forward 3	TM	Transmembrane
203	LG:349746.22:2001MAR30	1050	1282	forward 3	TM	Cytosolic
203	LG:349746.22:2001MAR30	1283	1305	forward 3	TM	Transmembrane
203	LG:349746.22:2001MAR30	1306	1892	forward 3	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	1893	1915	forward 3	TM	Transmembrane
203	LG:349746.22:2001MAR30	1916	1947	forward 3	TM	Cytosolic
203	LG:349746.22:2001MAR30	1948	1970	forward 3	TM	Transmembrane
203	LG:349746.22:2001MAR30	1971	2071	forward 3	TM	Non-Cytosolic
203	LG:349746.22:2001MAR30	2072	2094	forward 3	TM	Transmembrane
203	LG:349746.22:2001MAR30	2095	2118	forward 3	TM	Cytosolic
206	LG:440659.1:2001MAR30	1	164	forward 1	TM	Non-Cytosolic
206	LG:440659.1:2001MAR30	165	187	forward 1	TM	Transmembrane
206	LG:440659.1:2001MAR30	188	206	forward 1	TM	Cytosolic
207	LG:1081135.1:2001MAR30	1	349	forward 1	TM	Non-Cytosolic
207	LG:1081135.1:2001MAR30	350	372	forward 1	TM	Transmembrane
207	LG:1081135.1:2001MAR30	373	493	forward 1	TM	Cytosolic
207	LG:1081135.1:2001MAR30	494	516	forward 1	TM	Transmembrane
207	LG:1081135.1:2001MAR30	517	806	forward 1	TM	Non-Cytosolic
208	LG:1387341.2:2001MAR30	1	227	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
208	LG:1387341.2:2001MAR30	228	250	forward 1	TM	Transmembrane
208	LG:1387341.2:2001MAR30	251	270	forward 1	TM	Cytosolic
208	LG:1387341.2:2001MAR30	271	293	forward 1	TM	Transmembrane
208	LG:1387341.2:2001MAR30	294	339	forward 1	TM	Non-Cytosolic
208	LG:1387341.2:2001MAR30	340	359	forward 1	TM	Transmembrane
208	LG:1387341.2:2001MAR30	360	379	forward 1	TM	Cytosolic
208	LG:1387341.2:2001MAR30	380	399	forward 1	TM	Transmembrane
208	LG:1387341.2:2001MAR30	400	1094	forward 1	TM	Non-Cytosolic
208	LG:1387341.2:2001MAR30	1	119	forward 2	TM	Cytosolic
208	LG:1387341.2:2001MAR30	120	142	forward 2	TM	Transmembrane
208	LG:1387341.2:2001MAR30	143	182	forward 2	TM	Non-Cytosolic
208	LG:1387341.2:2001MAR30	183	202	forward 2	TM	Transmembrane
208	LG:1387341.2:2001MAR30	203	225	forward 2	TM	Cytosolic
208	LG:1387341.2:2001MAR30	226	248	forward 2	TM	Transmembrane
208	LG:1387341.2:2001MAR30	249	1093	forward 2	TM	Non-Cytosolic
209	LG:197915.17:2001MAR30	1	200	forward 3	TM	Cytosolic
209	LG:197915.17:2001MAR30	201	218	forward 3	TM	Transmembrane
209	LG:197915.17:2001MAR30	219	782	forward 3	TM	Non-Cytosolic
213	LI:233360.4:2001MAY17	1	259	forward 1	TM	Cytosolic
213	LI:233360.4:2001MAY17	260	282	forward 1	TM	Transmembrane
213	LI:233360.4:2001MAY17	283	291	forward 1	TM	Non-Cytosolic
213	LI:233360.4:2001MAY17	292	314	forward 1	TM	Transmembrane
213	LI:233360.4:2001MAY17	315	453	forward 1	TM	Cytosolic
213	LI:233360.4:2001MAY17	454	476	forward 1	TM	Transmembrane
213	LI:233360.4:2001MAY17	477	479	forward 1	TM	Non-Cytosolic
213	LI:233360.4:2001MAY17	480	502	forward 1	TM	Transmembrane
213	LI:233360.4:2001MAY17	503	514	forward 1	TM	Cytosolic
213	LI:233360.4:2001MAY17	515	537	forward 1	TM	Transmembrane
213	LI:233360.4:2001MAY17	538	562	forward 1	TM	Non-Cytosolic
213	LI:233360.4:2001MAY17	1	430	forward 2	TM	Non-Cytosolic
213	LI:233360.4:2001MAY17	431	449	forward 2	TM	Transmembrane
213	LI:233360.4:2001MAY17	450	453	forward 2	TM	Cytosolic
213	LI:233360.4:2001MAY17	454	476	forward 2	TM	Transmembrane
213	LI:233360.4:2001MAY17	477	485	forward 2	TM	Non-Cytosolic
213	LI:233360.4:2001MAY17	486	508	forward 2	TM	Transmembrane
213	LI:233360.4:2001MAY17	509	520	forward 2	TM	Cytosolic
213	LI:233360.4:2001MAY17	521	543	forward 2	TM	Transmembrane
213	LI:233360.4:2001MAY17	544	562	forward 2	TM	Non-Cytosolic
213	LI:233360.4:2001MAY17	1	296	forward 3	TM	Non-Cytosolic
213	LI:233360.4:2001MAY17	297	319	forward 3	TM	Transmembrane
213	LI:233360.4:2001MAY17	320	378	forward 3	TM	Cytosolic
213	LI:233360.4:2001MAY17	379	401	forward 3	TM	Transmembrane
213	LI:233360.4:2001MAY17	402	480	forward 3	TM	Non-Cytosolic
213	LI:233360.4:2001MAY17	481	503	forward 3	TM	Transmembrane
213	LI:233360.4:2001MAY17	504	562	forward 3	TM	Cytosolic
218	LG:1135945.19:2001JUN22	1	19	forward 1	TM	Cytosolic
218	LG:1135945.19:2001JUN22	20	42	forward 1	TM	Transmembrane
218	LG:1135945.19:2001JUN22	43	339	forward 1	TM	Non-Cytosolic
218	LG:1135945.19:2001JUN22	340	362	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
218	LG:1135945.19:2001JUN22	363	569	forward 1	TM	Cytosolic
218	LG:1135945.19:2001JUN22	1	19	forward 2	TM	Non-Cytosolic
218	LG:1135945.19:2001JUN22	20	42	forward 2	TM	Transmembrane
218	LG:1135945.19:2001JUN22	43	338	forward 2	TM	Cytosolic
218	LG:1135945.19:2001JUN22	339	361	forward 2	TM	Transmembrane
218	LG:1135945.19:2001JUN22	362	364	forward 2	TM	Non-Cytosolic
218	LG:1135945.19:2001JUN22	365	387	forward 2	TM	Transmembrane
218	LG:1135945.19:2001JUN22	388	407	forward 2	TM	Cytosolic
218	LG:1135945.19:2001JUN22	408	425	forward 2	TM	Transmembrane
218	LG:1135945.19:2001JUN22	426	428	forward 2	TM	Non-Cytosolic
218	LG:1135945.19:2001JUN22	429	448	forward 2	TM	Transmembrane
218	LG:1135945.19:2001JUN22	449	569	forward 2	TM	Cytosolic
218	LG:1135945.19:2001JUN22	1	309	forward 3	TM	Cytosolic
218	LG:1135945.19:2001JUN22	310	332	forward 3	TM	Transmembrane
218	LG:1135945.19:2001JUN22	333	346	forward 3	TM	Non-Cytosolic
218	LG:1135945.19:2001JUN22	347	369	forward 3	TM	Transmembrane
218	LG:1135945.19:2001JUN22	370	568	forward 3	TM	Cytosolic
221	LG:253987.9:2001JUN22	1	525	forward 1	TM	Non-Cytosolic
221	LG:253987.9:2001JUN22	526	545	forward 1	TM	Transmembrane
221	LG:253987.9:2001JUN22	546	556	forward 1	TM	Cytosolic
221	LG:253987.9:2001JUN22	557	579	forward 1	TM	Transmembrane
221	LG:253987.9:2001JUN22	580	1124	forward 1	TM	Non-Cytosolic
221	LG:253987.9:2001JUN22	1	47	forward 2	TM	Cytosolic
221	LG:253987.9:2001JUN22	48	70	forward 2	TM	Transmembrane
221	LG:253987.9:2001JUN22	71	1123	forward 2	TM	Non-Cytosolic
223	LG:7691137.1:2001JUN22	1	19	forward 3	TM	Non-Cytosolic
223	LG:7691137.1:2001JUN22	20	42	forward 3	TM	Transmembrane
223	LG:7691137.1:2001JUN22	43	358	forward 3	TM	Cytosolic
223	LG:7691137.1:2001JUN22	359	381	forward 3	TM	Transmembrane
223	LG:7691137.1:2001JUN22	382	403	forward 3	TM	Non-Cytosolic
225	LG:1088040.17:2001JUN22	1	1326	forward 3	TM	Non-Cytosolic
225	LG:1088040.17:2001JUN22	1327	1349	forward 3	TM	Transmembrane
225	LG:1088040.17:2001JUN22	1350	1652	forward 3	TM	Cytosolic
225	LG:1088040.17:2001JUN22	1653	1675	forward 3	TM	Transmembrane
225	LG:1088040.17:2001JUN22	1676	1696	forward 3	TM	Non-Cytosolic
225	LG:1088040.17:2001JUN22	1697	1714	forward 3	TM	Transmembrane
225	LG:1088040.17:2001JUN22	1715	1734	forward 3	TM	Cytosolic
225	LG:1088040.17:2001JUN22	1735	1757	forward 3	TM	Transmembrane
225	LG:1088040.17:2001JUN22	1758	2020	forward 3	TM	Non-Cytosolic
229	LG:276154.23:2001JUN22	1	858	forward 2	TM	Non-Cytosolic
229	LG:276154.23:2001JUN22	859	876	forward 2	TM	Transmembrane
229	LG:276154.23:2001JUN22	877	896	forward 2	TM	Cytosolic
229	LG:276154.23:2001JUN22	897	919	forward 2	TM	Transmembrane
229	LG:276154.23:2001JUN22	920	925	forward 2	TM	Non-Cytosolic
230	LG:332254.1:2001JUN22	1	382	forward 2	TM	Non-Cytosolic
230	LG:332254.1:2001JUN22	383	405	forward 2	TM	Transmembrane
230	LG:332254.1:2001JUN22	406	432	forward 2	TM	Cytosolic
230	LG:332254.1:2001JUN22	1	378	forward 3	TM	Non-Cytosolic
230	LG:332254.1:2001JUN22	379	401	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
230	LG:332254.1:2001JUN22	402	432	forward 3	TM	Cytosolic
232	LG:1064250.5:2001MAR30	1	1044	forward 3	TM	Non-Cytosolic
232	LG:1064250.5:2001MAR30	1045	1067	forward 3	TM	Transmembrane
232	LG:1064250.5:2001MAR30	1068	1153	forward 3	TM	Cytosolic
232	LG:1064250.5:2001MAR30	1154	1176	forward 3	TM	Transmembrane
232	LG:1064250.5:2001MAR30	1177	1507	forward 3	TM	Non-Cytosolic
233	LG:1065609.1:2001MAR30	1	181	forward 1	TM	Cytosolic
235	LG:1079476.6:2001MAR30	1	880	forward 3	TM	Non-Cytosolic
235	LG:1079476.6:2001MAR30	881	903	forward 3	TM	Transmembrane
235	LG:1079476.6:2001MAR30	904	930	forward 3	TM	Cytosolic
235	LG:1079476.6:2001MAR30	931	953	forward 3	TM	Transmembrane
235	LG:1079476.6:2001MAR30	954	981	forward 3	TM	Non-Cytosolic
235	LG:1079476.6:2001MAR30	982	1004	forward 3	TM	Transmembrane
235	LG:1079476.6:2001MAR30	1005	1025	forward 3	TM	Cytosolic
236	LG:1080579.9:2001MAR30	1	144	forward 1	TM	Non-Cytosolic
236	LG:1080579.9:2001MAR30	145	167	forward 1	TM	Transmembrane
236	LG:1080579.9:2001MAR30	168	173	forward 1	TM	Cytosolic
236	LG:1080579.9:2001MAR30	174	196	forward 1	TM	Transmembrane
236	LG:1080579.9:2001MAR30	197	243	forward 1	TM	Non-Cytosolic
236	LG:1080579.9:2001MAR30	244	263	forward 1	TM	Transmembrane
236	LG:1080579.9:2001MAR30	264	275	forward 1	TM	Cytosolic
236	LG:1080579.9:2001MAR30	1	148	forward 2	TM	Non-Cytosolic
236	LG:1080579.9:2001MAR30	149	171	forward 2	TM	Transmembrane
236	LG:1080579.9:2001MAR30	172	190	forward 2	TM	Cytosolic
236	LG:1080579.9:2001MAR30	191	213	forward 2	TM	Transmembrane
236	LG:1080579.9:2001MAR30	214	232	forward 2	TM	Non-Cytosolic
236	LG:1080579.9:2001MAR30	233	255	forward 2	TM	Transmembrane
236	LG:1080579.9:2001MAR30	256	275	forward 2	TM	Cytosolic
236	LG:1080579.9:2001MAR30	1	152	forward 3	TM	Non-Cytosolic
236	LG:1080579.9:2001MAR30	153	175	forward 3	TM	Transmembrane
236	LG:1080579.9:2001MAR30	176	226	forward 3	TM	Cytosolic
236	LG:1080579.9:2001MAR30	227	246	forward 3	TM	Transmembrane
236	LG:1080579.9:2001MAR30	247	275	forward 3	TM	Non-Cytosolic
237	LG:1082253.1:2001MAR30	1	270	forward 3	TM	Non-Cytosolic
237	LG:1082253.1:2001MAR30	271	293	forward 3	TM	Transmembrane
237	LG:1082253.1:2001MAR30	294	475	forward 3	TM	Cytosolic
238	LG:1082263.10:2001MAR30	1	246	forward 2	TM	Non-Cytosolic
238	LG:1082263.10:2001MAR30	247	264	forward 2	TM	Transmembrane
238	LG:1082263.10:2001MAR30	265	270	forward 2	TM	Cytosolic
238	LG:1082263.10:2001MAR30	271	293	forward 2	TM	Transmembrane
238	LG:1082263.10:2001MAR30	294	364	forward 2	TM	Non-Cytosolic
238	LG:1082263.10:2001MAR30	365	387	forward 2	TM	Transmembrane
238	LG:1082263.10:2001MAR30	388	390	forward 2	TM	Cytosolic
238	LG:1082263.10:2001MAR30	1	230	forward 3	TM	Non-Cytosolic
238	LG:1082263.10:2001MAR30	231	253	forward 3	TM	Transmembrane
238	LG:1082263.10:2001MAR30	254	390	forward 3	TM	Cytosolic
239	LG:1092343.1:2001MAR30	1	395	forward 3	TM	Non-Cytosolic
239	LG:1092343.1:2001MAR30	396	418	forward 3	TM	Transmembrane
239	LG:1092343.1:2001MAR30	419	422	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
242	LG:1384676.4:2001MAR30	1	287	forward 1	TM	Non-Cytosolic
242	LG:1384676.4:2001MAR30	288	310	forward 1	TM	Transmembrane
242	LG:1384676.4:2001MAR30	311	322	forward 1	TM	Cytosolic
242	LG:1384676.4:2001MAR30	323	340	forward 1	TM	Transmembrane
242	LG:1384676.4:2001MAR30	341	363	forward 1	TM	Non-Cytosolic
242	LG:1384676.4:2001MAR30	1	287	forward 3	TM	Non-Cytosolic
242	LG:1384676.4:2001MAR30	288	310	forward 3	TM	Transmembrane
242	LG:1384676.4:2001MAR30	311	326	forward 3	TM	Cytosolic
242	LG:1384676.4:2001MAR30	327	349	forward 3	TM	Transmembrane
242	LG:1384676.4:2001MAR30	350	363	forward 3	TM	Non-Cytosolic
245	LG:1500873.3:2001MAR30	1	1912	forward 1	TM	Non-Cytosolic
245	LG:1500873.3:2001MAR30	1913	1935	forward 1	TM	Transmembrane
245	LG:1500873.3:2001MAR30	1936	1974	forward 1	TM	Cytosolic
245	LG:1500873.3:2001MAR30	1975	1994	forward 1	TM	Transmembrane
245	LG:1500873.3:2001MAR30	1995	2003	forward 1	TM	Non-Cytosolic
245	LG:1500873.3:2001MAR30	2004	2026	forward 1	TM	Transmembrane
245	LG:1500873.3:2001MAR30	2027	2037	forward 1	TM	Cytosolic
245	LG:1500873.3:2001MAR30	2038	2060	forward 1	TM	Transmembrane
245	LG:1500873.3:2001MAR30	2061	2073	forward 1	TM	Non-Cytosolic
248	LG:208637.1:2001MAR30	1	625	forward 2	TM	Non-Cytosolic
248	LG:208637.1:2001MAR30	626	648	forward 2	TM	Transmembrane
248	LG:208637.1:2001MAR30	649	784	forward 2	TM	Cytosolic
248	LG:208637.1:2001MAR30	785	807	forward 2	TM	Transmembrane
248	LG:208637.1:2001MAR30	808	826	forward 2	TM	Non-Cytosolic
248	LG:208637.1:2001MAR30	827	849	forward 2	TM	Transmembrane
248	LG:208637.1:2001MAR30	850	879	forward 2	TM	Cytosolic
248	LG:208637.1:2001MAR30	880	902	forward 2	TM	Transmembrane
248	LG:208637.1:2001MAR30	903	921	forward 2	TM	Non-Cytosolic
248	LG:208637.1:2001MAR30	922	944	forward 2	TM	Transmembrane
248	LG:208637.1:2001MAR30	945	1058	forward 2	TM	Cytosolic
248	LG:208637.1:2001MAR30	1059	1081	forward 2	TM	Transmembrane
248	LG:208637.1:2001MAR30	1082	1113	forward 2	TM	Non-Cytosolic
248	LG:208637.1:2001MAR30	1114	1136	forward 2	TM	Transmembrane
248	LG:208637.1:2001MAR30	1137	1178	forward 2	TM	Cytosolic
248	LG:208637.1:2001MAR30	1179	1201	forward 2	TM	Transmembrane
248	LG:208637.1:2001MAR30	1202	1271	forward 2	TM	Non-Cytosolic
248	LG:208637.1:2001MAR30	1272	1294	forward 2	TM	Transmembrane
248	LG:208637.1:2001MAR30	1295	1310	forward 2	TM	Cytosolic
248	LG:208637.1:2001MAR30	1	913	forward 3	TM	Non-Cytosolic
248	LG:208637.1:2001MAR30	914	933	forward 3	TM	Transmembrane
248	LG:208637.1:2001MAR30	934	945	forward 3	TM	Cytosolic
248	LG:208637.1:2001MAR30	946	968	forward 3	TM	Transmembrane
248	LG:208637.1:2001MAR30	969	1012	forward 3	TM	Non-Cytosolic
248	LG:208637.1:2001MAR30	1013	1035	forward 3	TM	Transmembrane
248	LG:208637.1:2001MAR30	1036	1111	forward 3	TM	Cytosolic
248	LG:208637.1:2001MAR30	1112	1134	forward 3	TM	Transmembrane
248	LG:208637.1:2001MAR30	1135	1143	forward 3	TM	Non-Cytosolic
248	LG:208637.1:2001MAR30	1144	1161	forward 3	TM	Transmembrane
248	LG:208637.1:2001MAR30	1162	1244	forward 3	TM	Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
248	LG:208637.1:2001MAR30	1245	1267	forward 3	TM	Transmembrane
248	LG:208637.1:2001MAR30	1268	1281	forward 3	TM	Non-Cytosolic
248	LG:208637.1:2001MAR30	1282	1299	forward 3	TM	Transmembrane
248	LG:208637.1:2001MAR30	1300	1309	forward 3	TM	Cytosolic
249	LG:234936.67:2001MAR30	1	132	forward 2	TM	Cytosolic
249	LG:234936.67:2001MAR30	133	152	forward 2	TM	Transmembrane
249	LG:234936.67:2001MAR30	153	166	forward 2	TM	Non-Cytosolic
249	LG:234936.67:2001MAR30	167	186	forward 2	TM	Transmembrane
249	LG:234936.67:2001MAR30	187	419	forward 2	TM	Cytosolic
249	LG:234936.67:2001MAR30	420	442	forward 2	TM	Transmembrane
249	LG:234936.67:2001MAR30	443	678	forward 2	TM	Non-Cytosolic
250	LG:243305.3:2001MAR30	1	260	forward 2	TM	Non-Cytosolic
250	LG:243305.3:2001MAR30	261	283	forward 2	TM	Transmembrane
250	LG:243305.3:2001MAR30	284	335	forward 2	TM	Cytosolic
251	LG:334645.20:2001MAR30	1	6	forward 1	TM	Cytosolic
251	LG:334645.20:2001MAR30	7	29	forward 1	TM	Transmembrane
251	LG:334645.20:2001MAR30	30	43	forward 1	TM	Non-Cytosolic
251	LG:334645.20:2001MAR30	44	66	forward 1	TM	Transmembrane
251	LG:334645.20:2001MAR30	67	330	forward 1	TM	Cytosolic
251	LG:334645.20:2001MAR30	331	353	forward 1	TM	Transmembrane
251	LG:334645.20:2001MAR30	354	384	forward 1	TM	Non-Cytosolic
251	LG:334645.20:2001MAR30	385	407	forward 1	TM	Transmembrane
251	LG:334645.20:2001MAR30	408	427	forward 1	TM	Cytosolic
251	LG:334645.20:2001MAR30	428	450	forward 1	TM	Transmembrane
251	LG:334645.20:2001MAR30	451	469	forward 1	TM	Non-Cytosolic
251	LG:334645.20:2001MAR30	1	28	forward 2	TM	Non-Cytosolic
251	LG:334645.20:2001MAR30	29	51	forward 2	TM	Transmembrane
251	LG:334645.20:2001MAR30	52	283	forward 2	TM	Cytosolic
251	LG:334645.20:2001MAR30	284	303	forward 2	TM	Transmembrane
251	LG:334645.20:2001MAR30	304	332	forward 2	TM	Non-Cytosolic
251	LG:334645.20:2001MAR30	333	352	forward 2	TM	Transmembrane
251	LG:334645.20:2001MAR30	353	384	forward 2	TM	Cytosolic
251	LG:334645.20:2001MAR30	385	407	forward 2	TM	Transmembrane
251	LG:334645.20:2001MAR30	408	426	forward 2	TM	Non-Cytosolic
251	LG:334645.20:2001MAR30	427	449	forward 2	TM	Transmembrane
251	LG:334645.20:2001MAR30	450	468	forward 2	TM	Cytosolic
251	LG:334645.20:2001MAR30	1	3	forward 3	TM	Non-Cytosolic
251	LG:334645.20:2001MAR30	4	26	forward 3	TM	Transmembrane
251	LG:334645.20:2001MAR30	27	38	forward 3	TM	Cytosolic
251	LG:334645.20:2001MAR30	39	61	forward 3	TM	Transmembrane
251	LG:334645.20:2001MAR30	62	468	forward 3	TM	Non-Cytosolic
256	LG:404157.1:2001MAR30	1	845	forward 1	TM	Non-Cytosolic
256	LG:404157.1:2001MAR30	846	868	forward 1	TM	Transmembrane
256	LG:404157.1:2001MAR30	869	922	forward 1	TM	Cytosolic
256	LG:404157.1:2001MAR30	923	945	forward 1	TM	Transmembrane
256	LG:404157.1:2001MAR30	946	949	forward 1	TM	Non-Cytosolic
256	LG:404157.1:2001MAR30	950	972	forward 1	TM	Transmembrane
256	LG:404157.1:2001MAR30	973	981	forward 1	TM	Cytosolic
256	LG:404157.1:2001MAR30	1	836	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
256	LG:404157.1:2001MAR30	837	859	forward 2	TM	Transmembrane
256	LG:404157.1:2001MAR30	860	948	forward 2	TM	Cytosolic
256	LG:404157.1:2001MAR30	949	971	forward 2	TM	Transmembrane
256	LG:404157.1:2001MAR30	972	980	forward 2	TM	Non-Cytosolic
256	LG:404157.1:2001MAR30	1	503	forward 3	TM	Non-Cytosolic
256	LG:404157.1:2001MAR30	504	521	forward 3	TM	Transmembrane
256	LG:404157.1:2001MAR30	522	525	forward 3	TM	Cytosolic
256	LG:404157.1:2001MAR30	526	548	forward 3	TM	Transmembrane
256	LG:404157.1:2001MAR30	549	980	forward 3	TM	Non-Cytosolic
258	LG:981962.1:2001MAR30	1	338	forward 3	TM	Non-Cytosolic
258	LG:981962.1:2001MAR30	339	361	forward 3	TM	Transmembrane
258	LG:981962.1:2001MAR30	362	432	forward 3	TM	Cytosolic
258	LG:981962.1:2001MAR30	433	455	forward 3	TM	Transmembrane
258	LG:981962.1:2001MAR30	456	479	forward 3	TM	Non-Cytosolic
258	LG:981962.1:2001MAR30	480	502	forward 3	TM	Transmembrane
258	LG:981962.1:2001MAR30	503	513	forward 3	TM	Cytosolic
258	LG:981962.1:2001MAR30	514	536	forward 3	TM	Transmembrane
258	LG:981962.1:2001MAR30	537	550	forward 3	TM	Non-Cytosolic
258	LG:981962.1:2001MAR30	551	573	forward 3	TM	Transmembrane
258	LG:981962.1:2001MAR30	574	640	forward 3	TM	Cytosolic
260	LG:1448087.1:2001MAR30	1	102	forward 1	TM	Cytosolic
266	U:016933.2:2001MAY17	1	43	forward 1	TM	Cytosolic
266	U:016933.2:2001MAY17	44	66	forward 1	TM	Transmembrane
266	U:016933.2:2001MAY17	67	85	forward 1	TM	Non-Cytosolic
266	U:016933.2:2001MAY17	86	108	forward 1	TM	Transmembrane
266	U:016933.2:2001MAY17	109	112	forward 1	TM	Cytosolic
266	U:016933.2:2001MAY17	113	135	forward 1	TM	Transmembrane
266	U:016933.2:2001MAY17	136	138	forward 1	TM	Non-Cytosolic
266	U:016933.2:2001MAY17	139	161	forward 1	TM	Transmembrane
266	U:016933.2:2001MAY17	162	167	forward 1	TM	Cytosolic
266	U:016933.2:2001MAY17	168	190	forward 1	TM	Transmembrane
266	U:016933.2:2001MAY17	191	266	forward 1	TM	Non-Cytosolic
266	U:016933.2:2001MAY17	267	284	forward 1	TM	Transmembrane
266	U:016933.2:2001MAY17	285	290	forward 1	TM	Cytosolic
266	U:016933.2:2001MAY17	291	313	forward 1	TM	Transmembrane
266	U:016933.2:2001MAY17	314	377	forward 1	TM	Non-Cytosolic
266	U:016933.2:2001MAY17	378	400	forward 1	TM	Transmembrane
266	U:016933.2:2001MAY17	401	416	forward 1	TM	Cytosolic
266	U:016933.2:2001MAY17	1	86	forward 2	TM	Cytosolic
266	U:016933.2:2001MAY17	87	106	forward 2	TM	Transmembrane
266	U:016933.2:2001MAY17	107	132	forward 2	TM	Non-Cytosolic
266	U:016933.2:2001MAY17	133	155	forward 2	TM	Transmembrane
266	U:016933.2:2001MAY17	156	161	forward 2	TM	Cytosolic
266	U:016933.2:2001MAY17	162	179	forward 2	TM	Transmembrane
266	U:016933.2:2001MAY17	180	275	forward 2	TM	Non-Cytosolic
266	U:016933.2:2001MAY17	276	298	forward 2	TM	Transmembrane
266	U:016933.2:2001MAY17	299	375	forward 2	TM	Cytosolic
266	U:016933.2:2001MAY17	376	398	forward 2	TM	Transmembrane
266	U:016933.2:2001MAY17	399	416	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
266	U:016933.2:2001MAY17	1	46	forward 3	TM	Cytosolic
266	U:016933.2:2001MAY17	47	65	forward 3	TM	Transmembrane
266	U:016933.2:2001MAY17	66	84	forward 3	TM	Non-Cytosolic
266	U:016933.2:2001MAY17	85	107	forward 3	TM	Transmembrane
266	U:016933.2:2001MAY17	108	111	forward 3	TM	Cytosolic
266	U:016933.2:2001MAY17	112	134	forward 3	TM	Transmembrane
266	U:016933.2:2001MAY17	135	153	forward 3	TM	Non-Cytosolic
266	U:016933.2:2001MAY17	154	176	forward 3	TM	Transmembrane
266	U:016933.2:2001MAY17	177	270	forward 3	TM	Cytosolic
266	U:016933.2:2001MAY17	271	293	forward 3	TM	Transmembrane
266	U:016933.2:2001MAY17	294	307	forward 3	TM	Non-Cytosolic
266	U:016933.2:2001MAY17	308	330	forward 3	TM	Transmembrane
266	U:016933.2:2001MAY17	331	350	forward 3	TM	Cytosolic
266	U:016933.2:2001MAY17	351	373	forward 3	TM	Transmembrane
266	U:016933.2:2001MAY17	374	376	forward 3	TM	Non-Cytosolic
266	U:016933.2:2001MAY17	377	399	forward 3	TM	Transmembrane
266	U:016933.2:2001MAY17	400	415	forward 3	TM	Cytosolic
267	U:1072014.6:2001MAY17	1	685	forward 2	TM	Non-Cytosolic
267	U:1072014.6:2001MAY17	686	708	forward 2	TM	Transmembrane
267	U:1072014.6:2001MAY17	709	764	forward 2	TM	Cytosolic
267	U:1072014.6:2001MAY17	765	787	forward 2	TM	Transmembrane
267	U:1072014.6:2001MAY17	788	834	forward 2	TM	Non-Cytosolic
267	U:1072014.6:2001MAY17	835	857	forward 2	TM	Transmembrane
267	U:1072014.6:2001MAY17	858	932	forward 2	TM	Cytosolic
267	U:1072014.6:2001MAY17	1	762	forward 3	TM	Non-Cytosolic
267	U:1072014.6:2001MAY17	763	785	forward 3	TM	Transmembrane
267	U:1072014.6:2001MAY17	786	904	forward 3	TM	Cytosolic
267	U:1072014.6:2001MAY17	905	927	forward 3	TM	Transmembrane
267	U:1072014.6:2001MAY17	928	931	forward 3	TM	Non-Cytosolic
271	U:1170154.12:2001MAY17	1	444	forward 2	TM	Non-Cytosolic
271	U:1170154.12:2001MAY17	445	467	forward 2	TM	Transmembrane
271	U:1170154.12:2001MAY17	468	753	forward 2	TM	Cytosolic
271	U:1170154.12:2001MAY17	754	776	forward 2	TM	Transmembrane
271	U:1170154.12:2001MAY17	777	814	forward 2	TM	Non-Cytosolic
271	U:1170154.12:2001MAY17	1	425	forward 3	TM	Cytosolic
271	U:1170154.12:2001MAY17	426	448	forward 3	TM	Transmembrane
271	U:1170154.12:2001MAY17	449	493	forward 3	TM	Non-Cytosolic
271	U:1170154.12:2001MAY17	494	516	forward 3	TM	Transmembrane
271	U:1170154.12:2001MAY17	517	758	forward 3	TM	Cytosolic
271	U:1170154.12:2001MAY17	759	781	forward 3	TM	Transmembrane
271	U:1170154.12:2001MAY17	782	814	forward 3	TM	Non-Cytosolic
275	U:1179173.3:2001MAY17	1	732	forward 1	TM	Non-Cytosolic
275	U:1179173.3:2001MAY17	733	755	forward 1	TM	Transmembrane
275	U:1179173.3:2001MAY17	756	779	forward 1	TM	Cytosolic
275	U:1179173.3:2001MAY17	1	543	forward 2	TM	Non-Cytosolic
275	U:1179173.3:2001MAY17	544	566	forward 2	TM	Transmembrane
275	U:1179173.3:2001MAY17	567	779	forward 2	TM	Cytosolic
277	U:1181458.2:2001MAY17	1	754	forward 1	TM	Non-Cytosolic
277	U:1181458.2:2001MAY17	755	777	forward 1	TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
277	U:1181458.2:2001MAY17	778	830	forward 1	TM	Cytosolic
277	U:1181458.2:2001MAY17	831	853	forward 1	TM	Transmembrane
277	U:1181458.2:2001MAY17	854	854	forward 1	TM	Non-Cytosolic
278	U:1182817.8:2001MAY17	1	1047	forward 1	TM	Non-Cytosolic
278	U:1182817.8:2001MAY17	1048	1070	forward 1	TM	Transmembrane
278	U:1182817.8:2001MAY17	1071	1156	forward 1	TM	Cytosolic
278	U:1182817.8:2001MAY17	1157	1179	forward 1	TM	Transmembrane
278	U:1182817.8:2001MAY17	1180	1510	forward 1	TM	Non-Cytosolic
279	U:1182838.4:2001MAY17	1	883	forward 1	TM	Non-Cytosolic
279	U:1182838.4:2001MAY17	884	906	forward 1	TM	Transmembrane
279	U:1182838.4:2001MAY17	907	933	forward 1	TM	Cytosolic
279	U:1182838.4:2001MAY17	934	956	forward 1	TM	Transmembrane
279	U:1182838.4:2001MAY17	957	984	forward 1	TM	Non-Cytosolic
279	U:1182838.4:2001MAY17	985	1007	forward 1	TM	Transmembrane
279	U:1182838.4:2001MAY17	1008	1028	forward 1	TM	Cytosolic
280	U:2053637.1:2001MAY17	1	467	forward 2	TM	Non-Cytosolic
280	U:2053637.1:2001MAY17	468	487	forward 2	TM	Transmembrane
280	U:2053637.1:2001MAY17	488	493	forward 2	TM	Cytosolic
280	U:2053637.1:2001MAY17	494	511	forward 2	TM	Transmembrane
280	U:2053637.1:2001MAY17	512	525	forward 2	TM	Non-Cytosolic
280	U:2053637.1:2001MAY17	526	545	forward 2	TM	Transmembrane
280	U:2053637.1:2001MAY17	546	557	forward 2	TM	Cytosolic
280	U:2053637.1:2001MAY17	558	580	forward 2	TM	Transmembrane
280	U:2053637.1:2001MAY17	581	602	forward 2	TM	Non-Cytosolic
280	U:2053637.1:2001MAY17	1	562	forward 3	TM	Non-Cytosolic
280	U:2053637.1:2001MAY17	563	585	forward 3	TM	Transmembrane
280	U:2053637.1:2001MAY17	586	602	forward 3	TM	Cytosolic
284	U:2121899.1:2001MAY17	1	169	forward 1	TM	Non-Cytosolic
284	U:2121899.1:2001MAY17	170	192	forward 1	TM	Transmembrane
284	U:2121899.1:2001MAY17	193	374	forward 1	TM	Cytosolic
288	U:2195736.1:2001MAY17	1	308	forward 1	TM	Non-Cytosolic
288	U:2195736.1:2001MAY17	309	331	forward 1	TM	Transmembrane
288	U:2195736.1:2001MAY17	332	337	forward 1	TM	Cytosolic
288	U:2195736.1:2001MAY17	338	360	forward 1	TM	Transmembrane
288	U:2195736.1:2001MAY17	361	370	forward 1	TM	Non-Cytosolic
288	U:2195736.1:2001MAY17	1	337	forward 2	TM	Non-Cytosolic
288	U:2195736.1:2001MAY17	338	360	forward 2	TM	Transmembrane
288	U:2195736.1:2001MAY17	361	370	forward 2	TM	Cytosolic
288	U:2195736.1:2001MAY17	1	308	forward 3	TM	Non-Cytosolic
288	U:2195736.1:2001MAY17	309	331	forward 3	TM	Transmembrane
288	U:2195736.1:2001MAY17	332	337	forward 3	TM	Cytosolic
288	U:2195736.1:2001MAY17	338	360	forward 3	TM	Transmembrane
288	U:2195736.1:2001MAY17	361	369	forward 3	TM	Non-Cytosolic
290	U:2196327.1:2001MAY17	1	491	forward 1	TM	Non-Cytosolic
290	U:2196327.1:2001MAY17	492	514	forward 1	TM	Transmembrane
290	U:2196327.1:2001MAY17	515	572	forward 1	TM	Cytosolic
293	U:2206159.1:2001MAY17	1	345	forward 3	TM	Non-Cytosolic
293	U:2206159.1:2001MAY17	346	368	forward 3	TM	Transmembrane
293	U:2206159.1:2001MAY17	369	480	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
293	U:2206159.1:2001MAY17	481	503	forward 3	TM	Transmembrane
293	U:2206159.1:2001MAY17	504	512	forward 3	TM	Non-Cytosolic
293	U:2206159.1:2001MAY17	513	535	forward 3	TM	Transmembrane
293	U:2206159.1:2001MAY17	536	541	forward 3	TM	Cytosolic
293	U:2206159.1:2001MAY17	542	556	forward 3	TM	Transmembrane
293	U:2206159.1:2001MAY17	557	575	forward 3	TM	Non-Cytosolic
293	U:2206159.1:2001MAY17	576	598	forward 3	TM	Transmembrane
293	U:2206159.1:2001MAY17	599	618	forward 3	TM	Cytosolic
294	U:2208960.3:2001MAY17	1	1912	forward 3	TM	Non-Cytosolic
294	U:2208960.3:2001MAY17	1913	1935	forward 3	TM	Transmembrane
294	U:2208960.3:2001MAY17	1936	1974	forward 3	TM	Cytosolic
294	U:2208960.3:2001MAY17	1975	1994	forward 3	TM	Transmembrane
294	U:2208960.3:2001MAY17	1995	2003	forward 3	TM	Non-Cytosolic
294	U:2208960.3:2001MAY17	2004	2026	forward 3	TM	Transmembrane
294	U:2208960.3:2001MAY17	2027	2104	forward 3	TM	Cytosolic
298	U:480324.48:2001MAY17	1	179	forward 2	TM	Non-Cytosolic
298	U:480324.48:2001MAY17	180	202	forward 2	TM	Transmembrane
298	U:480324.48:2001MAY17	203	303	forward 2	TM	Cytosolic
300	U:796992.1:2001MAY17	1	747	forward 2	TM	Non-Cytosolic
300	U:796992.1:2001MAY17	748	770	forward 2	TM	Transmembrane
300	U:796992.1:2001MAY17	771	844	forward 2	TM	Cytosolic
300	U:796992.1:2001MAY17	845	867	forward 2	TM	Transmembrane
300	U:796992.1:2001MAY17	868	886	forward 2	TM	Non-Cytosolic
300	U:796992.1:2001MAY17	887	909	forward 2	TM	Transmembrane
300	U:796992.1:2001MAY17	910	921	forward 2	TM	Cytosolic
300	U:796992.1:2001MAY17	922	944	forward 2	TM	Transmembrane
300	U:796992.1:2001MAY17	945	948	forward 2	TM	Non-Cytosolic
300	U:796992.1:2001MAY17	949	971	forward 2	TM	Transmembrane
300	U:796992.1:2001MAY17	972	980	forward 2	TM	Cytosolic
300	U:796992.1:2001MAY17	1	503	forward 3	TM	Non-Cytosolic
300	U:796992.1:2001MAY17	504	521	forward 3	TM	Transmembrane
300	U:796992.1:2001MAY17	522	525	forward 3	TM	Cytosolic
300	U:796992.1:2001MAY17	526	548	forward 3	TM	Transmembrane
300	U:796992.1:2001MAY17	549	835	forward 3	TM	Non-Cytosolic
300	U:796992.1:2001MAY17	836	858	forward 3	TM	Transmembrane
300	U:796992.1:2001MAY17	859	947	forward 3	TM	Cytosolic
300	U:796992.1:2001MAY17	948	970	forward 3	TM	Transmembrane
300	U:796992.1:2001MAY17	971	979	forward 3	TM	Non-Cytosolic
306	U:1182999.3:2001MAY17	1	509	forward 2	TM	Non-Cytosolic
306	U:1182999.3:2001MAY17	510	532	forward 2	TM	Transmembrane
306	U:1182999.3:2001MAY17	533	538	forward 2	TM	Cytosolic
306	U:1182999.3:2001MAY17	539	561	forward 2	TM	Transmembrane
306	U:1182999.3:2001MAY17	562	571	forward 2	TM	Non-Cytosolic
306	U:1182999.3:2001MAY17	1	65	forward 3	TM	Cytosolic
306	U:1182999.3:2001MAY17	66	88	forward 3	TM	Transmembrane
306	U:1182999.3:2001MAY17	89	571	forward 3	TM	Non-Cytosolic
307	U:1183525.1:2001MAY17	1	160	forward 3	TM	Non-Cytosolic
307	U:1183525.1:2001MAY17	161	183	forward 3	TM	Transmembrane
307	U:1183525.1:2001MAY17	184	194	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
307	LI:1183525.1:2001MAY17	195	214	forward 3	TM	Transmembrane
307	LI:1183525.1:2001MAY17	215	447	forward 3	TM	Non-Cytosolic
308	LI:2121675.1:2001MAY17	1	168	forward 1	TM	Cytosolic
308	LI:2121675.1:2001MAY17	169	191	forward 1	TM	Transmembrane
308	LI:2121675.1:2001MAY17	192	200	forward 1	TM	Non-Cytosolic
308	LI:2121675.1:2001MAY17	201	223	forward 1	TM	Transmembrane
308	LI:2121675.1:2001MAY17	224	226	forward 1	TM	Cytosolic
308	LI:2121675.1:2001MAY17	1	195	forward 2	TM	Cytosolic
308	LI:2121675.1:2001MAY17	196	218	forward 2	TM	Transmembrane
308	LI:2121675.1:2001MAY17	219	226	forward 2	TM	Non-Cytosolic
308	LI:2121675.1:2001MAY17	1	130	forward 3	TM	Cytosolic
308	LI:2121675.1:2001MAY17	131	153	forward 3	TM	Transmembrane
308	LI:2121675.1:2001MAY17	154	162	forward 3	TM	Non-Cytosolic
308	LI:2121675.1:2001MAY17	163	180	forward 3	TM	Transmembrane
308	LI:2121675.1:2001MAY17	181	192	forward 3	TM	Cytosolic
308	LI:2121675.1:2001MAY17	193	212	forward 3	TM	Transmembrane
308	LI:2121675.1:2001MAY17	213	226	forward 3	TM	Non-Cytosolic
320	LG:208637.1:2001JUN22	1	840	forward 2	TM	Non-Cytosolic
320	LG:208637.1:2001JUN22	841	863	forward 2	TM	Transmembrane
320	LG:208637.1:2001JUN22	864	874	forward 2	TM	Cytosolic
320	LG:208637.1:2001JUN22	875	894	forward 2	TM	Transmembrane
320	LG:208637.1:2001JUN22	895	913	forward 2	TM	Non-Cytosolic
320	LG:208637.1:2001JUN22	914	936	forward 2	TM	Transmembrane
320	LG:208637.1:2001JUN22	937	966	forward 2	TM	Cytosolic
320	LG:208637.1:2001JUN22	967	989	forward 2	TM	Transmembrane
320	LG:208637.1:2001JUN22	990	1008	forward 2	TM	Non-Cytosolic
320	LG:208637.1:2001JUN22	1009	1031	forward 2	TM	Transmembrane
320	LG:208637.1:2001JUN22	1032	1145	forward 2	TM	Cytosolic
320	LG:208637.1:2001JUN22	1146	1168	forward 2	TM	Transmembrane
320	LG:208637.1:2001JUN22	1169	1200	forward 2	TM	Non-Cytosolic
320	LG:208637.1:2001JUN22	1201	1223	forward 2	TM	Transmembrane
320	LG:208637.1:2001JUN22	1224	1265	forward 2	TM	Cytosolic
320	LG:208637.1:2001JUN22	1266	1288	forward 2	TM	Transmembrane
320	LG:208637.1:2001JUN22	1289	1358	forward 2	TM	Non-Cytosolic
320	LG:208637.1:2001JUN22	1359	1381	forward 2	TM	Transmembrane
320	LG:208637.1:2001JUN22	1382	1397	forward 2	TM	Cytosolic
320	LG:208637.1:2001JUN22	1	866	forward 3	TM	Non-Cytosolic
320	LG:208637.1:2001JUN22	867	889	forward 3	TM	Transmembrane
320	LG:208637.1:2001JUN22	890	908	forward 3	TM	Cytosolic
320	LG:208637.1:2001JUN22	909	931	forward 3	TM	Transmembrane
320	LG:208637.1:2001JUN22	932	1000	forward 3	TM	Non-Cytosolic
320	LG:208637.1:2001JUN22	1001	1020	forward 3	TM	Transmembrane
320	LG:208637.1:2001JUN22	1021	1032	forward 3	TM	Cytosolic
320	LG:208637.1:2001JUN22	1033	1055	forward 3	TM	Transmembrane
320	LG:208637.1:2001JUN22	1056	1099	forward 3	TM	Non-Cytosolic
320	LG:208637.1:2001JUN22	1100	1122	forward 3	TM	Transmembrane
320	LG:208637.1:2001JUN22	1123	1198	forward 3	TM	Cytosolic
320	LG:208637.1:2001JUN22	1199	1221	forward 3	TM	Transmembrane
320	LG:208637.1:2001JUN22	1222	1230	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
320	LG:208637.1:2001JUN22	1231	1248	forward 3	TM	Transmembrane
320	LG:208637.1:2001JUN22	1249	1331	forward 3	TM	Cytosolic
320	LG:208637.1:2001JUN22	1332	1354	forward 3	TM	Transmembrane
320	LG:208637.1:2001JUN22	1355	1368	forward 3	TM	Non-Cytosolic
320	LG:208637.1:2001JUN22	1369	1386	forward 3	TM	Transmembrane
320	LG:208637.1:2001JUN22	1387	1396	forward 3	TM	Cytosolic
321	LG:233311.5:2001JUN22	1	39	forward 1	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	40	62	forward 1	TM	Transmembrane
321	LG:233311.5:2001JUN22	63	375	forward 1	TM	Cytosolic
321	LG:233311.5:2001JUN22	376	398	forward 1	TM	Transmembrane
321	LG:233311.5:2001JUN22	399	455	forward 1	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	456	478	forward 1	TM	Transmembrane
321	LG:233311.5:2001JUN22	479	688	forward 1	TM	Cytosolic
321	LG:233311.5:2001JUN22	689	711	forward 1	TM	Transmembrane
321	LG:233311.5:2001JUN22	712	740	forward 1	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	741	763	forward 1	TM	Transmembrane
321	LG:233311.5:2001JUN22	764	867	forward 1	TM	Cytosolic
321	LG:233311.5:2001JUN22	868	890	forward 1	TM	Transmembrane
321	LG:233311.5:2001JUN22	891	1147	forward 1	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	1	322	forward 2	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	323	345	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	346	356	forward 2	TM	Cytosolic
321	LG:233311.5:2001JUN22	357	379	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	380	388	forward 2	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	389	411	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	412	417	forward 2	TM	Cytosolic
321	LG:233311.5:2001JUN22	418	440	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	441	449	forward 2	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	450	472	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	473	609	forward 2	TM	Cytosolic
321	LG:233311.5:2001JUN22	610	629	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	630	643	forward 2	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	644	666	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	667	686	forward 2	TM	Cytosolic
321	LG:233311.5:2001JUN22	687	709	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	710	820	forward 2	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	821	843	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	844	863	forward 2	TM	Cytosolic
321	LG:233311.5:2001JUN22	864	886	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	887	900	forward 2	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	901	920	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	921	1079	forward 2	TM	Cytosolic
321	LG:233311.5:2001JUN22	1080	1102	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	1103	1116	forward 2	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	1117	1136	forward 2	TM	Transmembrane
321	LG:233311.5:2001JUN22	1137	1146	forward 2	TM	Cytosolic
321	LG:233311.5:2001JUN22	1	367	forward 3	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	368	390	forward 3	TM	Transmembrane
321	LG:233311.5:2001JUN22	391	445	forward 3	TM	Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
321	LG:233311.5:2001JUN22	446	468	forward 3	TM	Transmembrane
321	LG:233311.5:2001JUN22	469	578	forward 3	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	579	601	forward 3	TM	Transmembrane
321	LG:233311.5:2001JUN22	602	640	forward 3	TM	Cytosolic
321	LG:233311.5:2001JUN22	641	663	forward 3	TM	Transmembrane
321	LG:233311.5:2001JUN22	664	682	forward 3	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	683	700	forward 3	TM	Transmembrane
321	LG:233311.5:2001JUN22	701	706	forward 3	TM	Cytosolic
321	LG:233311.5:2001JUN22	707	729	forward 3	TM	Transmembrane
321	LG:233311.5:2001JUN22	730	811	forward 3	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	812	834	forward 3	TM	Transmembrane
321	LG:233311.5:2001JUN22	835	1072	forward 3	TM	Cytosolic
321	LG:233311.5:2001JUN22	1073	1095	forward 3	TM	Transmembrane
321	LG:233311.5:2001JUN22	1096	1109	forward 3	TM	Non-Cytosolic
321	LG:233311.5:2001JUN22	1110	1132	forward 3	TM	Transmembrane
321	LG:233311.5:2001JUN22	1133	1146	forward 3	TM	Cytosolic
323	LG:404157.1:2001JUN22	1	836	forward 1	TM	Non-Cytosolic
323	LG:404157.1:2001JUN22	837	859	forward 1	TM	Transmembrane
323	LG:404157.1:2001JUN22	860	948	forward 1	TM	Cytosolic
323	LG:404157.1:2001JUN22	949	971	forward 1	TM	Transmembrane
323	LG:404157.1:2001JUN22	972	980	forward 1	TM	Non-Cytosolic
323	LG:404157.1:2001JUN22	1	503	forward 3	TM	Non-Cytosolic
323	LG:404157.1:2001JUN22	504	521	forward 3	TM	Transmembrane
323	LG:404157.1:2001JUN22	522	525	forward 3	TM	Cytosolic
323	LG:404157.1:2001JUN22	526	548	forward 3	TM	Transmembrane
323	LG:404157.1:2001JUN22	549	747	forward 3	TM	Non-Cytosolic
323	LG:404157.1:2001JUN22	748	770	forward 3	TM	Transmembrane
323	LG:404157.1:2001JUN22	771	844	forward 3	TM	Cytosolic
323	LG:404157.1:2001JUN22	845	867	forward 3	TM	Transmembrane
323	LG:404157.1:2001JUN22	868	886	forward 3	TM	Non-Cytosolic
323	LG:404157.1:2001JUN22	887	909	forward 3	TM	Transmembrane
323	LG:404157.1:2001JUN22	910	921	forward 3	TM	Cytosolic
323	LG:404157.1:2001JUN22	922	944	forward 3	TM	Transmembrane
323	LG:404157.1:2001JUN22	945	948	forward 3	TM	Non-Cytosolic
323	LG:404157.1:2001JUN22	949	971	forward 3	TM	Transmembrane
323	LG:404157.1:2001JUN22	972	980	forward 3	TM	Cytosolic
324	LG:7684505.1:2001JUN22	1	260	forward 3	TM	Non-Cytosolic
324	LG:7684505.1:2001JUN22	261	283	forward 3	TM	Transmembrane
324	LG:7684505.1:2001JUN22	284	290	forward 3	TM	Cytosolic
325	LG:7687730.1:2001JUN22	1	1097	forward 1	TM	Non-Cytosolic
325	LG:7687730.1:2001JUN22	1098	1120	forward 1	TM	Transmembrane
325	LG:7687730.1:2001JUN22	1121	1159	forward 1	TM	Cytosolic
325	LG:7687730.1:2001JUN22	1160	1182	forward 1	TM	Transmembrane
325	LG:7687730.1:2001JUN22	1183	1201	forward 1	TM	Non-Cytosolic
325	LG:7687730.1:2001JUN22	1202	1224	forward 1	TM	Transmembrane
325	LG:7687730.1:2001JUN22	1225	1230	forward 1	TM	Cytosolic
325	LG:7687730.1:2001JUN22	1	1176	forward 2	TM	Non-Cytosolic
325	LG:7687730.1:2001JUN22	1177	1199	forward 2	TM	Transmembrane
325	LG:7687730.1:2001JUN22	1200	1229	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
325	LG:7687730.1:2001JUN22	1	1018	forward 3	TM	Non-Cytosolic
325	LG:7687730.1:2001JUN22	1019	1038	forward 3	TM	Transmembrane
325	LG:7687730.1:2001JUN22	1039	1049	forward 3	TM	Cytosolic
325	LG:7687730.1:2001JUN22	1050	1072	forward 3	TM	Transmembrane
325	LG:7687730.1:2001JUN22	1073	1099	forward 3	TM	Non-Cytosolic
325	LG:7687730.1:2001JUN22	1100	1117	forward 3	TM	Transmembrane
325	LG:7687730.1:2001JUN22	1118	1129	forward 3	TM	Cytosolic
325	LG:7687730.1:2001JUN22	1130	1152	forward 3	TM	Transmembrane
325	LG:7687730.1:2001JUN22	1153	1176	forward 3	TM	Non-Cytosolic
325	LG:7687730.1:2001JUN22	1177	1199	forward 3	TM	Transmembrane
325	LG:7687730.1:2001JUN22	1200	1229	forward 3	TM	Cytosolic
326	LG:7687809.2:2001JUN22	1	512	forward 3	TM	Non-Cytosolic
326	LG:7687809.2:2001JUN22	513	535	forward 3	TM	Transmembrane
326	LG:7687809.2:2001JUN22	536	593	forward 3	TM	Cytosolic
329	LG:7690362.3:2001JUN22	1	147	forward 1	TM	Cytosolic
332	LG:7691280.4:2001JUN22	1	190	forward 2	TM	Cytosolic
334	LG:7691685.3:2001JUN22	1	56	forward 2	TM	Cytosolic
334	LG:7691685.3:2001JUN22	57	79	forward 2	TM	Transmembrane
334	LG:7691685.3:2001JUN22	80	83	forward 2	TM	Non-Cytosolic
334	LG:7691685.3:2001JUN22	84	106	forward 2	TM	Transmembrane
334	LG:7691685.3:2001JUN22	107	163	forward 2	TM	Cytosolic
334	LG:7691685.3:2001JUN22	1	20	forward 3	TM	Cytosolic
334	LG:7691685.3:2001JUN22	21	43	forward 3	TM	Transmembrane
334	LG:7691685.3:2001JUN22	44	57	forward 3	TM	Non-Cytosolic
334	LG:7691685.3:2001JUN22	58	80	forward 3	TM	Transmembrane
334	LG:7691685.3:2001JUN22	81	163	forward 3	TM	Cytosolic
336	LG:981962.1:2001JUN22	1	338	forward 3	TM	Non-Cytosolic
336	LG:981962.1:2001JUN22	339	361	forward 3	TM	Transmembrane
336	LG:981962.1:2001JUN22	362	432	forward 3	TM	Cytosolic
336	LG:981962.1:2001JUN22	433	455	forward 3	TM	Transmembrane
336	LG:981962.1:2001JUN22	456	479	forward 3	TM	Non-Cytosolic
336	LG:981962.1:2001JUN22	480	502	forward 3	TM	Transmembrane
336	LG:981962.1:2001JUN22	503	513	forward 3	TM	Cytosolic
336	LG:981962.1:2001JUN22	514	536	forward 3	TM	Transmembrane
336	LG:981962.1:2001JUN22	537	550	forward 3	TM	Non-Cytosolic
336	LG:981962.1:2001JUN22	551	573	forward 3	TM	Transmembrane
336	LG:981962.1:2001JUN22	574	639	forward 3	TM	Cytosolic
339	LG:7690406.2:2001JUN22	1	18	forward 3	TM	Cytosolic
339	LG:7690406.2:2001JUN22	19	38	forward 3	TM	Transmembrane
339	LG:7690406.2:2001JUN22	39	332	forward 3	TM	Non-Cytosolic
340	LG:7690773.2:2001JUN22	1	284	forward 1	TM	Cytosolic
340	LG:7690773.2:2001JUN22	285	307	forward 1	TM	Transmembrane
340	LG:7690773.2:2001JUN22	308	310	forward 1	TM	Non-Cytosolic
340	LG:7690773.2:2001JUN22	1	214	forward 2	TM	Non-Cytosolic
340	LG:7690773.2:2001JUN22	215	237	forward 2	TM	Transmembrane
340	LG:7690773.2:2001JUN22	238	243	forward 2	TM	Cytosolic
340	LG:7690773.2:2001JUN22	244	266	forward 2	TM	Transmembrane
340	LG:7690773.2:2001JUN22	267	280	forward 2	TM	Non-Cytosolic
340	LG:7690773.2:2001JUN22	281	303	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
340	LG:7690773.2:2001JUN22	304	310	forward 2	TM	Cytosolic
340	LG:7690773.2:2001JUN22	1	251	forward 3	TM	Cytosolic
340	LG:7690773.2:2001JUN22	252	274	forward 3	TM	Transmembrane
340	LG:7690773.2:2001JUN22	275	283	forward 3	TM	Non-Cytosolic
340	LG:7690773.2:2001JUN22	284	306	forward 3	TM	Transmembrane
340	LG:7690773.2:2001JUN22	307	310	forward 3	TM	Cytosolic
341	LG:1347119.1:2001JUN22	1	717	forward 1	TM	Non-Cytosolic
341	LG:1347119.1:2001JUN22	718	740	forward 1	TM	Transmembrane
341	LG:1347119.1:2001JUN22	741	814	forward 1	TM	Cytosolic
341	LG:1347119.1:2001JUN22	815	837	forward 1	TM	Transmembrane
341	LG:1347119.1:2001JUN22	838	851	forward 1	TM	Non-Cytosolic
341	LG:1347119.1:2001JUN22	852	874	forward 1	TM	Transmembrane
341	LG:1347119.1:2001JUN22	875	894	forward 1	TM	Cytosolic
341	LG:1347119.1:2001JUN22	895	917	forward 1	TM	Transmembrane
341	LG:1347119.1:2001JUN22	918	1404	forward 1	TM	Non-Cytosolic
341	LG:1347119.1:2001JUN22	1	811	forward 3	TM	Non-Cytosolic
341	LG:1347119.1:2001JUN22	812	834	forward 3	TM	Transmembrane
341	LG:1347119.1:2001JUN22	835	840	forward 3	TM	Cytosolic
341	LG:1347119.1:2001JUN22	841	863	forward 3	TM	Transmembrane
341	LG:1347119.1:2001JUN22	864	1404	forward 3	TM	Non-Cytosolic
343	LG:023518.3:2001MAR30	1	474	forward 1	TM	Non-Cytosolic
343	LG:023518.3:2001MAR30	475	497	forward 1	TM	Transmembrane
343	LG:023518.3:2001MAR30	498	524	forward 1	TM	Cytosolic
343	LG:023518.3:2001MAR30	1	97	forward 2	TM	Cytosolic
343	LG:023518.3:2001MAR30	98	117	forward 2	TM	Transmembrane
343	LG:023518.3:2001MAR30	118	473	forward 2	TM	Non-Cytosolic
343	LG:023518.3:2001MAR30	474	496	forward 2	TM	Transmembrane
343	LG:023518.3:2001MAR30	497	523	forward 2	TM	Cytosolic
345	LG:235076.6:2001MAR30	1	1319	forward 1	TM	Non-Cytosolic
345	LG:235076.6:2001MAR30	1320	1342	forward 1	TM	Transmembrane
345	LG:235076.6:2001MAR30	1343	1354	forward 1	TM	Cytosolic
345	LG:235076.6:2001MAR30	1355	1372	forward 1	TM	Transmembrane
345	LG:235076.6:2001MAR30	1373	1378	forward 1	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	1	187	forward 1	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	188	210	forward 1	TM	Transmembrane
346	LG:270582.4:2001MAR30	211	216	forward 1	TM	Cytosolic
346	LG:270582.4:2001MAR30	217	239	forward 1	TM	Transmembrane
346	LG:270582.4:2001MAR30	240	268	forward 1	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	269	291	forward 1	TM	Transmembrane
346	LG:270582.4:2001MAR30	292	297	forward 1	TM	Cytosolic
346	LG:270582.4:2001MAR30	298	320	forward 1	TM	Transmembrane
346	LG:270582.4:2001MAR30	321	334	forward 1	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	335	357	forward 1	TM	Transmembrane
346	LG:270582.4:2001MAR30	358	577	forward 1	TM	Cytosolic
346	LG:270582.4:2001MAR30	578	597	forward 1	TM	Transmembrane
346	LG:270582.4:2001MAR30	598	776	forward 1	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	777	799	forward 1	TM	Transmembrane
346	LG:270582.4:2001MAR30	800	842	forward 1	TM	Cytosolic
346	LG:270582.4:2001MAR30	843	865	forward 1	TM	Transmembrane

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
346	LG:270582.4:2001MAR30	866	946	forward 1	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	947	964	forward 1	TM	Transmembrane
346	LG:270582.4:2001MAR30	965	975	forward 1	TM	Cytosolic
346	LG:270582.4:2001MAR30	976	998	forward 1	TM	Transmembrane
346	LG:270582.4:2001MAR30	999	1012	forward 1	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	1013	1035	forward 1	TM	Transmembrane
346	LG:270582.4:2001MAR30	1036	1131	forward 1	TM	Cytosolic
346	LG:270582.4:2001MAR30	1	107	forward 2	TM	Cytosolic
346	LG:270582.4:2001MAR30	108	127	forward 2	TM	Transmembrane
346	LG:270582.4:2001MAR30	128	749	forward 2	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	750	767	forward 2	TM	Transmembrane
346	LG:270582.4:2001MAR30	768	773	forward 2	TM	Cytosolic
346	LG:270582.4:2001MAR30	774	796	forward 2	TM	Transmembrane
346	LG:270582.4:2001MAR30	797	975	forward 2	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	976	998	forward 2	TM	Transmembrane
346	LG:270582.4:2001MAR30	999	1004	forward 2	TM	Cytosolic
346	LG:270582.4:2001MAR30	1005	1027	forward 2	TM	Transmembrane
346	LG:270582.4:2001MAR30	1028	1130	forward 2	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	1	749	forward 3	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	750	767	forward 3	TM	Transmembrane
346	LG:270582.4:2001MAR30	768	773	forward 3	TM	Cytosolic
346	LG:270582.4:2001MAR30	774	796	forward 3	TM	Transmembrane
346	LG:270582.4:2001MAR30	797	836	forward 3	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	837	859	forward 3	TM	Transmembrane
346	LG:270582.4:2001MAR30	860	871	forward 3	TM	Cytosolic
346	LG:270582.4:2001MAR30	872	894	forward 3	TM	Transmembrane
346	LG:270582.4:2001MAR30	895	946	forward 3	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	947	964	forward 3	TM	Transmembrane
346	LG:270582.4:2001MAR30	965	976	forward 3	TM	Cytosolic
346	LG:270582.4:2001MAR30	977	999	forward 3	TM	Transmembrane
346	LG:270582.4:2001MAR30	1000	1013	forward 3	TM	Non-Cytosolic
346	LG:270582.4:2001MAR30	1014	1036	forward 3	TM	Transmembrane
346	LG:270582.4:2001MAR30	1037	1130	forward 3	TM	Cytosolic
347	LG:334752.12:2001MAR30	1	157	forward 1	TM	Cytosolic
347	LG:334752.12:2001MAR30	158	180	forward 1	TM	Transmembrane
347	LG:334752.12:2001MAR30	181	208	forward 1	TM	Non-Cytosolic
347	LG:334752.12:2001MAR30	209	231	forward 1	TM	Transmembrane
347	LG:334752.12:2001MAR30	232	250	forward 1	TM	Cytosolic
347	LG:334752.12:2001MAR30	251	273	forward 1	TM	Transmembrane
347	LG:334752.12:2001MAR30	274	310	forward 1	TM	Non-Cytosolic
347	LG:334752.12:2001MAR30	311	333	forward 1	TM	Transmembrane
347	LG:334752.12:2001MAR30	334	401	forward 1	TM	Cytosolic
347	LG:334752.12:2001MAR30	402	424	forward 1	TM	Transmembrane
347	LG:334752.12:2001MAR30	425	427	forward 1	TM	Non-Cytosolic
347	LG:334752.12:2001MAR30	428	450	forward 1	TM	Transmembrane
347	LG:334752.12:2001MAR30	451	456	forward 1	TM	Cytosolic
347	LG:334752.12:2001MAR30	457	474	forward 1	TM	Transmembrane
347	LG:334752.12:2001MAR30	475	488	forward 1	TM	Non-Cytosolic
347	LG:334752.12:2001MAR30	489	511	forward 1	TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
347	LG:334752.12:2001MAR30	512	790	forward 1	TM	Cytosolic
348	LG:425641.11:2001MAR30	1	152	forward 1	TM	Cytosolic
348	LG:425641.11:2001MAR30	153	175	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	176	184	forward 1	TM	Non-Cytosolic
348	LG:425641.11:2001MAR30	185	207	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	208	219	forward 1	TM	Cytosolic
348	LG:425641.11:2001MAR30	220	242	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	243	270	forward 1	TM	Non-Cytosolic
348	LG:425641.11:2001MAR30	271	293	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	294	304	forward 1	TM	Cytosolic
348	LG:425641.11:2001MAR30	305	327	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	328	378	forward 1	TM	Non-Cytosolic
348	LG:425641.11:2001MAR30	379	401	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	402	421	forward 1	TM	Cytosolic
348	LG:425641.11:2001MAR30	422	444	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	445	471	forward 1	TM	Non-Cytosolic
348	LG:425641.11:2001MAR30	472	490	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	491	496	forward 1	TM	Cytosolic
348	LG:425641.11:2001MAR30	497	519	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	520	533	forward 1	TM	Non-Cytosolic
348	LG:425641.11:2001MAR30	534	553	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	554	559	forward 1	TM	Cytosolic
348	LG:425641.11:2001MAR30	560	579	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	580	1299	forward 1	TM	Non-Cytosolic
348	LG:425641.11:2001MAR30	1300	1322	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	1323	1367	forward 1	TM	Cytosolic
348	LG:425641.11:2001MAR30	1368	1390	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	1391	1404	forward 1	TM	Non-Cytosolic
348	LG:425641.11:2001MAR30	1405	1427	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	1428	1447	forward 1	TM	Cytosolic
348	LG:425641.11:2001MAR30	1448	1467	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	1468	2072	forward 1	TM	Non-Cytosolic
348	LG:425641.11:2001MAR30	2073	2095	forward 1	TM	Transmembrane
348	LG:425641.11:2001MAR30	2096	2134	forward 1	TM	Cytosolic
348	LG:425641.11:2001MAR30	1	1352	forward 2	TM	Non-Cytosolic
348	LG:425641.11:2001MAR30	1353	1375	forward 2	TM	Transmembrane
348	LG:425641.11:2001MAR30	1376	1679	forward 2	TM	Cytosolic
348	LG:425641.11:2001MAR30	1680	1702	forward 2	TM	Transmembrane
348	LG:425641.11:2001MAR30	1703	1716	forward 2	TM	Non-Cytosolic
348	LG:425641.11:2001MAR30	1717	1739	forward 2	TM	Transmembrane
348	LG:425641.11:2001MAR30	1740	2101	forward 2	TM	Cytosolic
348	LG:425641.11:2001MAR30	2102	2124	forward 2	TM	Transmembrane
348	LG:425641.11:2001MAR30	2125	2134	forward 2	TM	Non-Cytosolic
349	LG:980241.4:2001MAR30	1	34	forward 1	TM	Cytosolic
349	LG:980241.4:2001MAR30	35	57	forward 1	TM	Transmembrane
349	LG:980241.4:2001MAR30	58	66	forward 1	TM	Non-Cytosolic
349	LG:980241.4:2001MAR30	67	89	forward 1	TM	Transmembrane
349	LG:980241.4:2001MAR30	90	135	forward 1	TM	Cytosolic
349	LG:980241.4:2001MAR30	136	158	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
349	LG:980241.4:2001MAR30	159	205	forward 1	TM	Non-Cytosolic
349	LG:980241.4:2001MAR30	206	228	forward 1	TM	Transmembrane
349	LG:980241.4:2001MAR30	229	318	forward 1	TM	Cytosolic
349	LG:980241.4:2001MAR30	319	341	forward 1	TM	Transmembrane
349	LG:980241.4:2001MAR30	342	796	forward 1	TM	Non-Cytosolic
349	LG:980241.4:2001MAR30	797	819	forward 1	TM	Transmembrane
349	LG:980241.4:2001MAR30	820	846	forward 1	TM	Cytosolic
349	LG:980241.4:2001MAR30	1	33	forward 2	TM	Non-Cytosolic
349	LG:980241.4:2001MAR30	34	56	forward 2	TM	Transmembrane
349	LG:980241.4:2001MAR30	57	152	forward 2	TM	Cytosolic
349	LG:980241.4:2001MAR30	153	175	forward 2	TM	Transmembrane
349	LG:980241.4:2001MAR30	176	179	forward 2	TM	Non-Cytosolic
349	LG:980241.4:2001MAR30	180	202	forward 2	TM	Transmembrane
349	LG:980241.4:2001MAR30	203	206	forward 2	TM	Cytosolic
349	LG:980241.4:2001MAR30	207	229	forward 2	TM	Transmembrane
349	LG:980241.4:2001MAR30	230	467	forward 2	TM	Non-Cytosolic
349	LG:980241.4:2001MAR30	468	490	forward 2	TM	Transmembrane
349	LG:980241.4:2001MAR30	491	727	forward 2	TM	Cytosolic
349	LG:980241.4:2001MAR30	728	750	forward 2	TM	Transmembrane
349	LG:980241.4:2001MAR30	751	787	forward 2	TM	Non-Cytosolic
349	LG:980241.4:2001MAR30	788	810	forward 2	TM	Transmembrane
349	LG:980241.4:2001MAR30	811	846	forward 2	TM	Cytosolic
349	LG:980241.4:2001MAR30	1	205	forward 3	TM	Non-Cytosolic
349	LG:980241.4:2001MAR30	206	228	forward 3	TM	Transmembrane
349	LG:980241.4:2001MAR30	229	309	forward 3	TM	Cytosolic
349	LG:980241.4:2001MAR30	310	332	forward 3	TM	Transmembrane
349	LG:980241.4:2001MAR30	333	468	forward 3	TM	Non-Cytosolic
349	LG:980241.4:2001MAR30	469	491	forward 3	TM	Transmembrane
349	LG:980241.4:2001MAR30	492	511	forward 3	TM	Cytosolic
349	LG:980241.4:2001MAR30	512	534	forward 3	TM	Transmembrane
349	LG:980241.4:2001MAR30	535	846	forward 3	TM	Non-Cytosolic
350	U:1040737.102:2001MAY17	1	71	forward 2	TM	Cytosolic
350	U:1040737.102:2001MAY17	72	94	forward 2	TM	Transmembrane
350	U:1040737.102:2001MAY17	95	203	forward 2	TM	Non-Cytosolic
350	U:1040737.102:2001MAY17	1	137	forward 3	TM	Cytosolic
350	U:1040737.102:2001MAY17	138	157	forward 3	TM	Transmembrane
350	U:1040737.102:2001MAY17	158	202	forward 3	TM	Non-Cytosolic
351	U:1072888.10:2001MAY17	1	37	forward 1	TM	Cytosolic
351	U:1072888.10:2001MAY17	38	60	forward 1	TM	Transmembrane
351	U:1072888.10:2001MAY17	61	74	forward 1	TM	Non-Cytosolic
351	U:1072888.10:2001MAY17	75	97	forward 1	TM	Transmembrane
351	U:1072888.10:2001MAY17	98	103	forward 1	TM	Cytosolic
351	U:1072888.10:2001MAY17	104	123	forward 1	TM	Transmembrane
351	U:1072888.10:2001MAY17	124	153	forward 1	TM	Non-Cytosolic
351	U:1072888.10:2001MAY17	154	176	forward 1	TM	Transmembrane
351	U:1072888.10:2001MAY17	177	429	forward 1	TM	Cytosolic
351	U:1072888.10:2001MAY17	1	142	forward 2	TM	Cytosolic
351	U:1072888.10:2001MAY17	143	165	forward 2	TM	Transmembrane
351	U:1072888.10:2001MAY17	166	428	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
352	U:2048255.1:2001MAY17	1	57	forward 1	TM	Cytosolic
352	U:2048255.1:2001MAY17	58	77	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	78	86	forward 1	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	87	109	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	110	129	forward 1	TM	Cytosolic
352	U:2048255.1:2001MAY17	130	152	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	153	208	forward 1	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	209	226	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	227	238	forward 1	TM	Cytosolic
352	U:2048255.1:2001MAY17	239	261	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	262	290	forward 1	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	291	313	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	314	319	forward 1	TM	Cytosolic
352	U:2048255.1:2001MAY17	320	342	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	343	430	forward 1	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	431	453	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	454	473	forward 1	TM	Cytosolic
352	U:2048255.1:2001MAY17	474	491	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	492	505	forward 1	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	506	528	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	529	548	forward 1	TM	Cytosolic
352	U:2048255.1:2001MAY17	549	571	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	572	597	forward 1	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	598	620	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	621	714	forward 1	TM	Cytosolic
352	U:2048255.1:2001MAY17	715	737	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	738	798	forward 1	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	799	821	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	822	827	forward 1	TM	Cytosolic
352	U:2048255.1:2001MAY17	828	850	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	851	854	forward 1	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	855	874	forward 1	TM	Transmembrane
352	U:2048255.1:2001MAY17	875	1011	forward 1	TM	Cytosolic
352	U:2048255.1:2001MAY17	1	774	forward 2	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	775	797	forward 2	TM	Transmembrane
352	U:2048255.1:2001MAY17	798	817	forward 2	TM	Cytosolic
352	U:2048255.1:2001MAY17	818	840	forward 2	TM	Transmembrane
352	U:2048255.1:2001MAY17	841	844	forward 2	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	845	867	forward 2	TM	Transmembrane
352	U:2048255.1:2001MAY17	868	1011	forward 2	TM	Cytosolic
352	U:2048255.1:2001MAY17	1	427	forward 3	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	428	450	forward 3	TM	Transmembrane
352	U:2048255.1:2001MAY17	451	694	forward 3	TM	Cytosolic
352	U:2048255.1:2001MAY17	695	717	forward 3	TM	Transmembrane
352	U:2048255.1:2001MAY17	718	726	forward 3	TM	Non-Cytosolic
352	U:2048255.1:2001MAY17	727	749	forward 3	TM	Transmembrane
352	U:2048255.1:2001MAY17	750	769	forward 3	TM	Cytosolic
352	U:2048255.1:2001MAY17	770	792	forward 3	TM	Transmembrane
352	U:2048255.1:2001MAY17	793	811	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
352	U:2048255.1:2001MAY17	812	834	forward 3	TM	Transmembrane
352	U:2048255.1:2001MAY17	835	1010	forward 3	TM	Cytosolic
354	U:410188.4:2001MAY17	1	176	forward 1	TM	Cytosolic
354	U:410188.4:2001MAY17	177	199	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	200	242	forward 1	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	243	265	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	266	271	forward 1	TM	Cytosolic
354	U:410188.4:2001MAY17	272	294	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	295	303	forward 1	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	304	326	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	327	440	forward 1	TM	Cytosolic
354	U:410188.4:2001MAY17	441	463	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	464	763	forward 1	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	764	786	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	787	798	forward 1	TM	Cytosolic
354	U:410188.4:2001MAY17	799	821	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	822	830	forward 1	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	831	848	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	849	888	forward 1	TM	Cytosolic
354	U:410188.4:2001MAY17	889	911	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	912	925	forward 1	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	926	945	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	946	965	forward 1	TM	Cytosolic
354	U:410188.4:2001MAY17	966	988	forward 1	TM	Transmembrane
354	U:410188.4:2001MAY17	989	2836	forward 1	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	1	1300	forward 2	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	1301	1318	forward 2	TM	Transmembrane
354	U:410188.4:2001MAY17	1319	1324	forward 2	TM	Cytosolic
354	U:410188.4:2001MAY17	1325	1347	forward 2	TM	Transmembrane
354	U:410188.4:2001MAY17	1348	1388	forward 2	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	1389	1411	forward 2	TM	Transmembrane
354	U:410188.4:2001MAY17	1412	1459	forward 2	TM	Cytosolic
354	U:410188.4:2001MAY17	1460	1482	forward 2	TM	Transmembrane
354	U:410188.4:2001MAY17	1483	1501	forward 2	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	1502	1524	forward 2	TM	Transmembrane
354	U:410188.4:2001MAY17	1525	1584	forward 2	TM	Cytosolic
354	U:410188.4:2001MAY17	1585	1602	forward 2	TM	Transmembrane
354	U:410188.4:2001MAY17	1603	1611	forward 2	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	1612	1632	forward 2	TM	Transmembrane
354	U:410188.4:2001MAY17	1633	1644	forward 2	TM	Cytosolic
354	U:410188.4:2001MAY17	1645	1667	forward 2	TM	Transmembrane
354	U:410188.4:2001MAY17	1668	1714	forward 2	TM	Non-Cytosolic
354	U:410188.4:2001MAY17	1715	1737	forward 2	TM	Transmembrane
354	U:410188.4:2001MAY17	1738	1801	forward 2	TM	Cytosolic
354	U:410188.4:2001MAY17	1802	1824	forward 2	TM	Transmembrane
354	U:410188.4:2001MAY17	1825	2836	forward 2	TM	Non-Cytosolic
355	U:902565.38:2001MAY17	1	22	forward 1	TM	Non-Cytosolic
355	U:902565.38:2001MAY17	23	45	forward 1	TM	Transmembrane
355	U:902565.38:2001MAY17	46	244	forward 1	TM	Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
355	LI:902565.38:2001MAY17	245	267	forward 1	TM	Transmembrane
355	LI:902565.38:2001MAY17	268	490	forward 1	TM	Non-Cytosolic
355	LI:902565.38:2001MAY17	491	513	forward 1	TM	Transmembrane
355	LI:902565.38:2001MAY17	514	560	forward 1	TM	Cytosolic
355	LI:902565.38:2001MAY17	1	58	forward 2	TM	Non-Cytosolic
355	LI:902565.38:2001MAY17	59	81	forward 2	TM	Transmembrane
355	LI:902565.38:2001MAY17	82	135	forward 2	TM	Cytosolic
355	LI:902565.38:2001MAY17	136	158	forward 2	TM	Transmembrane
355	LI:902565.38:2001MAY17	159	560	forward 2	TM	Non-Cytosolic
357	LI:2192055.1:2001MAY17	1	9	forward 1	TM	Non-Cytosolic
357	LI:2192055.1:2001MAY17	10	32	forward 1	TM	Transmembrane
357	LI:2192055.1:2001MAY17	33	177	forward 1	TM	Cytosolic
357	LI:2192055.1:2001MAY17	1	14	forward 2	TM	Non-Cytosolic
357	LI:2192055.1:2001MAY17	15	37	forward 2	TM	Transmembrane
357	LI:2192055.1:2001MAY17	38	177	forward 2	TM	Cytosolic
357	LI:2192055.1:2001MAY17	1	6	forward 3	TM	Cytosolic
357	LI:2192055.1:2001MAY17	7	29	forward 3	TM	Transmembrane
357	LI:2192055.1:2001MAY17	30	176	forward 3	TM	Non-Cytosolic
358	LG:133851.16:2001JUN22	1	574	forward 2	TM	Non-Cytosolic
358	LG:133851.16:2001JUN22	575	597	forward 2	TM	Transmembrane
358	LG:133851.16:2001JUN22	598	753	forward 2	TM	Cytosolic
359	LG:1398822.1:2001JUN22	1	37	forward 1	TM	Cytosolic
359	LG:1398822.1:2001JUN22	38	60	forward 1	TM	Transmembrane
359	LG:1398822.1:2001JUN22	61	69	forward 1	TM	Non-Cytosolic
359	LG:1398822.1:2001JUN22	70	92	forward 1	TM	Transmembrane
359	LG:1398822.1:2001JUN22	93	111	forward 1	TM	Cytosolic
359	LG:1398822.1:2001JUN22	112	134	forward 1	TM	Transmembrane
359	LG:1398822.1:2001JUN22	135	153	forward 1	TM	Non-Cytosolic
359	LG:1398822.1:2001JUN22	154	176	forward 1	TM	Transmembrane
359	LG:1398822.1:2001JUN22	177	230	forward 1	TM	Cytosolic
359	LG:1398822.1:2001JUN22	231	253	forward 1	TM	Transmembrane
359	LG:1398822.1:2001JUN22	254	1390	forward 1	TM	Non-Cytosolic
362	LG:235076.15:2001JUN22	1	1210	forward 2	TM	Non-Cytosolic
362	LG:235076.15:2001JUN22	1211	1233	forward 2	TM	Transmembrane
362	LG:235076.15:2001JUN22	1234	1245	forward 2	TM	Cytosolic
362	LG:235076.15:2001JUN22	1246	1263	forward 2	TM	Transmembrane
362	LG:235076.15:2001JUN22	1264	1269	forward 2	TM	Non-Cytosolic
363	LG:7689943.1:2001JUN22	1	173	forward 1	TM	Non-Cytosolic
363	LG:7689943.1:2001JUN22	174	196	forward 1	TM	Transmembrane
363	LG:7689943.1:2001JUN22	197	289	forward 1	TM	Cytosolic
364	LG:7693319.3:2001JUN22	1	14	forward 1	TM	Non-Cytosolic
364	LG:7693319.3:2001JUN22	15	37	forward 1	TM	Transmembrane
364	LG:7693319.3:2001JUN22	38	262	forward 1	TM	Cytosolic
364	LG:7693319.3:2001JUN22	263	285	forward 1	TM	Transmembrane
364	LG:7693319.3:2001JUN22	286	315	forward 1	TM	Non-Cytosolic
364	LG:7693319.3:2001JUN22	1	262	forward 3	TM	Cytosolic
364	LG:7693319.3:2001JUN22	263	285	forward 3	TM	Transmembrane
364	LG:7693319.3:2001JUN22	286	314	forward 3	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	1	601	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
365	LG:980241.4:2001JUN22	602	624	forward 1	TM	Transmembrane
365	LG:980241.4:2001JUN22	625	628	forward 1	TM	Cytosolic
365	LG:980241.4:2001JUN22	629	651	forward 1	TM	Transmembrane
365	LG:980241.4:2001JUN22	652	670	forward 1	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	671	693	forward 1	TM	Transmembrane
365	LG:980241.4:2001JUN22	694	705	forward 1	TM	Cytosolic
365	LG:980241.4:2001JUN22	706	728	forward 1	TM	Transmembrane
365	LG:980241.4:2001JUN22	729	806	forward 1	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	807	829	forward 1	TM	Transmembrane
365	LG:980241.4:2001JUN22	830	1089	forward 1	TM	Cytosolic
365	LG:980241.4:2001JUN22	1090	1112	forward 1	TM	Transmembrane
365	LG:980241.4:2001JUN22	1113	1133	forward 1	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	1134	1156	forward 1	TM	Transmembrane
365	LG:980241.4:2001JUN22	1157	1237	forward 1	TM	Cytosolic
365	LG:980241.4:2001JUN22	1238	1260	forward 1	TM	Transmembrane
365	LG:980241.4:2001JUN22	1261	1396	forward 1	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	1397	1419	forward 1	TM	Transmembrane
365	LG:980241.4:2001JUN22	1420	1439	forward 1	TM	Cytosolic
365	LG:980241.4:2001JUN22	1440	1462	forward 1	TM	Transmembrane
365	LG:980241.4:2001JUN22	1463	1774	forward 1	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	1	775	forward 2	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	776	798	forward 2	TM	Transmembrane
365	LG:980241.4:2001JUN22	799	810	forward 2	TM	Cytosolic
365	LG:980241.4:2001JUN22	811	833	forward 2	TM	Transmembrane
365	LG:980241.4:2001JUN22	834	1132	forward 2	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	1133	1155	forward 2	TM	Transmembrane
365	LG:980241.4:2001JUN22	1156	1245	forward 2	TM	Cytosolic
365	LG:980241.4:2001JUN22	1246	1268	forward 2	TM	Transmembrane
365	LG:980241.4:2001JUN22	1269	1723	forward 2	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	1724	1746	forward 2	TM	Transmembrane
365	LG:980241.4:2001JUN22	1747	1773	forward 2	TM	Cytosolic
365	LG:980241.4:2001JUN22	1	336	forward 3	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	337	356	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	357	415	forward 3	TM	Cytosolic
365	LG:980241.4:2001JUN22	416	438	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	439	530	forward 3	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	531	553	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	554	580	forward 3	TM	Cytosolic
365	LG:980241.4:2001JUN22	581	603	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	604	709	forward 3	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	710	732	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	733	751	forward 3	TM	Cytosolic
365	LG:980241.4:2001JUN22	752	770	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	771	805	forward 3	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	806	828	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	829	834	forward 3	TM	Cytosolic
365	LG:980241.4:2001JUN22	835	857	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	858	876	forward 3	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	877	899	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
365	LG:980241.4:2001JUN22	900	926	forward 3	TM	Cytosolic
365	LG:980241.4:2001JUN22	927	949	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	950	963	forward 3	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	964	983	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	984	1079	forward 3	TM	Cytosolic
365	LG:980241.4:2001JUN22	1080	1102	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	1103	1106	forward 3	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	1107	1129	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	1130	1133	forward 3	TM	Cytosolic
365	LG:980241.4:2001JUN22	1134	1156	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	1157	1394	forward 3	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	1395	1417	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	1418	1654	forward 3	TM	Cytosolic
365	LG:980241.4:2001JUN22	1655	1677	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	1678	1714	forward 3	TM	Non-Cytosolic
365	LG:980241.4:2001JUN22	1715	1737	forward 3	TM	Transmembrane
365	LG:980241.4:2001JUN22	1738	1773	forward 3	TM	Cytosolic
366	LG:226475.15:2001JUN22	1	509	forward 1	TM	Non-Cytosolic
366	LG:226475.15:2001JUN22	510	527	forward 1	TM	Transmembrane
366	LG:226475.15:2001JUN22	528	585	forward 1	TM	Cytosolic
366	LG:226475.15:2001JUN22	586	608	forward 1	TM	Transmembrane
366	LG:226475.15:2001JUN22	609	863	forward 1	TM	Non-Cytosolic
366	LG:226475.15:2001JUN22	1	504	forward 2	TM	Non-Cytosolic
366	LG:226475.15:2001JUN22	505	527	forward 2	TM	Transmembrane
366	LG:226475.15:2001JUN22	528	690	forward 2	TM	Cytosolic
366	LG:226475.15:2001JUN22	691	710	forward 2	TM	Transmembrane
366	LG:226475.15:2001JUN22	711	714	forward 2	TM	Non-Cytosolic
366	LG:226475.15:2001JUN22	715	737	forward 2	TM	Transmembrane
366	LG:226475.15:2001JUN22	738	863	forward 2	TM	Cytosolic
366	LG:226475.15:2001JUN22	1	505	forward 3	TM	Non-Cytosolic
366	LG:226475.15:2001JUN22	506	528	forward 3	TM	Transmembrane
366	LG:226475.15:2001JUN22	529	563	forward 3	TM	Cytosolic
366	LG:226475.15:2001JUN22	564	586	forward 3	TM	Transmembrane
366	LG:226475.15:2001JUN22	587	605	forward 3	TM	Non-Cytosolic
366	LG:226475.15:2001JUN22	606	628	forward 3	TM	Transmembrane
366	LG:226475.15:2001JUN22	629	754	forward 3	TM	Cytosolic
366	LG:226475.15:2001JUN22	755	777	forward 3	TM	Transmembrane
366	LG:226475.15:2001JUN22	778	805	forward 3	TM	Non-Cytosolic
366	LG:226475.15:2001JUN22	806	825	forward 3	TM	Transmembrane
366	LG:226475.15:2001JUN22	826	863	forward 3	TM	Cytosolic
367	LG:422564.11:2001JUN22	1	380	forward 1	TM	Non-Cytosolic
367	LG:422564.11:2001JUN22	381	403	forward 1	TM	Transmembrane
367	LG:422564.11:2001JUN22	404	466	forward 1	TM	Cytosolic
367	LG:422564.11:2001JUN22	467	486	forward 1	TM	Transmembrane
367	LG:422564.11:2001JUN22	487	500	forward 1	TM	Non-Cytosolic
367	LG:422564.11:2001JUN22	501	523	forward 1	TM	Transmembrane
367	LG:422564.11:2001JUN22	524	535	forward 1	TM	Cytosolic
367	LG:422564.11:2001JUN22	536	553	forward 1	TM	Transmembrane
367	LG:422564.11:2001JUN22	554	555	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
367	LG:422564.11:2001JUN22	1	374	forward 2	TM	Non-Cytosolic
367	LG:422564.11:2001JUN22	375	397	forward 2	TM	Transmembrane
367	LG:422564.11:2001JUN22	398	500	forward 2	TM	Cytosolic
367	LG:422564.11:2001JUN22	501	523	forward 2	TM	Transmembrane
367	LG:422564.11:2001JUN22	524	532	forward 2	TM	Non-Cytosolic
367	LG:422564.11:2001JUN22	533	549	forward 2	TM	Transmembrane
367	LG:422564.11:2001JUN22	550	555	forward 2	TM	Cytosolic
367	LG:422564.11:2001JUN22	1	301	forward 3	TM	Non-Cytosolic
367	LG:422564.11:2001JUN22	302	324	forward 3	TM	Transmembrane
367	LG:422564.11:2001JUN22	325	330	forward 3	TM	Cytosolic
367	LG:422564.11:2001JUN22	331	350	forward 3	TM	Transmembrane
367	LG:422564.11:2001JUN22	351	380	forward 3	TM	Non-Cytosolic
367	LG:422564.11:2001JUN22	381	403	forward 3	TM	Transmembrane
367	LG:422564.11:2001JUN22	404	554	forward 3	TM	Cytosolic
369	LG:1087811.6:2001MAR30	1	750	forward 2	TM	Non-Cytosolic
369	LG:1087811.6:2001MAR30	751	773	forward 2	TM	Transmembrane
369	LG:1087811.6:2001MAR30	774	849	forward 2	TM	Cytosolic
369	LG:1087811.6:2001MAR30	1	542	forward 3	TM	Non-Cytosolic
369	LG:1087811.6:2001MAR30	543	565	forward 3	TM	Transmembrane
369	LG:1087811.6:2001MAR30	566	635	forward 3	TM	Cytosolic
369	LG:1087811.6:2001MAR30	636	654	forward 3	TM	Transmembrane
369	LG:1087811.6:2001MAR30	655	768	forward 3	TM	Non-Cytosolic
369	LG:1087811.6:2001MAR30	769	791	forward 3	TM	Transmembrane
369	LG:1087811.6:2001MAR30	792	819	forward 3	TM	Cytosolic
369	LG:1087811.6:2001MAR30	820	842	forward 3	TM	Transmembrane
369	LG:1087811.6:2001MAR30	843	848	forward 3	TM	Non-Cytosolic
372	LG:331078.21:2001MAR30	1	272	forward 3	TM	Cytosolic
372	LG:331078.21:2001MAR30	273	295	forward 3	TM	Transmembrane
372	LG:331078.21:2001MAR30	296	769	forward 3	TM	Non-Cytosolic
375	LG:400109.5:2001MAR30	1	413	forward 2	TM	Non-Cytosolic
375	LG:400109.5:2001MAR30	414	433	forward 2	TM	Transmembrane
375	LG:400109.5:2001MAR30	434	452	forward 2	TM	Cytosolic
375	LG:400109.5:2001MAR30	453	475	forward 2	TM	Transmembrane
375	LG:400109.5:2001MAR30	476	487	forward 2	TM	Non-Cytosolic
376	LG:001294.11:2001MAR30	1	1292	forward 1	TM	Non-Cytosolic
376	LG:001294.11:2001MAR30	1293	1315	forward 1	TM	Transmembrane
376	LG:001294.11:2001MAR30	1316	1645	forward 1	TM	Cytosolic
376	LG:001294.11:2001MAR30	1646	1668	forward 1	TM	Transmembrane
376	LG:001294.11:2001MAR30	1669	1763	forward 1	TM	Non-Cytosolic
376	LG:001294.11:2001MAR30	1	1478	forward 2	TM	Non-Cytosolic
376	LG:001294.11:2001MAR30	1479	1501	forward 2	TM	Transmembrane
376	LG:001294.11:2001MAR30	1502	1557	forward 2	TM	Cytosolic
376	LG:001294.11:2001MAR30	1558	1580	forward 2	TM	Transmembrane
376	LG:001294.11:2001MAR30	1581	1635	forward 2	TM	Non-Cytosolic
376	LG:001294.11:2001MAR30	1636	1658	forward 2	TM	Transmembrane
376	LG:001294.11:2001MAR30	1659	1763	forward 2	TM	Cytosolic
376	LG:001294.11:2001MAR30	1	1048	forward 3	TM	Non-Cytosolic
376	LG:001294.11:2001MAR30	1049	1071	forward 3	TM	Transmembrane
376	LG:001294.11:2001MAR30	1072	1082	forward 3	TM	Cytosolic



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
376	LG:001294.11:2001MAR30	1083	1105	forward 3	TM	Transmembrane
376	LG:001294.11:2001MAR30	1106	1647	forward 3	TM	Non-Cytosolic
376	LG:001294.11:2001MAR30	1648	1667	forward 3	TM	Transmembrane
376	LG:001294.11:2001MAR30	1668	1762	forward 3	TM	Cytosolic
377	LG:230895.5:2001MAR30	1	563	forward 1	TM	Non-Cytosolic
377	LG:230895.5:2001MAR30	564	586	forward 1	TM	Transmembrane
377	LG:230895.5:2001MAR30	587	620	forward 1	TM	Cytosolic
377	LG:230895.5:2001MAR30	621	643	forward 1	TM	Transmembrane
377	LG:230895.5:2001MAR30	644	656	forward 1	TM	Non-Cytosolic
377	LG:230895.5:2001MAR30	1	138	forward 2	TM	Cytosolic
377	LG:230895.5:2001MAR30	139	161	forward 2	TM	Transmembrane
377	LG:230895.5:2001MAR30	162	656	forward 2	TM	Non-Cytosolic
379	LI:1072276.1:2001MAY17	1	250	forward 2	TM	Non-Cytosolic
379	LI:1072276.1:2001MAY17	251	273	forward 2	TM	Transmembrane
379	LI:1072276.1:2001MAY17	274	297	forward 2	TM	Cytosolic
379	LI:1072276.1:2001MAY17	1	241	forward 3	TM	Non-Cytosolic
379	LI:1072276.1:2001MAY17	242	264	forward 3	TM	Transmembrane
379	LI:1072276.1:2001MAY17	265	297	forward 3	TM	Cytosolic
383	LI:2032264.3:2001MAY17	1	173	forward 3	TM	Non-Cytosolic
383	LI:2032264.3:2001MAY17	174	196	forward 3	TM	Transmembrane
383	LI:2032264.3:2001MAY17	197	212	forward 3	TM	Cytosolic
384	LI:2070168.1:2001MAY17	1	375	forward 3	TM	Non-Cytosolic
384	LI:2070168.1:2001MAY17	376	398	forward 3	TM	Transmembrane
384	LI:2070168.1:2001MAY17	399	409	forward 3	TM	Cytosolic
388	LI:237520.26:2001MAY17	1	54	forward 3	TM	Cytosolic
388	LI:237520.26:2001MAY17	55	77	forward 3	TM	Transmembrane
388	LI:237520.26:2001MAY17	78	264	forward 3	TM	Non-Cytosolic
389	LI:243892.46:2001MAY17	2	55	forward 2	SP	
390	LI:400590.4:2001MAY17	1	300	forward 1	TM	Non-Cytosolic
390	LI:400590.4:2001MAY17	301	323	forward 1	TM	Transmembrane
390	LI:400590.4:2001MAY17	324	496	forward 1	TM	Cytosolic
390	LI:400590.4:2001MAY17	497	519	forward 1	TM	Transmembrane
390	LI:400590.4:2001MAY17	520	538	forward 1	TM	Non-Cytosolic
390	LI:400590.4:2001MAY17	539	561	forward 1	TM	Transmembrane
390	LI:400590.4:2001MAY17	562	650	forward 1	TM	Cytosolic
390	LI:400590.4:2001MAY17	651	668	forward 1	TM	Transmembrane
390	LI:400590.4:2001MAY17	669	1039	forward 1	TM	Non-Cytosolic
390	LI:400590.4:2001MAY17	1040	1062	forward 1	TM	Transmembrane
390	LI:400590.4:2001MAY17	1063	1126	forward 1	TM	Cytosolic
390	LI:400590.4:2001MAY17	1	735	forward 3	TM	Non-Cytosolic
390	LI:400590.4:2001MAY17	736	758	forward 3	TM	Transmembrane
390	LI:400590.4:2001MAY17	759	933	forward 3	TM	Cytosolic
390	LI:400590.4:2001MAY17	934	956	forward 3	TM	Transmembrane
390	LI:400590.4:2001MAY17	957	1033	forward 3	TM	Non-Cytosolic
390	LI:400590.4:2001MAY17	1034	1056	forward 3	TM	Transmembrane
390	LI:400590.4:2001MAY17	1057	1068	forward 3	TM	Cytosolic
390	LI:400590.4:2001MAY17	1069	1091	forward 3	TM	Transmembrane
390	LI:400590.4:2001MAY17	1092	1126	forward 3	TM	Non-Cytosolic
391	LI:407084.4:2001MAY17	1	173	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
391	U:407084.4:2001MAY17	174	196	forward 1	TM	Transmembrane
391	U:407084.4:2001MAY17	197	286	forward 1	TM	Cytosolic
391	U:407084.4:2001MAY17	1	173	forward 2	TM	Non-Cytosolic
391	U:407084.4:2001MAY17	174	196	forward 2	TM	Transmembrane
391	U:407084.4:2001MAY17	197	285	forward 2	TM	Cytosolic
391	U:407084.4:2001MAY17	1	158	forward 3	TM	Cytosolic
391	U:407084.4:2001MAY17	159	181	forward 3	TM	Transmembrane
391	U:407084.4:2001MAY17	182	285	forward 3	TM	Non-Cytosolic
392	U:2052211.9:2001MAY17	1	658	forward 1	TM	Non-Cytosolic
392	U:2052211.9:2001MAY17	659	676	forward 1	TM	Transmembrane
392	U:2052211.9:2001MAY17	677	683	forward 1	TM	Cytosolic
392	U:2052211.9:2001MAY17	1	521	forward 2	TM	Non-Cytosolic
392	U:2052211.9:2001MAY17	522	539	forward 2	TM	Transmembrane
392	U:2052211.9:2001MAY17	540	621	forward 2	TM	Cytosolic
392	U:2052211.9:2001MAY17	622	644	forward 2	TM	Transmembrane
392	U:2052211.9:2001MAY17	645	653	forward 2	TM	Non-Cytosolic
392	U:2052211.9:2001MAY17	654	676	forward 2	TM	Transmembrane
392	U:2052211.9:2001MAY17	677	682	forward 2	TM	Cytosolic
392	U:2052211.9:2001MAY17	1	622	forward 3	TM	Non-Cytosolic
392	U:2052211.9:2001MAY17	623	640	forward 3	TM	Transmembrane
392	U:2052211.9:2001MAY17	641	682	forward 3	TM	Cytosolic
395	U:401586.1:2001MAY17	1	440	forward 1	TM	Non-Cytosolic
395	U:401586.1:2001MAY17	441	463	forward 1	TM	Transmembrane
395	U:401586.1:2001MAY17	464	483	forward 1	TM	Cytosolic
396	LG:1093982.21:2001JUN22	1	158	forward 2	TM	Cytosolic
396	LG:1093982.21:2001JUN22	159	181	forward 2	TM	Transmembrane
396	LG:1093982.21:2001JUN22	182	337	forward 2	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1	726	forward 1	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	727	746	forward 1	TM	Transmembrane
398	LG:199121.19:2001JUN22	747	953	forward 1	TM	Cytosolic
398	LG:199121.19:2001JUN22	954	976	forward 1	TM	Transmembrane
398	LG:199121.19:2001JUN22	977	999	forward 1	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1000	1022	forward 1	TM	Transmembrane
398	LG:199121.19:2001JUN22	1023	1052	forward 1	TM	Cytosolic
398	LG:199121.19:2001JUN22	1053	1075	forward 1	TM	Transmembrane
398	LG:199121.19:2001JUN22	1076	1202	forward 1	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1203	1225	forward 1	TM	Transmembrane
398	LG:199121.19:2001JUN22	1226	1245	forward 1	TM	Cytosolic
398	LG:199121.19:2001JUN22	1246	1268	forward 1	TM	Transmembrane
398	LG:199121.19:2001JUN22	1269	1311	forward 1	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1312	1334	forward 1	TM	Transmembrane
398	LG:199121.19:2001JUN22	1335	1387	forward 1	TM	Cytosolic
398	LG:199121.19:2001JUN22	1388	1405	forward 1	TM	Transmembrane
398	LG:199121.19:2001JUN22	1406	1409	forward 1	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1410	1429	forward 1	TM	Transmembrane
398	LG:199121.19:2001JUN22	1430	1441	forward 1	TM	Cytosolic
398	LG:199121.19:2001JUN22	1442	1461	forward 1	TM	Transmembrane
398	LG:199121.19:2001JUN22	1462	1478	forward 1	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1	831	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
398	LG:199121.19:2001JUN22	832	854	forward 2	TM	Transmembrane
398	LG:199121.19:2001JUN22	855	860	forward 2	TM	Cytosolic
398	LG:199121.19:2001JUN22	861	880	forward 2	TM	Transmembrane
398	LG:199121.19:2001JUN22	881	1247	forward 2	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1248	1270	forward 2	TM	Transmembrane
398	LG:199121.19:2001JUN22	1271	1281	forward 2	TM	Cytosolic
398	LG:199121.19:2001JUN22	1282	1304	forward 2	TM	Transmembrane
398	LG:199121.19:2001JUN22	1305	1439	forward 2	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1440	1462	forward 2	TM	Transmembrane
398	LG:199121.19:2001JUN22	1463	1477	forward 2	TM	Cytosolic
398	LG:199121.19:2001JUN22	1	1158	forward 3	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1159	1181	forward 3	TM	Transmembrane
398	LG:199121.19:2001JUN22	1182	1201	forward 3	TM	Cytosolic
398	LG:199121.19:2001JUN22	1202	1224	forward 3	TM	Transmembrane
398	LG:199121.19:2001JUN22	1225	1243	forward 3	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1244	1266	forward 3	TM	Transmembrane
398	LG:199121.19:2001JUN22	1267	1405	forward 3	TM	Cytosolic
398	LG:199121.19:2001JUN22	1406	1428	forward 3	TM	Transmembrane
398	LG:199121.19:2001JUN22	1429	1437	forward 3	TM	Non-Cytosolic
398	LG:199121.19:2001JUN22	1438	1457	forward 3	TM	Transmembrane
398	LG:199121.19:2001JUN22	1458	1477	forward 3	TM	Cytosolic
399	LG:482411.11:2001JUN22	1	443	forward 3	TM	Non-Cytosolic
399	LG:482411.11:2001JUN22	444	466	forward 3	TM	Transmembrane
399	LG:482411.11:2001JUN22	467	511	forward 3	TM	Cytosolic
399	LG:482411.11:2001JUN22	512	534	forward 3	TM	Transmembrane
399	LG:482411.11:2001JUN22	535	1042	forward 3	TM	Non-Cytosolic
401	LG:1500347.6:2001JUN22	1	572	forward 1	TM	Non-Cytosolic
401	LG:1500347.6:2001JUN22	573	590	forward 1	TM	Transmembrane
401	LG:1500347.6:2001JUN22	591	620	forward 1	TM	Cytosolic
401	LG:1500347.6:2001JUN22	621	643	forward 1	TM	Transmembrane
401	LG:1500347.6:2001JUN22	644	646	forward 1	TM	Non-Cytosolic
401	LG:1500347.6:2001JUN22	647	666	forward 1	TM	Transmembrane
401	LG:1500347.6:2001JUN22	667	672	forward 1	TM	Cytosolic
401	LG:1500347.6:2001JUN22	673	695	forward 1	TM	Transmembrane
401	LG:1500347.6:2001JUN22	696	698	forward 1	TM	Non-Cytosolic
401	LG:1500347.6:2001JUN22	699	721	forward 1	TM	Transmembrane
401	LG:1500347.6:2001JUN22	722	727	forward 1	TM	Cytosolic
401	LG:1500347.6:2001JUN22	728	750	forward 1	TM	Transmembrane
401	LG:1500347.6:2001JUN22	751	1165	forward 1	TM	Non-Cytosolic
401	LG:1500347.6:2001JUN22	1	620	forward 2	TM	Non-Cytosolic
401	LG:1500347.6:2001JUN22	621	640	forward 2	TM	Transmembrane
401	LG:1500347.6:2001JUN22	641	646	forward 2	TM	Cytosolic
401	LG:1500347.6:2001JUN22	647	669	forward 2	TM	Transmembrane
401	LG:1500347.6:2001JUN22	670	683	forward 2	TM	Non-Cytosolic
401	LG:1500347.6:2001JUN22	684	703	forward 2	TM	Transmembrane
401	LG:1500347.6:2001JUN22	704	723	forward 2	TM	Cytosolic
401	LG:1500347.6:2001JUN22	724	746	forward 2	TM	Transmembrane
401	LG:1500347.6:2001JUN22	747	1165	forward 2	TM	Non-Cytosolic
401	LG:1500347.6:2001JUN22	1	629	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
401	LG:1500347.6:2001JUN22	630	652	forward 3	TM	Transmembrane
401	LG:1500347.6:2001JUN22	653	727	forward 3	TM	Cytosolic
401	LG:1500347.6:2001JUN22	728	750	forward 3	TM	Transmembrane
401	LG:1500347.6:2001JUN22	751	1165	forward 3	TM	Non-Cytosolic
403	LG:010761.6:2001MAR30	1	476	forward 2	TM	Non-Cytosolic
403	LG:010761.6:2001MAR30	477	499	forward 2	TM	Transmembrane
403	LG:010761.6:2001MAR30	500	511	forward 2	TM	Cytosolic
403	LG:010761.6:2001MAR30	512	531	forward 2	TM	Transmembrane
403	LG:010761.6:2001MAR30	532	583	forward 2	TM	Non-Cytosolic
403	LG:010761.6:2001MAR30	584	606	forward 2	TM	Transmembrane
403	LG:010761.6:2001MAR30	607	638	forward 2	TM	Cytosolic
403	LG:010761.6:2001MAR30	639	656	forward 2	TM	Transmembrane
403	LG:010761.6:2001MAR30	657	661	forward 2	TM	Non-Cytosolic
404	LG:104970.6:2001MAR30	1	735	forward 2	TM	Non-Cytosolic
404	LG:104970.6:2001MAR30	736	758	forward 2	TM	Transmembrane
404	LG:104970.6:2001MAR30	759	911	forward 2	TM	Cytosolic
404	LG:104970.6:2001MAR30	912	931	forward 2	TM	Transmembrane
404	LG:104970.6:2001MAR30	932	934	forward 2	TM	Non-Cytosolic
404	LG:104970.6:2001MAR30	935	957	forward 2	TM	Transmembrane
404	LG:104970.6:2001MAR30	958	1024	forward 2	TM	Cytosolic
404	LG:104970.6:2001MAR30	1	908	forward 3	TM	Non-Cytosolic
404	LG:104970.6:2001MAR30	909	931	forward 3	TM	Transmembrane
404	LG:104970.6:2001MAR30	932	942	forward 3	TM	Cytosolic
404	LG:104970.6:2001MAR30	943	962	forward 3	TM	Transmembrane
404	LG:104970.6:2001MAR30	963	981	forward 3	TM	Non-Cytosolic
404	LG:104970.6:2001MAR30	982	1004	forward 3	TM	Transmembrane
404	LG:104970.6:2001MAR30	1005	1023	forward 3	TM	Cytosolic
406	LG:1094182.9:2001MAR30	1	331	forward 1	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	332	354	forward 1	TM	Transmembrane
406	LG:1094182.9:2001MAR30	355	397	forward 1	TM	Cytosolic
406	LG:1094182.9:2001MAR30	398	420	forward 1	TM	Transmembrane
406	LG:1094182.9:2001MAR30	421	439	forward 1	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	440	462	forward 1	TM	Transmembrane
406	LG:1094182.9:2001MAR30	463	876	forward 1	TM	Cytosolic
406	LG:1094182.9:2001MAR30	877	899	forward 1	TM	Transmembrane
406	LG:1094182.9:2001MAR30	900	928	forward 1	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	929	951	forward 1	TM	Transmembrane
406	LG:1094182.9:2001MAR30	952	1026	forward 1	TM	Cytosolic
406	LG:1094182.9:2001MAR30	1	317	forward 2	TM	Cytosolic
406	LG:1094182.9:2001MAR30	318	340	forward 2	TM	Transmembrane
406	LG:1094182.9:2001MAR30	341	359	forward 2	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	360	379	forward 2	TM	Transmembrane
406	LG:1094182.9:2001MAR30	380	399	forward 2	TM	Cytosolic
406	LG:1094182.9:2001MAR30	400	422	forward 2	TM	Transmembrane
406	LG:1094182.9:2001MAR30	423	436	forward 2	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	437	459	forward 2	TM	Transmembrane
406	LG:1094182.9:2001MAR30	460	487	forward 2	TM	Cytosolic
406	LG:1094182.9:2001MAR30	488	510	forward 2	TM	Transmembrane
406	LG:1094182.9:2001MAR30	511	529	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
406	LG:1094182.9:2001MAR30	530	552	forward 2	TM	Transmembrane
406	LG:1094182.9:2001MAR30	553	683	forward 2	TM	Cytosolic
406	LG:1094182.9:2001MAR30	684	701	forward 2	TM	Transmembrane
406	LG:1094182.9:2001MAR30	702	715	forward 2	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	716	738	forward 2	TM	Transmembrane
406	LG:1094182.9:2001MAR30	739	874	forward 2	TM	Cytosolic
406	LG:1094182.9:2001MAR30	875	906	forward 2	TM	Transmembrane
406	LG:1094182.9:2001MAR30	907	1026	forward 2	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	1	329	forward 3	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	330	352	forward 3	TM	Transmembrane
406	LG:1094182.9:2001MAR30	353	358	forward 3	TM	Cytosolic
406	LG:1094182.9:2001MAR30	359	378	forward 3	TM	Transmembrane
406	LG:1094182.9:2001MAR30	379	397	forward 3	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	398	420	forward 3	TM	Transmembrane
406	LG:1094182.9:2001MAR30	421	436	forward 3	TM	Cytosolic
406	LG:1094182.9:2001MAR30	437	459	forward 3	TM	Transmembrane
406	LG:1094182.9:2001MAR30	460	478	forward 3	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	479	498	forward 3	TM	Transmembrane
406	LG:1094182.9:2001MAR30	499	528	forward 3	TM	Cytosolic
406	LG:1094182.9:2001MAR30	529	551	forward 3	TM	Transmembrane
406	LG:1094182.9:2001MAR30	552	555	forward 3	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	556	573	forward 3	TM	Transmembrane
406	LG:1094182.9:2001MAR30	574	860	forward 3	TM	Cytosolic
406	LG:1094182.9:2001MAR30	861	883	forward 3	TM	Transmembrane
406	LG:1094182.9:2001MAR30	884	897	forward 3	TM	Non-Cytosolic
406	LG:1094182.9:2001MAR30	898	920	forward 3	TM	Transmembrane
406	LG:1094182.9:2001MAR30	921	987	forward 3	TM	Cytosolic
406	LG:1094182.9:2001MAR30	988	1010	forward 3	TM	Transmembrane
406	LG:1094182.9:2001MAR30	1011	1025	forward 3	TM	Non-Cytosolic
407	LG:1399075.18:2001MAR30	1	59	forward 1	TM	Cytosolic
407	LG:1399075.18:2001MAR30	60	77	forward 1	TM	Transmembrane
407	LG:1399075.18:2001MAR30	78	394	forward 1	TM	Non-Cytosolic
407	LG:1399075.18:2001MAR30	395	417	forward 1	TM	Transmembrane
407	LG:1399075.18:2001MAR30	418	580	forward 1	TM	Cytosolic
407	LG:1399075.18:2001MAR30	581	603	forward 1	TM	Transmembrane
407	LG:1399075.18:2001MAR30	604	909	forward 1	TM	Non-Cytosolic
407	LG:1399075.18:2001MAR30	1	320	forward 2	TM	Non-Cytosolic
407	LG:1399075.18:2001MAR30	321	343	forward 2	TM	Transmembrane
407	LG:1399075.18:2001MAR30	344	399	forward 2	TM	Cytosolic
407	LG:1399075.18:2001MAR30	400	417	forward 2	TM	Transmembrane
407	LG:1399075.18:2001MAR30	418	479	forward 2	TM	Non-Cytosolic
407	LG:1399075.18:2001MAR30	480	502	forward 2	TM	Transmembrane
407	LG:1399075.18:2001MAR30	503	578	forward 2	TM	Cytosolic
407	LG:1399075.18:2001MAR30	579	601	forward 2	TM	Transmembrane
407	LG:1399075.18:2001MAR30	602	909	forward 2	TM	Non-Cytosolic
407	LG:1399075.18:2001MAR30	1	3	forward 3	TM	Non-Cytosolic
407	LG:1399075.18:2001MAR30	4	21	forward 3	TM	Transmembrane
407	LG:1399075.18:2001MAR30	22	41	forward 3	TM	Cytosolic
407	LG:1399075.18:2001MAR30	42	61	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
407	LG:1399075.18:2001MAR30	62	64	forward 3	TM	Non-Cytosolic
407	LG:1399075.18:2001MAR30	65	87	forward 3	TM	Transmembrane
407	LG:1399075.18:2001MAR30	88	213	forward 3	TM	Cytosolic
407	LG:1399075.18:2001MAR30	214	236	forward 3	TM	Transmembrane
407	LG:1399075.18:2001MAR30	237	320	forward 3	TM	Non-Cytosolic
407	LG:1399075.18:2001MAR30	321	343	forward 3	TM	Transmembrane
407	LG:1399075.18:2001MAR30	344	387	forward 3	TM	Cytosolic
407	LG:1399075.18:2001MAR30	388	410	forward 3	TM	Transmembrane
407	LG:1399075.18:2001MAR30	411	476	forward 3	TM	Non-Cytosolic
407	LG:1399075.18:2001MAR30	477	499	forward 3	TM	Transmembrane
407	LG:1399075.18:2001MAR30	500	581	forward 3	TM	Cytosolic
407	LG:1399075.18:2001MAR30	582	604	forward 3	TM	Transmembrane
407	LG:1399075.18:2001MAR30	605	908	forward 3	TM	Non-Cytosolic
408	LG:1501344.7:2001MAR30	1	73	forward 1	TM	Cytosolic
408	LG:1501344.7:2001MAR30	74	96	forward 1	TM	Transmembrane
408	LG:1501344.7:2001MAR30	97	99	forward 1	TM	Non-Cytosolic
408	LG:1501344.7:2001MAR30	100	122	forward 1	TM	Transmembrane
408	LG:1501344.7:2001MAR30	123	193	forward 1	TM	Cytosolic
408	LG:1501344.7:2001MAR30	1	70	forward 2	TM	Non-Cytosolic
408	LG:1501344.7:2001MAR30	71	93	forward 2	TM	Transmembrane
408	LG:1501344.7:2001MAR30	94	192	forward 2	TM	Cytosolic
409	U:1144484.3:2001MAY17	1	68	forward 1	TM	Cytosolic
409	U:1144484.3:2001MAY17	69	91	forward 1	TM	Transmembrane
409	U:1144484.3:2001MAY17	92	448	forward 1	TM	Non-Cytosolic
409	U:1144484.3:2001MAY17	1	70	forward 3	TM	Cytosolic
409	U:1144484.3:2001MAY17	71	90	forward 3	TM	Transmembrane
409	U:1144484.3:2001MAY17	91	447	forward 3	TM	Non-Cytosolic
410	U:337388.11:2001MAY17	1	93	forward 3	TM	Cytosolic
410	U:337388.11:2001MAY17	94	116	forward 3	TM	Transmembrane
410	U:337388.11:2001MAY17	117	645	forward 3	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	1	258	forward 1	TM	Cytosolic
412	U:480238.8:2001MAY17	259	276	forward 1	TM	Transmembrane
412	U:480238.8:2001MAY17	277	305	forward 1	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	306	328	forward 1	TM	Transmembrane
412	U:480238.8:2001MAY17	329	340	forward 1	TM	Cytosolic
412	U:480238.8:2001MAY17	341	363	forward 1	TM	Transmembrane
412	U:480238.8:2001MAY17	364	372	forward 1	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	373	395	forward 1	TM	Transmembrane
412	U:480238.8:2001MAY17	396	415	forward 1	TM	Cytosolic
412	U:480238.8:2001MAY17	416	433	forward 1	TM	Transmembrane
412	U:480238.8:2001MAY17	434	442	forward 1	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	443	465	forward 1	TM	Transmembrane
412	U:480238.8:2001MAY17	466	477	forward 1	TM	Cytosolic
412	U:480238.8:2001MAY17	478	500	forward 1	TM	Transmembrane
412	U:480238.8:2001MAY17	501	728	forward 1	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	729	751	forward 1	TM	Transmembrane
412	U:480238.8:2001MAY17	752	906	forward 1	TM	Cytosolic
412	U:480238.8:2001MAY17	1	270	forward 2	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	271	293	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
412	U:480238.8:2001MAY17	294	305	forward 2	TM	Cytosolic
412	U:480238.8:2001MAY17	306	328	forward 2	TM	Transmembrane
412	U:480238.8:2001MAY17	329	478	forward 2	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	479	501	forward 2	TM	Transmembrane
412	U:480238.8:2001MAY17	502	600	forward 2	TM	Cytosolic
412	U:480238.8:2001MAY17	601	623	forward 2	TM	Transmembrane
412	U:480238.8:2001MAY17	624	665	forward 2	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	666	688	forward 2	TM	Transmembrane
412	U:480238.8:2001MAY17	689	707	forward 2	TM	Cytosolic
412	U:480238.8:2001MAY17	708	730	forward 2	TM	Transmembrane
412	U:480238.8:2001MAY17	731	733	forward 2	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	734	751	forward 2	TM	Transmembrane
412	U:480238.8:2001MAY17	752	906	forward 2	TM	Cytosolic
412	U:480238.8:2001MAY17	1	262	forward 3	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	263	285	forward 3	TM	Transmembrane
412	U:480238.8:2001MAY17	286	305	forward 3	TM	Cytosolic
412	U:480238.8:2001MAY17	306	328	forward 3	TM	Transmembrane
412	U:480238.8:2001MAY17	329	337	forward 3	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	338	360	forward 3	TM	Transmembrane
412	U:480238.8:2001MAY17	361	436	forward 3	TM	Cytosolic
412	U:480238.8:2001MAY17	437	459	forward 3	TM	Transmembrane
412	U:480238.8:2001MAY17	460	478	forward 3	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	479	501	forward 3	TM	Transmembrane
412	U:480238.8:2001MAY17	502	564	forward 3	TM	Cytosolic
412	U:480238.8:2001MAY17	565	582	forward 3	TM	Transmembrane
412	U:480238.8:2001MAY17	583	591	forward 3	TM	Non-Cytosolic
412	U:480238.8:2001MAY17	592	611	forward 3	TM	Transmembrane
412	U:480238.8:2001MAY17	612	623	forward 3	TM	Cytosolic
412	U:480238.8:2001MAY17	624	646	forward 3	TM	Transmembrane
412	U:480238.8:2001MAY17	647	906	forward 3	TM	Non-Cytosolic
413	U:2121656.1:2001MAY17	1	93	forward 1	TM	Cytosolic
413	U:2121656.1:2001MAY17	94	116	forward 1	TM	Transmembrane
413	U:2121656.1:2001MAY17	117	404	forward 1	TM	Non-Cytosolic
413	U:2121656.1:2001MAY17	1	6	forward 2	TM	Cytosolic
413	U:2121656.1:2001MAY17	7	26	forward 2	TM	Transmembrane
413	U:2121656.1:2001MAY17	27	132	forward 2	TM	Non-Cytosolic
413	U:2121656.1:2001MAY17	133	155	forward 2	TM	Transmembrane
413	U:2121656.1:2001MAY17	156	161	forward 2	TM	Cytosolic
413	U:2121656.1:2001MAY17	162	184	forward 2	TM	Transmembrane
413	U:2121656.1:2001MAY17	185	217	forward 2	TM	Non-Cytosolic
413	U:2121656.1:2001MAY17	218	240	forward 2	TM	Transmembrane
413	U:2121656.1:2001MAY17	241	281	forward 2	TM	Cytosolic
413	U:2121656.1:2001MAY17	282	304	forward 2	TM	Transmembrane
413	U:2121656.1:2001MAY17	305	340	forward 2	TM	Non-Cytosolic
413	U:2121656.1:2001MAY17	341	363	forward 2	TM	Transmembrane
413	U:2121656.1:2001MAY17	364	375	forward 2	TM	Cytosolic
413	U:2121656.1:2001MAY17	376	398	forward 2	TM	Transmembrane
413	U:2121656.1:2001MAY17	399	404	forward 2	TM	Non-Cytosolic
413	U:2121656.1:2001MAY17	1	67	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
413	U:2121656.1:2001MAY17	68	90	forward 3	TM	Transmembrane
413	U:2121656.1:2001MAY17	91	104	forward 3	TM	Non-Cytosolic
413	U:2121656.1:2001MAY17	105	127	forward 3	TM	Transmembrane
413	U:2121656.1:2001MAY17	128	200	forward 3	TM	Cytosolic
413	U:2121656.1:2001MAY17	201	223	forward 3	TM	Transmembrane
413	U:2121656.1:2001MAY17	224	324	forward 3	TM	Non-Cytosolic
413	U:2121656.1:2001MAY17	325	344	forward 3	TM	Transmembrane
413	U:2121656.1:2001MAY17	345	350	forward 3	TM	Cytosolic
413	U:2121656.1:2001MAY17	351	368	forward 3	TM	Transmembrane
413	U:2121656.1:2001MAY17	369	377	forward 3	TM	Non-Cytosolic
413	U:2121656.1:2001MAY17	378	395	forward 3	TM	Transmembrane
413	U:2121656.1:2001MAY17	396	404	forward 3	TM	Cytosolic
414	LG:1328038.5:2001JUN22	1	158	forward 3	TM	Cytosolic
415	LG:437443.21:2001JUN22	1	237	forward 1	TM	Cytosolic
415	LG:437443.21:2001JUN22	238	260	forward 1	TM	Transmembrane
415	LG:437443.21:2001JUN22	261	279	forward 1	TM	Non-Cytosolic
415	LG:437443.21:2001JUN22	280	302	forward 1	TM	Transmembrane
415	LG:437443.21:2001JUN22	303	314	forward 1	TM	Cytosolic
415	LG:437443.21:2001JUN22	315	334	forward 1	TM	Transmembrane
415	LG:437443.21:2001JUN22	335	405	forward 1	TM	Non-Cytosolic
415	LG:437443.21:2001JUN22	1	278	forward 2	TM	Non-Cytosolic
415	LG:437443.21:2001JUN22	279	301	forward 2	TM	Transmembrane
415	LG:437443.21:2001JUN22	302	313	forward 2	TM	Cytosolic
415	LG:437443.21:2001JUN22	314	336	forward 2	TM	Transmembrane
415	LG:437443.21:2001JUN22	337	366	forward 2	TM	Non-Cytosolic
415	LG:437443.21:2001JUN22	367	389	forward 2	TM	Transmembrane
415	LG:437443.21:2001JUN22	390	405	forward 2	TM	Cytosolic
417	LG:7689014.1:2001JUN22	1	141	forward 2	TM	Cytosolic
417	LG:7689014.1:2001JUN22	142	164	forward 2	TM	Transmembrane
417	LG:7689014.1:2001JUN22	165	342	forward 2	TM	Non-Cytosolic
418	LG:984007.4:2001JUN22	1	4	forward 1	TM	Cytosolic
418	LG:984007.4:2001JUN22	5	27	forward 1	TM	Transmembrane
418	LG:984007.4:2001JUN22	28	36	forward 1	TM	Non-Cytosolic
418	LG:984007.4:2001JUN22	37	59	forward 1	TM	Transmembrane
418	LG:984007.4:2001JUN22	60	65	forward 1	TM	Cytosolic
418	LG:984007.4:2001JUN22	66	88	forward 1	TM	Transmembrane
418	LG:984007.4:2001JUN22	89	1172	forward 1	TM	Non-Cytosolic
418	LG:984007.4:2001JUN22	1	4	forward 2	TM	Non-Cytosolic
418	LG:984007.4:2001JUN22	5	27	forward 2	TM	Transmembrane
418	LG:984007.4:2001JUN22	28	39	forward 2	TM	Cytosolic
418	LG:984007.4:2001JUN22	40	62	forward 2	TM	Transmembrane
418	LG:984007.4:2001JUN22	63	71	forward 2	TM	Non-Cytosolic
418	LG:984007.4:2001JUN22	72	94	forward 2	TM	Transmembrane
418	LG:984007.4:2001JUN22	95	462	forward 2	TM	Cytosolic
418	LG:984007.4:2001JUN22	463	481	forward 2	TM	Transmembrane
418	LG:984007.4:2001JUN22	482	485	forward 2	TM	Non-Cytosolic
418	LG:984007.4:2001JUN22	486	505	forward 2	TM	Transmembrane
418	LG:984007.4:2001JUN22	506	839	forward 2	TM	Cytosolic
418	LG:984007.4:2001JUN22	840	862	forward 2	TM	Transmembrane



TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
418	LG:984007.4:2001JUN22	863	866	forward 2	TM	Non-Cytosolic
418	LG:984007.4:2001JUN22	867	884	forward 2	TM	Transmembrane
418	LG:984007.4:2001JUN22	885	888	forward 2	TM	Cytosolic
418	LG:984007.4:2001JUN22	889	906	forward 2	TM	Transmembrane
418	LG:984007.4:2001JUN22	907	920	forward 2	TM	Non-Cytosolic
418	LG:984007.4:2001JUN22	921	943	forward 2	TM	Transmembrane
418	LG:984007.4:2001JUN22	944	1172	forward 2	TM	Cytosolic
418	LG:984007.4:2001JUN22	1	47	forward 3	TM	Non-Cytosolic
418	LG:984007.4:2001JUN22	48	70	forward 3	TM	Transmembrane
418	LG:984007.4:2001JUN22	71	76	forward 3	TM	Cytosolic
418	LG:984007.4:2001JUN22	77	99	forward 3	TM	Transmembrane
418	LG:984007.4:2001JUN22	100	1171	forward 3	TM	Non-Cytosolic
419	LG:008606.21:2001JUN22	1	371	forward 2	TM	Non-Cytosolic
419	LG:008606.21:2001JUN22	372	394	forward 2	TM	Transmembrane
419	LG:008606.21:2001JUN22	395	481	forward 2	TM	Cytosolic
419	LG:008606.21:2001JUN22	482	504	forward 2	TM	Transmembrane
419	LG:008606.21:2001JUN22	505	1013	forward 2	TM	Non-Cytosolic
419	LG:008606.21:2001JUN22	1	12	forward 3	TM	Cytosolic
419	LG:008606.21:2001JUN22	13	35	forward 3	TM	Transmembrane
419	LG:008606.21:2001JUN22	36	40	forward 3	TM	Non-Cytosolic
419	LG:008606.21:2001JUN22	41	63	forward 3	TM	Transmembrane
419	LG:008606.21:2001JUN22	64	380	forward 3	TM	Cytosolic
419	LG:008606.21:2001JUN22	381	398	forward 3	TM	Transmembrane
419	LG:008606.21:2001JUN22	399	412	forward 3	TM	Non-Cytosolic
419	LG:008606.21:2001JUN22	413	435	forward 3	TM	Transmembrane
419	LG:008606.21:2001JUN22	436	447	forward 3	TM	Cytosolic
419	LG:008606.21:2001JUN22	448	470	forward 3	TM	Transmembrane
419	LG:008606.21:2001JUN22	471	484	forward 3	TM	Non-Cytosolic
419	LG:008606.21:2001JUN22	485	504	forward 3	TM	Transmembrane
419	LG:008606.21:2001JUN22	505	510	forward 3	TM	Cytosolic
419	LG:008606.21:2001JUN22	511	533	forward 3	TM	Transmembrane
419	LG:008606.21:2001JUN22	534	1013	forward 3	TM	Non-Cytosolic
420	LG:240680.1:2001JUN22	1	70	forward 3	TM	Cytosolic
420	LG:240680.1:2001JUN22	71	93	forward 3	TM	Transmembrane
420	LG:240680.1:2001JUN22	94	112	forward 3	TM	Non-Cytosolic
420	LG:240680.1:2001JUN22	113	135	forward 3	TM	Transmembrane
420	LG:240680.1:2001JUN22	136	139	forward 3	TM	Cytosolic
420	LG:240680.1:2001JUN22	140	162	forward 3	TM	Transmembrane
420	LG:240680.1:2001JUN22	163	206	forward 3	TM	Non-Cytosolic
421	LG:160481.1:2001MAR30	1	6	forward 1	TM	Cytosolic
421	LG:160481.1:2001MAR30	7	29	forward 1	TM	Transmembrane
421	LG:160481.1:2001MAR30	30	355	forward 1	TM	Non-Cytosolic
421	LG:160481.1:2001MAR30	1	14	forward 2	TM	Non-Cytosolic
421	LG:160481.1:2001MAR30	15	37	forward 2	TM	Transmembrane
421	LG:160481.1:2001MAR30	38	355	forward 2	TM	Cytosolic
423	LG:407582.21:2001MAR30	1	901	forward 2	TM	Non-Cytosolic
423	LG:407582.21:2001MAR30	902	924	forward 2	TM	Transmembrane
423	LG:407582.21:2001MAR30	925	1142	forward 2	TM	Cytosolic
423	LG:407582.21:2001MAR30	1	310	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
423	LG:407582.21:2001MAR30	311	333	forward 3	TM	Transmembrane
423	LG:407582.21:2001MAR30	334	1142	forward 3	TM	Non-Cytosolic
424	LI:2051428.9:2001MAY17	1	148	forward 1	TM	Cytosolic
424	LI:2051428.9:2001MAY17	149	171	forward 1	TM	Transmembrane
424	LI:2051428.9:2001MAY17	172	713	forward 1	TM	Non-Cytosolic
424	LI:2051428.9:2001MAY17	714	736	forward 1	TM	Transmembrane
424	LI:2051428.9:2001MAY17	737	756	forward 1	TM	Cytosolic
424	LI:2051428.9:2001MAY17	757	775	forward 1	TM	Transmembrane
424	LI:2051428.9:2001MAY17	776	1548	forward 1	TM	Non-Cytosolic
424	LI:2051428.9:2001MAY17	1	963	forward 3	TM	Non-Cytosolic
424	LI:2051428.9:2001MAY17	964	986	forward 3	TM	Transmembrane
424	LI:2051428.9:2001MAY17	987	1298	forward 3	TM	Cytosolic
424	LI:2051428.9:2001MAY17	1299	1321	forward 3	TM	Transmembrane
424	LI:2051428.9:2001MAY17	1322	1345	forward 3	TM	Non-Cytosolic
424	LI:2051428.9:2001MAY17	1346	1368	forward 3	TM	Transmembrane
424	LI:2051428.9:2001MAY17	1369	1548	forward 3	TM	Cytosolic
426	LI:375954.18:2001MAY17	1	639	forward 1	TM	Non-Cytosolic
426	LI:375954.18:2001MAY17	640	662	forward 1	TM	Transmembrane
426	LI:375954.18:2001MAY17	663	669	forward 1	TM	Cytosolic
427	LI:480115.132:2001MAY17	1	310	forward 2	TM	Non-Cytosolic
427	LI:480115.132:2001MAY17	311	333	forward 2	TM	Transmembrane
427	LI:480115.132:2001MAY17	334	365	forward 2	TM	Cytosolic
427	LI:480115.132:2001MAY17	366	388	forward 2	TM	Transmembrane
427	LI:480115.132:2001MAY17	389	425	forward 2	TM	Non-Cytosolic
427	LI:480115.132:2001MAY17	426	448	forward 2	TM	Transmembrane
427	LI:480115.132:2001MAY17	449	450	forward 2	TM	Cytosolic
432	LG:1401132.92:2001MAR30	10	81	forward 1	SP	
432	LG:1401132.92:2001MAR30	16	78	forward 1	SP	
433	LG:1401165.155:2001MAR30	1	112	forward 1	TM	Cytosolic
433	LG:1401165.155:2001MAR30	1	112	forward 2	TM	Cytosolic
436	LG:411364.13:2001MAR30	1	461	forward 1	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	462	484	forward 1	TM	Transmembrane
436	LG:411364.13:2001MAR30	485	490	forward 1	TM	Cytosolic
436	LG:411364.13:2001MAR30	491	513	forward 1	TM	Transmembrane
436	LG:411364.13:2001MAR30	514	789	forward 1	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	790	812	forward 1	TM	Transmembrane
436	LG:411364.13:2001MAR30	813	1048	forward 1	TM	Cytosolic
436	LG:411364.13:2001MAR30	1049	1071	forward 1	TM	Transmembrane
436	LG:411364.13:2001MAR30	1072	1080	forward 1	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	1081	1100	forward 1	TM	Transmembrane
436	LG:411364.13:2001MAR30	1101	1106	forward 1	TM	Cytosolic
436	LG:411364.13:2001MAR30	1107	1129	forward 1	TM	Transmembrane
436	LG:411364.13:2001MAR30	1130	1143	forward 1	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	1144	1161	forward 1	TM	Transmembrane
436	LG:411364.13:2001MAR30	1162	1167	forward 1	TM	Cytosolic
436	LG:411364.13:2001MAR30	1168	1190	forward 1	TM	Transmembrane
436	LG:411364.13:2001MAR30	1191	1199	forward 1	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	1200	1222	forward 1	TM	Transmembrane
436	LG:411364.13:2001MAR30	1223	1235	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
436	LG:411364.13:2001MAR30	1	39	forward 2	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	40	62	forward 2	TM	Transmembrane
436	LG:411364.13:2001MAR30	63	462	forward 2	TM	Cytosolic
436	LG:411364.13:2001MAR30	463	485	forward 2	TM	Transmembrane
436	LG:411364.13:2001MAR30	486	786	forward 2	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	787	809	forward 2	TM	Transmembrane
436	LG:411364.13:2001MAR30	810	1042	forward 2	TM	Cytosolic
436	LG:411364.13:2001MAR30	1043	1060	forward 2	TM	Transmembrane
436	LG:411364.13:2001MAR30	1061	1074	forward 2	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	1075	1097	forward 2	TM	Transmembrane
436	LG:411364.13:2001MAR30	1098	1105	forward 2	TM	Cytosolic
436	LG:411364.13:2001MAR30	1106	1128	forward 2	TM	Transmembrane
436	LG:411364.13:2001MAR30	1129	1142	forward 2	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	1143	1165	forward 2	TM	Transmembrane
436	LG:411364.13:2001MAR30	1166	1235	forward 2	TM	Cytosolic
436	LG:411364.13:2001MAR30	1	1050	forward 3	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	1051	1073	forward 3	TM	Transmembrane
436	LG:411364.13:2001MAR30	1074	1079	forward 3	TM	Cytosolic
436	LG:411364.13:2001MAR30	1080	1102	forward 3	TM	Transmembrane
436	LG:411364.13:2001MAR30	1103	1145	forward 3	TM	Non-Cytosolic
436	LG:411364.13:2001MAR30	1146	1168	forward 3	TM	Transmembrane
436	LG:411364.13:2001MAR30	1169	1172	forward 3	TM	Cytosolic
436	LG:411364.13:2001MAR30	1173	1195	forward 3	TM	Transmembrane
436	LG:411364.13:2001MAR30	1196	1234	forward 3	TM	Non-Cytosolic
438	LG:235157.34:2001MAR30	1	77	forward 1	TM	Cytosolic
438	LG:235157.34:2001MAR30	78	100	forward 1	TM	Transmembrane
438	LG:235157.34:2001MAR30	101	119	forward 1	TM	Non-Cytosolic
438	LG:235157.34:2001MAR30	120	138	forward 1	TM	Transmembrane
438	LG:235157.34:2001MAR30	139	144	forward 1	TM	Cytosolic
438	LG:235157.34:2001MAR30	145	167	forward 1	TM	Transmembrane
438	LG:235157.34:2001MAR30	168	544	forward 1	TM	Non-Cytosolic
438	LG:235157.34:2001MAR30	1	257	forward 3	TM	Non-Cytosolic
438	LG:235157.34:2001MAR30	258	280	forward 3	TM	Transmembrane
438	LG:235157.34:2001MAR30	281	286	forward 3	TM	Cytosolic
438	LG:235157.34:2001MAR30	287	309	forward 3	TM	Transmembrane
438	LG:235157.34:2001MAR30	310	334	forward 3	TM	Non-Cytosolic
438	LG:235157.34:2001MAR30	335	354	forward 3	TM	Transmembrane
438	LG:235157.34:2001MAR30	355	366	forward 3	TM	Cytosolic
438	LG:235157.34:2001MAR30	367	389	forward 3	TM	Transmembrane
438	LG:235157.34:2001MAR30	390	393	forward 3	TM	Non-Cytosolic
438	LG:235157.34:2001MAR30	394	413	forward 3	TM	Transmembrane
438	LG:235157.34:2001MAR30	414	543	forward 3	TM	Cytosolic
440	LI:105160.28:2001MAY17	1	40	forward 3	TM	Non-Cytosolic
440	LI:105160.28:2001MAY17	41	63	forward 3	TM	Transmembrane
440	LI:105160.28:2001MAY17	64	214	forward 3	TM	Cytosolic
441	LI:1073108.49:2001MAY17	1	270	forward 3	TM	Non-Cytosolic
441	LI:1073108.49:2001MAY17	271	293	forward 3	TM	Transmembrane
441	LI:1073108.49:2001MAY17	294	304	forward 3	TM	Cytosolic
443	LI:2191073.14:2001MAY17	1	76	forward 3	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
444	U:2191348.6:2001MAY17	1	64	forward 3	TM	Cytosolic
445	U:2191424.12:2001MAY17	43	102	forward 1	SP	
448	U:392902.48:2001MAY17	1	938	forward 2	TM	Non-Cytosolic
448	U:392902.48:2001MAY17	939	961	forward 2	TM	Transmembrane
448	U:392902.48:2001MAY17	962	971	forward 2	TM	Cytosolic
449	U:411364.14:2001MAY17	1	599	forward 1	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	600	622	forward 1	TM	Transmembrane
449	U:411364.14:2001MAY17	623	628	forward 1	TM	Cytosolic
449	U:411364.14:2001MAY17	629	651	forward 1	TM	Transmembrane
449	U:411364.14:2001MAY17	652	927	forward 1	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	928	950	forward 1	TM	Transmembrane
449	U:411364.14:2001MAY17	951	1187	forward 1	TM	Cytosolic
449	U:411364.14:2001MAY17	1188	1210	forward 1	TM	Transmembrane
449	U:411364.14:2001MAY17	1211	1219	forward 1	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	1220	1242	forward 1	TM	Transmembrane
449	U:411364.14:2001MAY17	1243	1285	forward 1	TM	Cytosolic
449	U:411364.14:2001MAY17	1286	1308	forward 1	TM	Transmembrane
449	U:411364.14:2001MAY17	1309	1311	forward 1	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	1312	1334	forward 1	TM	Transmembrane
449	U:411364.14:2001MAY17	1335	1373	forward 1	TM	Cytosolic
449	U:411364.14:2001MAY17	1	25	forward 2	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	26	48	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	49	90	forward 2	TM	Cytosolic
449	U:411364.14:2001MAY17	91	113	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	114	177	forward 2	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	178	200	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	201	600	forward 2	TM	Cytosolic
449	U:411364.14:2001MAY17	601	623	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	624	924	forward 2	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	925	947	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	948	1186	forward 2	TM	Cytosolic
449	U:411364.14:2001MAY17	1187	1209	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	1210	1218	forward 2	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	1219	1238	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	1239	1244	forward 2	TM	Cytosolic
449	U:411364.14:2001MAY17	1245	1267	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	1268	1281	forward 2	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	1282	1299	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	1300	1305	forward 2	TM	Cytosolic
449	U:411364.14:2001MAY17	1306	1328	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	1329	1337	forward 2	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	1338	1360	forward 2	TM	Transmembrane
449	U:411364.14:2001MAY17	1361	1373	forward 2	TM	Cytosolic
449	U:411364.14:2001MAY17	1	1212	forward 3	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	1213	1235	forward 3	TM	Transmembrane
449	U:411364.14:2001MAY17	1236	1243	forward 3	TM	Cytosolic
449	U:411364.14:2001MAY17	1244	1266	forward 3	TM	Transmembrane
449	U:411364.14:2001MAY17	1267	1280	forward 3	TM	Non-Cytosolic
449	U:411364.14:2001MAY17	1281	1303	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
449	LI:411364.14:2001MAY17	1304	1373	forward 3	TM	Cytosolic
450	LI:417464.1:2001MAY17	1	91	forward 3	TM	Cytosolic
450	LI:417464.1:2001MAY17	92	114	forward 3	TM	Transmembrane
450	LI:417464.1:2001MAY17	115	533	forward 3	TM	Non-Cytosolic
450	LI:417464.1:2001MAY17	534	556	forward 3	TM	Transmembrane
450	LI:417464.1:2001MAY17	557	593	forward 3	TM	Cytosolic
451	LI:439077.1:2001MAY17	1	20	forward 1	TM	Cytosolic
451	LI:439077.1:2001MAY17	21	43	forward 1	TM	Transmembrane
451	LI:439077.1:2001MAY17	44	232	forward 1	TM	Non-Cytosolic
451	LI:439077.1:2001MAY17	1	20	forward 2	TM	Cytosolic
451	LI:439077.1:2001MAY17	21	43	forward 2	TM	Transmembrane
451	LI:439077.1:2001MAY17	44	232	forward 2	TM	Non-Cytosolic
451	LI:439077.1:2001MAY17	1	11	forward 3	TM	Cytosolic
451	LI:439077.1:2001MAY17	12	34	forward 3	TM	Transmembrane
451	LI:439077.1:2001MAY17	35	146	forward 3	TM	Non-Cytosolic
451	LI:439077.1:2001MAY17	147	169	forward 3	TM	Transmembrane
451	LI:439077.1:2001MAY17	170	231	forward 3	TM	Cytosolic
453	LG:1225513.19:2001JUN22	15	86	forward 3	SP	
455	LG:239410.21:2001JUN22	1	37	forward 2	TM	Cytosolic
455	LG:239410.21:2001JUN22	38	60	forward 2	TM	Transmembrane
455	LG:239410.21:2001JUN22	61	906	forward 2	TM	Non-Cytosolic
455	LG:239410.21:2001JUN22	907	924	forward 2	TM	Transmembrane
455	LG:239410.21:2001JUN22	925	1053	forward 2	TM	Cytosolic
455	LG:239410.21:2001JUN22	1	229	forward 3	TM	Non-Cytosolic
455	LG:239410.21:2001JUN22	230	252	forward 3	TM	Transmembrane
455	LG:239410.21:2001JUN22	253	253	forward 3	TM	Cytosolic
455	LG:239410.21:2001JUN22	254	276	forward 3	TM	Transmembrane
455	LG:239410.21:2001JUN22	277	309	forward 3	TM	Non-Cytosolic
455	LG:239410.21:2001JUN22	310	332	forward 3	TM	Transmembrane
455	LG:239410.21:2001JUN22	333	357	forward 3	TM	Cytosolic
455	LG:239410.21:2001JUN22	358	380	forward 3	TM	Transmembrane
455	LG:239410.21:2001JUN22	381	455	forward 3	TM	Non-Cytosolic
455	LG:239410.21:2001JUN22	456	478	forward 3	TM	Transmembrane
455	LG:239410.21:2001JUN22	479	498	forward 3	TM	Cytosolic
455	LG:239410.21:2001JUN22	499	521	forward 3	TM	Transmembrane
455	LG:239410.21:2001JUN22	522	560	forward 3	TM	Non-Cytosolic
455	LG:239410.21:2001JUN22	561	583	forward 3	TM	Transmembrane
455	LG:239410.21:2001JUN22	584	598	forward 3	TM	Cytosolic
455	LG:239410.21:2001JUN22	599	621	forward 3	TM	Transmembrane
455	LG:239410.21:2001JUN22	622	640	forward 3	TM	Non-Cytosolic
455	LG:239410.21:2001JUN22	641	663	forward 3	TM	Transmembrane
455	LG:239410.21:2001JUN22	664	1053	forward 3	TM	Cytosolic
458	LG:7696542.11:2001JUN22	1	270	forward 3	TM	Non-Cytosolic
458	LG:7696542.11:2001JUN22	271	293	forward 3	TM	Transmembrane
458	LG:7696542.11:2001JUN22	294	304	forward 3	TM	Cytosolic
460	LG:7696586.3:2001JUN22	1	129	forward 2	TM	Cytosolic
463	LI:2173928.1:2001MAY17	1	195	forward 2	TM	Cytosolic
465	LI:368098.26:2001MAY17	1	41	forward 3	TM	Non-Cytosolic
465	LI:368098.26:2001MAY17	42	64	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
465	LI:368098.26:2001MAY17	65	232	forward 3	TM	Cytosolic
467	LI:480845.50:2001MAY17	1	193	forward 2	TM	Cytosolic
467	LI:480845.50:2001MAY17	194	211	forward 2	TM	Transmembrane
467	LI:480845.50:2001MAY17	212	304	forward 2	TM	Non-Cytosolic
467	LI:480845.50:2001MAY17	1	19	forward 3	TM	Non-Cytosolic
467	LI:480845.50:2001MAY17	20	42	forward 3	TM	Transmembrane
467	LI:480845.50:2001MAY17	43	304	forward 3	TM	Cytosolic
468	LI:2205863.1:2001MAY17	1	247	forward 1	TM	Cytosolic
468	LI:2205863.1:2001MAY17	248	270	forward 1	TM	Transmembrane
468	LI:2205863.1:2001MAY17	271	284	forward 1	TM	Non-Cytosolic
468	LI:2205863.1:2001MAY17	285	307	forward 1	TM	Transmembrane
468	LI:2205863.1:2001MAY17	308	476	forward 1	TM	Cytosolic
468	LI:2205863.1:2001MAY17	477	499	forward 1	TM	Transmembrane
468	LI:2205863.1:2001MAY17	500	503	forward 1	TM	Non-Cytosolic
468	LI:2205863.1:2001MAY17	504	526	forward 1	TM	Transmembrane
468	LI:2205863.1:2001MAY17	527	571	forward 1	TM	Cytosolic
468	LI:2205863.1:2001MAY17	1	135	forward 3	TM	Cytosolic
468	LI:2205863.1:2001MAY17	136	158	forward 3	TM	Transmembrane
468	LI:2205863.1:2001MAY17	159	251	forward 3	TM	Non-Cytosolic
468	LI:2205863.1:2001MAY17	252	274	forward 3	TM	Transmembrane
468	LI:2205863.1:2001MAY17	275	294	forward 3	TM	Cytosolic
468	LI:2205863.1:2001MAY17	295	317	forward 3	TM	Transmembrane
468	LI:2205863.1:2001MAY17	318	570	forward 3	TM	Non-Cytosolic
469	LG:201188.2:2001JUN22	1	767	forward 2	TM	Non-Cytosolic
469	LG:201188.2:2001JUN22	768	790	forward 2	TM	Transmembrane
469	LG:201188.2:2001JUN22	791	848	forward 2	TM	Cytosolic
469	LG:201188.2:2001JUN22	849	871	forward 2	TM	Transmembrane
469	LG:201188.2:2001JUN22	872	890	forward 2	TM	Non-Cytosolic
469	LG:201188.2:2001JUN22	891	913	forward 2	TM	Transmembrane
469	LG:201188.2:2001JUN22	914	925	forward 2	TM	Cytosolic
469	LG:201188.2:2001JUN22	926	948	forward 2	TM	Transmembrane
469	LG:201188.2:2001JUN22	949	1356	forward 2	TM	Non-Cytosolic
472	LG:952182.4:2001MAR30	1	4	forward 1	TM	Cytosolic
472	LG:952182.4:2001MAR30	5	22	forward 1	TM	Transmembrane
472	LG:952182.4:2001MAR30	23	228	forward 1	TM	Non-Cytosolic
472	LG:952182.4:2001MAR30	1	20	forward 3	TM	Cytosolic
472	LG:952182.4:2001MAR30	21	43	forward 3	TM	Transmembrane
472	LG:952182.4:2001MAR30	44	62	forward 3	TM	Non-Cytosolic
472	LG:952182.4:2001MAR30	63	80	forward 3	TM	Transmembrane
472	LG:952182.4:2001MAR30	81	227	forward 3	TM	Cytosolic
473	LI:197195.10:2001MAY17	1	256	forward 1	TM	Cytosolic
473	LI:197195.10:2001MAY17	257	279	forward 1	TM	Transmembrane
473	LI:197195.10:2001MAY17	280	288	forward 1	TM	Non-Cytosolic
473	LI:197195.10:2001MAY17	289	308	forward 1	TM	Transmembrane
473	LI:197195.10:2001MAY17	309	348	forward 1	TM	Cytosolic
473	LI:197195.10:2001MAY17	1	111	forward 2	TM	Non-Cytosolic
473	LI:197195.10:2001MAY17	112	129	forward 2	TM	Transmembrane
473	LI:197195.10:2001MAY17	130	217	forward 2	TM	Cytosolic
473	LI:197195.10:2001MAY17	218	240	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
473	U:197195.10:2001MAY17	241	249	forward 2	TM	Non-Cytosolic
473	U:197195.10:2001MAY17	250	272	forward 2	TM	Transmembrane
473	U:197195.10:2001MAY17	273	348	forward 2	TM	Cytosolic
477	U:234507.10:2001MAY17	51	107	forward 3	SP	
477	U:234507.10:2001MAY17	1	294	forward 2	TM	Non-Cytosolic
477	U:234507.10:2001MAY17	295	317	forward 2	TM	Transmembrane
477	U:234507.10:2001MAY17	318	357	forward 2	TM	Cytosolic
477	U:234507.10:2001MAY17	358	380	forward 2	TM	Transmembrane
477	U:234507.10:2001MAY17	381	1163	forward 2	TM	Non-Cytosolic
477	U:234507.10:2001MAY17	1	585	forward 3	TM	Non-Cytosolic
477	U:234507.10:2001MAY17	586	608	forward 3	TM	Transmembrane
477	U:234507.10:2001MAY17	609	658	forward 3	TM	Cytosolic
477	U:234507.10:2001MAY17	659	681	forward 3	TM	Transmembrane
477	U:234507.10:2001MAY17	682	1162	forward 3	TM	Non-Cytosolic
479	U:244935.47:2001MAY17	1	14	forward 1	TM	Non-Cytosolic
479	U:244935.47:2001MAY17	15	37	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	38	90	forward 1	TM	Cytosolic
479	U:244935.47:2001MAY17	91	113	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	114	204	forward 1	TM	Non-Cytosolic
479	U:244935.47:2001MAY17	205	222	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	223	246	forward 1	TM	Cytosolic
479	U:244935.47:2001MAY17	247	269	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	270	273	forward 1	TM	Non-Cytosolic
479	U:244935.47:2001MAY17	274	293	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	294	400	forward 1	TM	Cytosolic
479	U:244935.47:2001MAY17	401	423	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	424	432	forward 1	TM	Non-Cytosolic
479	U:244935.47:2001MAY17	433	455	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	456	489	forward 1	TM	Cytosolic
479	U:244935.47:2001MAY17	490	509	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	510	518	forward 1	TM	Non-Cytosolic
479	U:244935.47:2001MAY17	519	541	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	542	756	forward 1	TM	Cytosolic
479	U:244935.47:2001MAY17	757	779	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	780	1013	forward 1	TM	Non-Cytosolic
479	U:244935.47:2001MAY17	1014	1036	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	1037	1099	forward 1	TM	Cytosolic
479	U:244935.47:2001MAY17	1100	1122	forward 1	TM	Transmembrane
479	U:244935.47:2001MAY17	1123	1362	forward 1	TM	Non-Cytosolic
479	U:244935.47:2001MAY17	1	569	forward 2	TM	Non-Cytosolic
479	U:244935.47:2001MAY17	570	592	forward 2	TM	Transmembrane
479	U:244935.47:2001MAY17	593	598	forward 2	TM	Cytosolic
479	U:244935.47:2001MAY17	599	621	forward 2	TM	Transmembrane
479	U:244935.47:2001MAY17	622	625	forward 2	TM	Non-Cytosolic
479	U:244935.47:2001MAY17	626	648	forward 2	TM	Transmembrane
479	U:244935.47:2001MAY17	649	668	forward 2	TM	Cytosolic
479	U:244935.47:2001MAY17	669	691	forward 2	TM	Transmembrane
479	U:244935.47:2001MAY17	692	1362	forward 2	TM	Non-Cytosolic
480	U:257664.143:2001MAY17	1	166	forward 1	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
480	U:257664.143:2001MAY17	167	189	forward 1	TM	Transmembrane
480	U:257664.143:2001MAY17	190	691	forward 1	TM	Non-Cytosolic
480	U:257664.143:2001MAY17	1	622	forward 2	TM	Non-Cytosolic
480	U:257664.143:2001MAY17	623	645	forward 2	TM	Transmembrane
480	U:257664.143:2001MAY17	646	690	forward 2	TM	Cytosolic
480	U:257664.143:2001MAY17	1	176	forward 3	TM	Non-Cytosolic
480	U:257664.143:2001MAY17	177	199	forward 3	TM	Transmembrane
480	U:257664.143:2001MAY17	200	623	forward 3	TM	Cytosolic
480	U:257664.143:2001MAY17	624	646	forward 3	TM	Transmembrane
480	U:257664.143:2001MAY17	647	660	forward 3	TM	Non-Cytosolic
480	U:257664.143:2001MAY17	661	683	forward 3	TM	Transmembrane
480	U:257664.143:2001MAY17	684	690	forward 3	TM	Cytosolic
482	U:346724.22:2001MAY17	1	380	forward 1	TM	Non-Cytosolic
482	U:346724.22:2001MAY17	381	400	forward 1	TM	Transmembrane
482	U:346724.22:2001MAY17	401	497	forward 1	TM	Cytosolic
482	U:346724.22:2001MAY17	498	520	forward 1	TM	Transmembrane
482	U:346724.22:2001MAY17	521	599	forward 1	TM	Non-Cytosolic
482	U:346724.22:2001MAY17	600	622	forward 1	TM	Transmembrane
482	U:346724.22:2001MAY17	623	761	forward 1	TM	Cytosolic
482	U:346724.22:2001MAY17	762	784	forward 1	TM	Transmembrane
482	U:346724.22:2001MAY17	785	863	forward 1	TM	Non-Cytosolic
482	U:346724.22:2001MAY17	864	886	forward 1	TM	Transmembrane
482	U:346724.22:2001MAY17	887	1074	forward 1	TM	Cytosolic
482	U:346724.22:2001MAY17	1	11	forward 2	TM	Cytosolic
482	U:346724.22:2001MAY17	12	34	forward 2	TM	Transmembrane
482	U:346724.22:2001MAY17	35	497	forward 2	TM	Non-Cytosolic
482	U:346724.22:2001MAY17	498	520	forward 2	TM	Transmembrane
482	U:346724.22:2001MAY17	521	601	forward 2	TM	Cytosolic
482	U:346724.22:2001MAY17	602	621	forward 2	TM	Transmembrane
482	U:346724.22:2001MAY17	622	1074	forward 2	TM	Non-Cytosolic
482	U:346724.22:2001MAY17	1	500	forward 3	TM	Non-Cytosolic
482	U:346724.22:2001MAY17	501	520	forward 3	TM	Transmembrane
482	U:346724.22:2001MAY17	521	602	forward 3	TM	Cytosolic
482	U:346724.22:2001MAY17	603	625	forward 3	TM	Transmembrane
482	U:346724.22:2001MAY17	626	658	forward 3	TM	Non-Cytosolic
482	U:346724.22:2001MAY17	659	681	forward 3	TM	Transmembrane
482	U:346724.22:2001MAY17	682	701	forward 3	TM	Cytosolic
482	U:346724.22:2001MAY17	702	724	forward 3	TM	Transmembrane
482	U:346724.22:2001MAY17	725	764	forward 3	TM	Non-Cytosolic
482	U:346724.22:2001MAY17	765	787	forward 3	TM	Transmembrane
482	U:346724.22:2001MAY17	788	860	forward 3	TM	Cytosolic
482	U:346724.22:2001MAY17	861	883	forward 3	TM	Transmembrane
482	U:346724.22:2001MAY17	884	931	forward 3	TM	Non-Cytosolic
482	U:346724.22:2001MAY17	932	954	forward 3	TM	Transmembrane
482	U:346724.22:2001MAY17	955	997	forward 3	TM	Cytosolic
482	U:346724.22:2001MAY17	998	1020	forward 3	TM	Transmembrane
482	U:346724.22:2001MAY17	1021	1073	forward 3	TM	Non-Cytosolic
484	U:889399.7:2001MAY17	1	251	forward 1	TM	Non-Cytosolic
484	U:889399.7:2001MAY17	252	274	forward 1	TM	Transmembrane



TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
484	U:889399.7:2001MAY17	275	294	forward 1	TM	Cytosolic
484	U:889399.7:2001MAY17	295	317	forward 1	TM	Transmembrane
484	U:889399.7:2001MAY17	318	332	forward 1	TM	Non-Cytosolic
485	U:1088907.2:2001MAY17	1	226	forward 3	TM	Cytosolic
485	U:1088907.2:2001MAY17	227	249	forward 3	TM	Transmembrane
485	U:1088907.2:2001MAY17	250	335	forward 3	TM	Non-Cytosolic
485	U:1088907.2:2001MAY17	336	358	forward 3	TM	Transmembrane
485	U:1088907.2:2001MAY17	359	508	forward 3	TM	Cytosolic
489	LG:900035.56:2001JUN22	1	369	forward 3	TM	Non-Cytosolic
489	LG:900035.56:2001JUN22	370	392	forward 3	TM	Transmembrane
489	LG:900035.56:2001JUN22	393	403	forward 3	TM	Cytosolic
489	LG:900035.56:2001JUN22	404	426	forward 3	TM	Transmembrane
489	LG:900035.56:2001JUN22	427	885	forward 3	TM	Non-Cytosolic
489	LG:900035.56:2001JUN22	886	908	forward 3	TM	Transmembrane
489	LG:900035.56:2001JUN22	909	939	forward 3	TM	Cytosolic
489	LG:900035.56:2001JUN22	940	962	forward 3	TM	Transmembrane
489	LG:900035.56:2001JUN22	963	981	forward 3	TM	Non-Cytosolic
489	LG:900035.56:2001JUN22	982	1004	forward 3	TM	Transmembrane
489	LG:900035.56:2001JUN22	1005	1285	forward 3	TM	Cytosolic
489	LG:900035.56:2001JUN22	1286	1308	forward 3	TM	Transmembrane
489	LG:900035.56:2001JUN22	1309	1650	forward 3	TM	Non-Cytosolic
491	LG:1384720.130:2001MAR30	1	72	forward 1	TM	Cytosolic
491	LG:1384720.130:2001MAR30	73	92	forward 1	TM	Transmembrane
491	LG:1384720.130:2001MAR30	93	211	forward 1	TM	Non-Cytosolic
491	LG:1384720.130:2001MAR30	212	234	forward 1	TM	Transmembrane
491	LG:1384720.130:2001MAR30	235	286	forward 1	TM	Cytosolic
491	LG:1384720.130:2001MAR30	1	72	forward 2	TM	Non-Cytosolic
491	LG:1384720.130:2001MAR30	73	92	forward 2	TM	Transmembrane
491	LG:1384720.130:2001MAR30	93	286	forward 2	TM	Cytosolic
491	LG:1384720.130:2001MAR30	1	72	forward 3	TM	Non-Cytosolic
491	LG:1384720.130:2001MAR30	73	95	forward 3	TM	Transmembrane
491	LG:1384720.130:2001MAR30	96	286	forward 3	TM	Cytosolic
495	LG:1502796.1:2001MAR30	1	6	forward 3	TM	Cytosolic
495	LG:1502796.1:2001MAR30	7	29	forward 3	TM	Transmembrane
495	LG:1502796.1:2001MAR30	30	218	forward 3	TM	Non-Cytosolic
499	LG:897867.1:2001MAR30	1	172	forward 3	TM	Cytosolic
499	LG:897867.1:2001MAR30	173	195	forward 3	TM	Transmembrane
499	LG:897867.1:2001MAR30	196	234	forward 3	TM	Non-Cytosolic
499	LG:897867.1:2001MAR30	235	257	forward 3	TM	Transmembrane
499	LG:897867.1:2001MAR30	258	268	forward 3	TM	Cytosolic
502	U:257715.58:2001MAY17	1	6	forward 1	TM	Cytosolic
502	U:257715.58:2001MAY17	7	29	forward 1	TM	Transmembrane
502	U:257715.58:2001MAY17	30	1122	forward 1	TM	Non-Cytosolic
503	U:333453.9:2001MAY17	1	1168	forward 1	TM	Non-Cytosolic
503	U:333453.9:2001MAY17	1169	1191	forward 1	TM	Transmembrane
503	U:333453.9:2001MAY17	1192	1199	forward 1	TM	Cytosolic
503	U:333453.9:2001MAY17	1200	1222	forward 1	TM	Transmembrane
503	U:333453.9:2001MAY17	1223	1364	forward 1	TM	Non-Cytosolic
503	U:333453.9:2001MAY17	1	685	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
503	U:333453.9:2001MAY17	686	708	forward 3	TM	Transmembrane
503	U:333453.9:2001MAY17	709	769	forward 3	TM	Cytosolic
503	U:333453.9:2001MAY17	770	792	forward 3	TM	Transmembrane
503	U:333453.9:2001MAY17	793	1363	forward 3	TM	Non-Cytosolic
504	U:412658.111:2001MAY17	1	1313	forward 1	TM	Non-Cytosolic
504	U:412658.111:2001MAY17	1314	1336	forward 1	TM	Transmembrane
504	U:412658.111:2001MAY17	1337	1379	forward 1	TM	Cytosolic
504	U:412658.111:2001MAY17	1	1000	forward 3	TM	Non-Cytosolic
504	U:412658.111:2001MAY17	1001	1018	forward 3	TM	Transmembrane
504	U:412658.111:2001MAY17	1019	1024	forward 3	TM	Cytosolic
504	U:412658.111:2001MAY17	1025	1047	forward 3	TM	Transmembrane
504	U:412658.111:2001MAY17	1048	1321	forward 3	TM	Non-Cytosolic
504	U:412658.111:2001MAY17	1322	1344	forward 3	TM	Transmembrane
504	U:412658.111:2001MAY17	1345	1378	forward 3	TM	Cytosolic
506	U:765245.9:2001MAY17	1	333	forward 1	TM	Cytosolic
506	U:765245.9:2001MAY17	334	353	forward 1	TM	Transmembrane
506	U:765245.9:2001MAY17	354	720	forward 1	TM	Non-Cytosolic
508	U:897867.1:2001MAY17	1	172	forward 3	TM	Cytosolic
508	U:897867.1:2001MAY17	173	195	forward 3	TM	Transmembrane
508	U:897867.1:2001MAY17	196	200	forward 3	TM	Non-Cytosolic
511	LG:1088618.90:2001JUN22	1	1267	forward 1	TM	Non-Cytosolic
511	LG:1088618.90:2001JUN22	1268	1290	forward 1	TM	Transmembrane
511	LG:1088618.90:2001JUN22	1291	1306	forward 1	TM	Cytosolic
511	LG:1088618.90:2001JUN22	1	1195	forward 2	TM	Non-Cytosolic
511	LG:1088618.90:2001JUN22	1196	1218	forward 2	TM	Transmembrane
511	LG:1088618.90:2001JUN22	1219	1306	forward 2	TM	Cytosolic
511	LG:1088618.90:2001JUN22	1	1217	forward 3	TM	Non-Cytosolic
511	LG:1088618.90:2001JUN22	1218	1240	forward 3	TM	Transmembrane
511	LG:1088618.90:2001JUN22	1241	1260	forward 3	TM	Cytosolic
511	LG:1088618.90:2001JUN22	1261	1283	forward 3	TM	Transmembrane
511	LG:1088618.90:2001JUN22	1284	1306	forward 3	TM	Non-Cytosolic
512	LG:1446318.6:2001JUN22	1	667	forward 1	TM	Non-Cytosolic
512	LG:1446318.6:2001JUN22	668	690	forward 1	TM	Transmembrane
512	LG:1446318.6:2001JUN22	691	801	forward 1	TM	Cytosolic
512	LG:1446318.6:2001JUN22	802	821	forward 1	TM	Transmembrane
512	LG:1446318.6:2001JUN22	822	1337	forward 1	TM	Non-Cytosolic
512	LG:1446318.6:2001JUN22	1	668	forward 2	TM	Non-Cytosolic
512	LG:1446318.6:2001JUN22	669	691	forward 2	TM	Transmembrane
512	LG:1446318.6:2001JUN22	692	832	forward 2	TM	Cytosolic
512	LG:1446318.6:2001JUN22	833	855	forward 2	TM	Transmembrane
512	LG:1446318.6:2001JUN22	856	877	forward 2	TM	Non-Cytosolic
512	LG:1446318.6:2001JUN22	878	900	forward 2	TM	Transmembrane
512	LG:1446318.6:2001JUN22	901	1109	forward 2	TM	Cytosolic
512	LG:1446318.6:2001JUN22	1110	1132	forward 2	TM	Transmembrane
512	LG:1446318.6:2001JUN22	1133	1218	forward 2	TM	Non-Cytosolic
512	LG:1446318.6:2001JUN22	1219	1241	forward 2	TM	Transmembrane
512	LG:1446318.6:2001JUN22	1242	1337	forward 2	TM	Cytosolic
512	LG:1446318.6:2001JUN22	1	732	forward 3	TM	Non-Cytosolic
512	LG:1446318.6:2001JUN22	733	755	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
512	LG:1446318.6:2001JUN22	756	875	forward 3	TM	Cytosolic
512	LG:1446318.6:2001JUN22	876	898	forward 3	TM	Transmembrane
512	LG:1446318.6:2001JUN22	899	998	forward 3	TM	Non-Cytosolic
512	LG:1446318.6:2001JUN22	999	1021	forward 3	TM	Transmembrane
512	LG:1446318.6:2001JUN22	1022	1102	forward 3	TM	Cytosolic
512	LG:1446318.6:2001JUN22	1103	1125	forward 3	TM	Transmembrane
512	LG:1446318.6:2001JUN22	1126	1337	forward 3	TM	Non-Cytosolic
515	LG:7697194.7:2001JUN22	1	865	forward 1	TM	Non-Cytosolic
515	LG:7697194.7:2001JUN22	866	888	forward 1	TM	Transmembrane
515	LG:7697194.7:2001JUN22	889	987	forward 1	TM	Cytosolic
515	LG:7697194.7:2001JUN22	988	1010	forward 1	TM	Transmembrane
515	LG:7697194.7:2001JUN22	1011	1097	forward 1	TM	Non-Cytosolic
515	LG:7697194.7:2001JUN22	1098	1120	forward 1	TM	Transmembrane
515	LG:7697194.7:2001JUN22	1121	1129	forward 1	TM	Cytosolic
515	LG:7697194.7:2001JUN22	1	620	forward 2	TM	Non-Cytosolic
515	LG:7697194.7:2001JUN22	621	643	forward 2	TM	Transmembrane
515	LG:7697194.7:2001JUN22	644	663	forward 2	TM	Cytosolic
515	LG:7697194.7:2001JUN22	664	686	forward 2	TM	Transmembrane
515	LG:7697194.7:2001JUN22	687	1096	forward 2	TM	Non-Cytosolic
515	LG:7697194.7:2001JUN22	1097	1119	forward 2	TM	Transmembrane
515	LG:7697194.7:2001JUN22	1120	1129	forward 2	TM	Cytosolic
517	LG:248005.17:2001JUN22	1	2251	forward 2	TM	Non-Cytosolic
517	LG:248005.17:2001JUN22	2252	2274	forward 2	TM	Transmembrane
517	LG:248005.17:2001JUN22	2275	2504	forward 2	TM	Cytosolic
521	LG:363612.2:2001MAR30	1	299	forward 2	TM	Non-Cytosolic
521	LG:363612.2:2001MAR30	300	322	forward 2	TM	Transmembrane
521	LG:363612.2:2001MAR30	323	356	forward 2	TM	Cytosolic
521	LG:363612.2:2001MAR30	357	379	forward 2	TM	Transmembrane
521	LG:363612.2:2001MAR30	380	393	forward 2	TM	Non-Cytosolic
521	LG:363612.2:2001MAR30	394	416	forward 2	TM	Transmembrane
521	LG:363612.2:2001MAR30	417	486	forward 2	TM	Cytosolic
522	LG:468481.1:2001MAR30	1	6	forward 1	TM	Cytosolic
522	LG:468481.1:2001MAR30	7	29	forward 1	TM	Transmembrane
522	LG:468481.1:2001MAR30	30	115	forward 1	TM	Non-Cytosolic
522	LG:468481.1:2001MAR30	116	138	forward 1	TM	Transmembrane
522	LG:468481.1:2001MAR30	139	157	forward 1	TM	Cytosolic
522	LG:468481.1:2001MAR30	158	180	forward 1	TM	Transmembrane
522	LG:468481.1:2001MAR30	181	211	forward 1	TM	Non-Cytosolic
522	LG:468481.1:2001MAR30	212	229	forward 1	TM	Transmembrane
522	LG:468481.1:2001MAR30	230	299	forward 1	TM	Cytosolic
522	LG:468481.1:2001MAR30	300	322	forward 1	TM	Transmembrane
522	LG:468481.1:2001MAR30	323	345	forward 1	TM	Non-Cytosolic
522	LG:468481.1:2001MAR30	346	363	forward 1	TM	Transmembrane
522	LG:468481.1:2001MAR30	364	555	forward 1	TM	Cytosolic
522	LG:468481.1:2001MAR30	556	578	forward 1	TM	Transmembrane
522	LG:468481.1:2001MAR30	579	677	forward 1	TM	Non-Cytosolic
522	LG:468481.1:2001MAR30	678	695	forward 1	TM	Transmembrane
522	LG:468481.1:2001MAR30	696	836	forward 1	TM	Cytosolic
522	LG:468481.1:2001MAR30	1	253	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
522	LG:468481.1:2001MAR30	254	276	forward 2	TM	Transmembrane
522	LG:468481.1:2001MAR30	277	345	forward 2	TM	Cytosolic
522	LG:468481.1:2001MAR30	346	368	forward 2	TM	Transmembrane
522	LG:468481.1:2001MAR30	369	515	forward 2	TM	Non-Cytosolic
522	LG:468481.1:2001MAR30	516	538	forward 2	TM	Transmembrane
522	LG:468481.1:2001MAR30	539	558	forward 2	TM	Cytosolic
522	LG:468481.1:2001MAR30	559	581	forward 2	TM	Transmembrane
522	LG:468481.1:2001MAR30	582	650	forward 2	TM	Non-Cytosolic
522	LG:468481.1:2001MAR30	651	668	forward 2	TM	Transmembrane
522	LG:468481.1:2001MAR30	669	756	forward 2	TM	Cytosolic
522	LG:468481.1:2001MAR30	757	779	forward 2	TM	Transmembrane
522	LG:468481.1:2001MAR30	780	798	forward 2	TM	Non-Cytosolic
522	LG:468481.1:2001MAR30	799	818	forward 2	TM	Transmembrane
522	LG:468481.1:2001MAR30	819	836	forward 2	TM	Cytosolic
523	LG:966475.1:2001MAR30	1	4	forward 1	TM	Non-Cytosolic
523	LG:966475.1:2001MAR30	5	22	forward 1	TM	Transmembrane
523	LG:966475.1:2001MAR30	23	41	forward 1	TM	Cytosolic
523	LG:966475.1:2001MAR30	42	59	forward 1	TM	Transmembrane
523	LG:966475.1:2001MAR30	60	220	forward 1	TM	Non-Cytosolic
523	LG:966475.1:2001MAR30	1	62	forward 3	TM	Cytosolic
523	LG:966475.1:2001MAR30	63	85	forward 3	TM	Transmembrane
523	LG:966475.1:2001MAR30	86	126	forward 3	TM	Non-Cytosolic
523	LG:966475.1:2001MAR30	127	149	forward 3	TM	Transmembrane
523	LG:966475.1:2001MAR30	150	220	forward 3	TM	Cytosolic
524	LG:1135422.1:2001MAR30	1	229	forward 3	TM	Cytosolic
524	LG:1135422.1:2001MAR30	230	252	forward 3	TM	Transmembrane
524	LG:1135422.1:2001MAR30	253	269	forward 3	TM	Non-Cytosolic
525	U:1010121.1:2001MAY17	1	49	forward 2	TM	Cytosolic
525	U:1010121.1:2001MAY17	50	72	forward 2	TM	Transmembrane
525	U:1010121.1:2001MAY17	73	81	forward 2	TM	Non-Cytosolic
525	U:1010121.1:2001MAY17	82	104	forward 2	TM	Transmembrane
525	U:1010121.1:2001MAY17	105	181	forward 2	TM	Cytosolic
525	U:1010121.1:2001MAY17	182	204	forward 2	TM	Transmembrane
525	U:1010121.1:2001MAY17	205	599	forward 2	TM	Non-Cytosolic
527	U:1188564.7:2001MAY17	1	222	forward 1	TM	Cytosolic
527	U:1188564.7:2001MAY17	223	245	forward 1	TM	Transmembrane
527	U:1188564.7:2001MAY17	246	259	forward 1	TM	Non-Cytosolic
527	U:1188564.7:2001MAY17	260	282	forward 1	TM	Transmembrane
527	U:1188564.7:2001MAY17	283	298	forward 1	TM	Cytosolic
529	U:2206501.1:2001MAY17	1	176	forward 1	TM	Non-Cytosolic
529	U:2206501.1:2001MAY17	177	199	forward 1	TM	Transmembrane
529	U:2206501.1:2001MAY17	200	260	forward 1	TM	Cytosolic
529	U:2206501.1:2001MAY17	261	283	forward 1	TM	Transmembrane
529	U:2206501.1:2001MAY17	284	327	forward 1	TM	Non-Cytosolic
529	U:2206501.1:2001MAY17	328	350	forward 1	TM	Transmembrane
529	U:2206501.1:2001MAY17	351	384	forward 1	TM	Cytosolic
530	U:337830.1:2001MAY17	241	327	forward 1	SP	
530	U:337830.1:2001MAY17	1	308	forward 1	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	309	331	forward 1	TM	Transmembrane

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
530	U:337830.1:2001MAY17	332	337	forward 1	TM	Cytosolic
530	U:337830.1:2001MAY17	338	360	forward 1	TM	Transmembrane
530	U:337830.1:2001MAY17	361	369	forward 1	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	370	392	forward 1	TM	Transmembrane
530	U:337830.1:2001MAY17	393	420	forward 1	TM	Cytosolic
530	U:337830.1:2001MAY17	421	443	forward 1	TM	Transmembrane
530	U:337830.1:2001MAY17	444	544	forward 1	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	545	567	forward 1	TM	Transmembrane
530	U:337830.1:2001MAY17	568	573	forward 1	TM	Cytosolic
530	U:337830.1:2001MAY17	574	596	forward 1	TM	Transmembrane
530	U:337830.1:2001MAY17	597	599	forward 1	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	600	617	forward 1	TM	Transmembrane
530	U:337830.1:2001MAY17	618	650	forward 1	TM	Cytosolic
530	U:337830.1:2001MAY17	651	673	forward 1	TM	Transmembrane
530	U:337830.1:2001MAY17	674	687	forward 1	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	688	710	forward 1	TM	Transmembrane
530	U:337830.1:2001MAY17	711	946	forward 1	TM	Cytosolic
530	U:337830.1:2001MAY17	1	419	forward 2	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	420	442	forward 2	TM	Transmembrane
530	U:337830.1:2001MAY17	443	563	forward 2	TM	Cytosolic
530	U:337830.1:2001MAY17	564	586	forward 2	TM	Transmembrane
530	U:337830.1:2001MAY17	587	595	forward 2	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	596	618	forward 2	TM	Transmembrane
530	U:337830.1:2001MAY17	619	670	forward 2	TM	Cytosolic
530	U:337830.1:2001MAY17	671	693	forward 2	TM	Transmembrane
530	U:337830.1:2001MAY17	694	946	forward 2	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	1	267	forward 3	TM	Cytosolic
530	U:337830.1:2001MAY17	268	290	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	291	304	forward 3	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	305	327	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	328	333	forward 3	TM	Cytosolic
530	U:337830.1:2001MAY17	334	356	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	357	368	forward 3	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	369	391	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	392	411	forward 3	TM	Cytosolic
530	U:337830.1:2001MAY17	412	431	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	432	445	forward 3	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	446	465	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	466	485	forward 3	TM	Cytosolic
530	U:337830.1:2001MAY17	486	505	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	506	563	forward 3	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	564	586	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	587	592	forward 3	TM	Cytosolic
530	U:337830.1:2001MAY17	593	612	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	613	615	forward 3	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	616	638	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	639	649	forward 3	TM	Cytosolic
530	U:337830.1:2001MAY17	650	672	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	673	686	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
530	U:337830.1:2001MAY17	687	709	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	710	811	forward 3	TM	Cytosolic
530	U:337830.1:2001MAY17	812	834	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	835	905	forward 3	TM	Non-Cytosolic
530	U:337830.1:2001MAY17	906	928	forward 3	TM	Transmembrane
530	U:337830.1:2001MAY17	929	945	forward 3	TM	Cytosolic
532	U:253580.4:2001MAY17	1	614	forward 1	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	615	636	forward 1	TM	Transmembrane
532	U:253580.4:2001MAY17	637	642	forward 1	TM	Cytosolic
532	U:253580.4:2001MAY17	643	665	forward 1	TM	Transmembrane
532	U:253580.4:2001MAY17	666	711	forward 1	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	712	734	forward 1	TM	Transmembrane
532	U:253580.4:2001MAY17	735	841	forward 1	TM	Cytosolic
532	U:253580.4:2001MAY17	842	864	forward 1	TM	Transmembrane
532	U:253580.4:2001MAY17	865	873	forward 1	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	874	896	forward 1	TM	Transmembrane
532	U:253580.4:2001MAY17	897	950	forward 1	TM	Cytosolic
532	U:253580.4:2001MAY17	951	973	forward 1	TM	Transmembrane
532	U:253580.4:2001MAY17	974	1008	forward 1	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	1009	1031	forward 1	TM	Transmembrane
532	U:253580.4:2001MAY17	1032	1082	forward 1	TM	Cytosolic
532	U:253580.4:2001MAY17	1083	1105	forward 1	TM	Transmembrane
532	U:253580.4:2001MAY17	1106	1124	forward 1	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	1125	1147	forward 1	TM	Transmembrane
532	U:253580.4:2001MAY17	1148	1283	forward 1	TM	Cytosolic
532	U:253580.4:2001MAY17	1284	1306	forward 1	TM	Transmembrane
532	U:253580.4:2001MAY17	1307	1402	forward 1	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	1	478	forward 2	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	479	501	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	502	561	forward 2	TM	Cytosolic
532	U:253580.4:2001MAY17	562	584	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	585	613	forward 2	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	614	636	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	637	642	forward 2	TM	Cytosolic
532	U:253580.4:2001MAY17	643	660	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	661	664	forward 2	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	665	687	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	688	706	forward 2	TM	Cytosolic
532	U:253580.4:2001MAY17	707	726	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	727	745	forward 2	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	746	768	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	769	953	forward 2	TM	Cytosolic
532	U:253580.4:2001MAY17	954	976	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	977	995	forward 2	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	996	1018	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	1019	1029	forward 2	TM	Cytosolic
532	U:253580.4:2001MAY17	1030	1052	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	1053	1073	forward 2	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	1074	1091	forward 2	TM	Transmembrane

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
532	U:253580.4:2001MAY17	1092	1127	forward 2	TM	Cytosolic
532	U:253580.4:2001MAY17	1128	1145	forward 2	TM	Transmembrane
532	U:253580.4:2001MAY17	1146	1402	forward 2	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	1	252	forward 3	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	253	275	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	276	377	forward 3	TM	Cytosolic
532	U:253580.4:2001MAY17	378	400	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	401	476	forward 3	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	477	494	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	495	563	forward 3	TM	Cytosolic
532	U:253580.4:2001MAY17	564	586	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	587	589	forward 3	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	590	607	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	608	613	forward 3	TM	Cytosolic
532	U:253580.4:2001MAY17	614	636	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	637	645	forward 3	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	646	668	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	669	709	forward 3	TM	Cytosolic
532	U:253580.4:2001MAY17	710	732	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	733	844	forward 3	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	845	867	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	868	879	forward 3	TM	Cytosolic
532	U:253580.4:2001MAY17	880	902	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	903	960	forward 3	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	961	983	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	984	995	forward 3	TM	Cytosolic
532	U:253580.4:2001MAY17	996	1015	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	1016	1029	forward 3	TM	Non-Cytosolic
532	U:253580.4:2001MAY17	1030	1050	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	1051	1123	forward 3	TM	Cytosolic
532	U:253580.4:2001MAY17	1124	1146	forward 3	TM	Transmembrane
532	U:253580.4:2001MAY17	1147	1401	forward 3	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1	1269	forward 1	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1270	1292	forward 1	TM	Transmembrane
533	LG:330850.3:2001JUN22	1293	1298	forward 1	TM	Cytosolic
533	LG:330850.3:2001JUN22	1299	1321	forward 1	TM	Transmembrane
533	LG:330850.3:2001JUN22	1322	1597	forward 1	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1598	1620	forward 1	TM	Transmembrane
533	LG:330850.3:2001JUN22	1621	1667	forward 1	TM	Cytosolic
533	LG:330850.3:2001JUN22	1668	1687	forward 1	TM	Transmembrane
533	LG:330850.3:2001JUN22	1688	2309	forward 1	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	2310	2332	forward 1	TM	Transmembrane
533	LG:330850.3:2001JUN22	2333	2338	forward 1	TM	Cytosolic
533	LG:330850.3:2001JUN22	2339	2361	forward 1	TM	Transmembrane
533	LG:330850.3:2001JUN22	2362	2370	forward 1	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	2371	2390	forward 1	TM	Transmembrane
533	LG:330850.3:2001JUN22	2391	2454	forward 1	TM	Cytosolic
533	LG:330850.3:2001JUN22	1	1567	forward 2	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1568	1585	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
533	LG:330850.3:2001JUN22	1586	1596	forward 2	TM	Cytosolic
533	LG:330850.3:2001JUN22	1597	1619	forward 2	TM	Transmembrane
533	LG:330850.3:2001JUN22	1620	1665	forward 2	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1666	1688	forward 2	TM	Transmembrane
533	LG:330850.3:2001JUN22	1689	1960	forward 2	TM	Cytosolic
533	LG:330850.3:2001JUN22	1961	1983	forward 2	TM	Transmembrane
533	LG:330850.3:2001JUN22	1984	2002	forward 2	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	2003	2025	forward 2	TM	Transmembrane
533	LG:330850.3:2001JUN22	2026	2104	forward 2	TM	Cytosolic
533	LG:330850.3:2001JUN22	2105	2127	forward 2	TM	Transmembrane
533	LG:330850.3:2001JUN22	2128	2130	forward 2	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	2131	2153	forward 2	TM	Transmembrane
533	LG:330850.3:2001JUN22	2154	2312	forward 2	TM	Cytosolic
533	LG:330850.3:2001JUN22	2313	2332	forward 2	TM	Transmembrane
533	LG:330850.3:2001JUN22	2333	2454	forward 2	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1	1258	forward 3	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1259	1281	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	1282	1301	forward 3	TM	Cytosolic
533	LG:330850.3:2001JUN22	1302	1319	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	1320	1376	forward 3	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1377	1399	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	1400	1603	forward 3	TM	Cytosolic
533	LG:330850.3:2001JUN22	1604	1626	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	1627	1635	forward 3	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1636	1653	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	1654	1665	forward 3	TM	Cytosolic
533	LG:330850.3:2001JUN22	1666	1688	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	1689	1697	forward 3	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1698	1720	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	1721	1823	forward 3	TM	Cytosolic
533	LG:330850.3:2001JUN22	1824	1846	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	1847	1924	forward 3	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	1925	1947	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	1948	2311	forward 3	TM	Cytosolic
533	LG:330850.3:2001JUN22	2312	2329	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	2330	2332	forward 3	TM	Non-Cytosolic
533	LG:330850.3:2001JUN22	2333	2350	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	2351	2356	forward 3	TM	Cytosolic
533	LG:330850.3:2001JUN22	2357	2379	forward 3	TM	Transmembrane
533	LG:330850.3:2001JUN22	2380	2454	forward 3	TM	Non-Cytosolic
534	LG:464722.13:2001JUN22	1	181	forward 1	TM	Non-Cytosolic
534	LG:464722.13:2001JUN22	182	204	forward 1	TM	Transmembrane
534	LG:464722.13:2001JUN22	205	451	forward 1	TM	Cytosolic
535	LG:7686119.1:2001JUN22	1	208	forward 2	TM	Non-Cytosolic
535	LG:7686119.1:2001JUN22	209	231	forward 2	TM	Transmembrane
535	LG:7686119.1:2001JUN22	232	290	forward 2	TM	Cytosolic
536	LG:903691.14:2001JUN22	1	700	forward 2	TM	Non-Cytosolic
536	LG:903691.14:2001JUN22	701	723	forward 2	TM	Transmembrane
536	LG:903691.14:2001JUN22	724	1145	forward 2	TM	Cytosolic



TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
536	LG:903691.14:2001JUN22	1146	1168	forward 2	TM	Transmembrane
536	LG:903691.14:2001JUN22	1169	1485	forward 2	TM	Non-Cytosolic
539	LG:1138457.20:2001MAR30	1	44	forward 1	TM	Cytosolic
539	LG:1138457.20:2001MAR30	45	67	forward 1	TM	Transmembrane
539	LG:1138457.20:2001MAR30	68	100	forward 1	TM	Non-Cytosolic
539	LG:1138457.20:2001MAR30	101	123	forward 1	TM	Transmembrane
539	LG:1138457.20:2001MAR30	124	139	forward 1	TM	Cytosolic
539	LG:1138457.20:2001MAR30	1	96	forward 2	TM	Non-Cytosolic
539	LG:1138457.20:2001MAR30	97	119	forward 2	TM	Transmembrane
539	LG:1138457.20:2001MAR30	120	139	forward 2	TM	Cytosolic
539	LG:1138457.20:2001MAR30	1	99	forward 3	TM	Non-Cytosolic
539	LG:1138457.20:2001MAR30	100	122	forward 3	TM	Transmembrane
539	LG:1138457.20:2001MAR30	123	138	forward 3	TM	Cytosolic
546	LG:255713.1:2001MAR30	1	128	forward 3	TM	Cytosolic
546	LG:255713.1:2001MAR30	129	151	forward 3	TM	Transmembrane
546	LG:255713.1:2001MAR30	152	170	forward 3	TM	Non-Cytosolic
546	LG:255713.1:2001MAR30	171	188	forward 3	TM	Transmembrane
546	LG:255713.1:2001MAR30	189	232	forward 3	TM	Cytosolic
546	LG:255713.1:2001MAR30	233	255	forward 3	TM	Transmembrane
546	LG:255713.1:2001MAR30	256	271	forward 3	TM	Non-Cytosolic
549	LG:997599.1:2001MAR30	1	278	forward 3	TM	Non-Cytosolic
549	LG:997599.1:2001MAR30	279	301	forward 3	TM	Transmembrane
549	LG:997599.1:2001MAR30	302	303	forward 3	TM	Cytosolic
550	LG:232776.8:2001MAR30	1	251	forward 1	TM	Cytosolic
550	LG:232776.8:2001MAR30	252	274	forward 1	TM	Transmembrane
550	LG:232776.8:2001MAR30	275	335	forward 1	TM	Non-Cytosolic
550	LG:232776.8:2001MAR30	336	353	forward 1	TM	Transmembrane
550	LG:232776.8:2001MAR30	354	428	forward 1	TM	Cytosolic
550	LG:232776.8:2001MAR30	429	451	forward 1	TM	Transmembrane
550	LG:232776.8:2001MAR30	452	472	forward 1	TM	Non-Cytosolic
550	LG:232776.8:2001MAR30	473	495	forward 1	TM	Transmembrane
550	LG:232776.8:2001MAR30	496	515	forward 1	TM	Cytosolic
550	LG:232776.8:2001MAR30	516	535	forward 1	TM	Transmembrane
550	LG:232776.8:2001MAR30	536	549	forward 1	TM	Non-Cytosolic
550	LG:232776.8:2001MAR30	550	572	forward 1	TM	Transmembrane
550	LG:232776.8:2001MAR30	573	732	forward 1	TM	Cytosolic
550	LG:232776.8:2001MAR30	733	755	forward 1	TM	Transmembrane
550	LG:232776.8:2001MAR30	756	774	forward 1	TM	Non-Cytosolic
550	LG:232776.8:2001MAR30	775	797	forward 1	TM	Transmembrane
550	LG:232776.8:2001MAR30	798	808	forward 1	TM	Cytosolic
550	LG:232776.8:2001MAR30	809	831	forward 1	TM	Transmembrane
550	LG:232776.8:2001MAR30	832	856	forward 1	TM	Non-Cytosolic
550	LG:232776.8:2001MAR30	857	879	forward 1	TM	Transmembrane
550	LG:232776.8:2001MAR30	880	890	forward 1	TM	Cytosolic
550	LG:232776.8:2001MAR30	1	204	forward 2	TM	Cytosolic
550	LG:232776.8:2001MAR30	205	227	forward 2	TM	Transmembrane
550	LG:232776.8:2001MAR30	228	889	forward 2	TM	Non-Cytosolic
550	LG:232776.8:2001MAR30	1	216	forward 3	TM	Non-Cytosolic
550	LG:232776.8:2001MAR30	217	239	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
550	LG:232776.8:2001MAR30	240	323	forward 3	TM	Cytosolic
550	LG:232776.8:2001MAR30	324	346	forward 3	TM	Transmembrane
550	LG:232776.8:2001MAR30	347	430	forward 3	TM	Non-Cytosolic
550	LG:232776.8:2001MAR30	431	453	forward 3	TM	Transmembrane
550	LG:232776.8:2001MAR30	454	672	forward 3	TM	Cytosolic
550	LG:232776.8:2001MAR30	673	692	forward 3	TM	Transmembrane
550	LG:232776.8:2001MAR30	693	701	forward 3	TM	Non-Cytosolic
550	LG:232776.8:2001MAR30	702	719	forward 3	TM	Transmembrane
550	LG:232776.8:2001MAR30	720	856	forward 3	TM	Cytosolic
550	LG:232776.8:2001MAR30	857	879	forward 3	TM	Transmembrane
550	LG:232776.8:2001MAR30	880	889	forward 3	TM	Non-Cytosolic
552	LI:1086565.6:2001MAY17	1	317	forward 1	TM	Non-Cytosolic
552	LI:1086565.6:2001MAY17	318	340	forward 1	TM	Transmembrane
552	LI:1086565.6:2001MAY17	341	346	forward 1	TM	Cytosolic
552	LI:1086565.6:2001MAY17	347	366	forward 1	TM	Transmembrane
552	LI:1086565.6:2001MAY17	367	375	forward 1	TM	Non-Cytosolic
552	LI:1086565.6:2001MAY17	376	398	forward 1	TM	Transmembrane
552	LI:1086565.6:2001MAY17	399	409	forward 1	TM	Cytosolic
552	LI:1086565.6:2001MAY17	410	432	forward 1	TM	Transmembrane
552	LI:1086565.6:2001MAY17	433	775	forward 1	TM	Non-Cytosolic
558	LI:2199688.3:2001MAY17	1	77	forward 1	TM	Cytosolic
558	LI:2199688.3:2001MAY17	78	100	forward 1	TM	Transmembrane
558	LI:2199688.3:2001MAY17	101	114	forward 1	TM	Non-Cytosolic
558	LI:2199688.3:2001MAY17	115	134	forward 1	TM	Transmembrane
558	LI:2199688.3:2001MAY17	135	184	forward 1	TM	Cytosolic
558	LI:2199688.3:2001MAY17	185	207	forward 1	TM	Transmembrane
558	LI:2199688.3:2001MAY17	208	275	forward 1	TM	Non-Cytosolic
558	LI:2199688.3:2001MAY17	1	79	forward 2	TM	Cytosolic
558	LI:2199688.3:2001MAY17	80	102	forward 2	TM	Transmembrane
558	LI:2199688.3:2001MAY17	103	111	forward 2	TM	Non-Cytosolic
558	LI:2199688.3:2001MAY17	112	134	forward 2	TM	Transmembrane
558	LI:2199688.3:2001MAY17	135	246	forward 2	TM	Cytosolic
558	LI:2199688.3:2001MAY17	247	269	forward 2	TM	Transmembrane
558	LI:2199688.3:2001MAY17	270	275	forward 2	TM	Non-Cytosolic
559	LI:790138.64:2001MAY17	1	131	forward 1	TM	Non-Cytosolic
559	LI:790138.64:2001MAY17	132	154	forward 1	TM	Transmembrane
559	LI:790138.64:2001MAY17	155	166	forward 1	TM	Cytosolic
559	LI:790138.64:2001MAY17	167	184	forward 1	TM	Transmembrane
559	LI:790138.64:2001MAY17	185	198	forward 1	TM	Non-Cytosolic
559	LI:790138.64:2001MAY17	199	218	forward 1	TM	Transmembrane
559	LI:790138.64:2001MAY17	219	322	forward 1	TM	Cytosolic
559	LI:790138.64:2001MAY17	1	126	forward 2	TM	Cytosolic
559	LI:790138.64:2001MAY17	127	149	forward 2	TM	Transmembrane
559	LI:790138.64:2001MAY17	150	322	forward 2	TM	Non-Cytosolic
559	LI:790138.64:2001MAY17	1	120	forward 3	TM	Cytosolic
559	LI:790138.64:2001MAY17	121	143	forward 3	TM	Transmembrane
559	LI:790138.64:2001MAY17	144	321	forward 3	TM	Non-Cytosolic
560	LI:757871.10:2001MAY17	1	240	forward 1	TM	Non-Cytosolic
560	LI:757871.10:2001MAY17	241	263	forward 1	TM	Transmembrane

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
560	LI:757871.10:2001MAY17	264	269	forward 1	TM	Cytosolic
560	LI:757871.10:2001MAY17	270	292	forward 1	TM	Transmembrane
560	LI:757871.10:2001MAY17	293	744	forward 1	TM	Non-Cytosolic
560	LI:757871.10:2001MAY17	1	284	forward 2	TM	Non-Cytosolic
560	LI:757871.10:2001MAY17	285	307	forward 2	TM	Transmembrane
560	LI:757871.10:2001MAY17	308	499	forward 2	TM	Cytosolic
560	LI:757871.10:2001MAY17	500	522	forward 2	TM	Transmembrane
560	LI:757871.10:2001MAY17	523	744	forward 2	TM	Non-Cytosolic
560	LI:757871.10:2001MAY17	1	63	forward 3	TM	Cytosolic
560	LI:757871.10:2001MAY17	64	86	forward 3	TM	Transmembrane
560	LI:757871.10:2001MAY17	87	395	forward 3	TM	Non-Cytosolic
560	LI:757871.10:2001MAY17	396	418	forward 3	TM	Transmembrane
560	LI:757871.10:2001MAY17	419	556	forward 3	TM	Cytosolic
560	LI:757871.10:2001MAY17	557	576	forward 3	TM	Transmembrane
560	LI:757871.10:2001MAY17	577	590	forward 3	TM	Non-Cytosolic
560	LI:757871.10:2001MAY17	591	613	forward 3	TM	Transmembrane
560	LI:757871.10:2001MAY17	614	743	forward 3	TM	Cytosolic
564	LG:1453540.34:2001JUN22	1	90	forward 2	TM	Cytosolic
565	LG:249518.11:2001JUN22	1	143	forward 2	TM	Cytosolic
566	LG:041656.5:2001JUN22	1	12	forward 1	TM	Cytosolic
566	LG:041656.5:2001JUN22	13	35	forward 1	TM	Transmembrane
566	LG:041656.5:2001JUN22	36	1030	forward 1	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	1	4	forward 2	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	5	23	forward 2	TM	Transmembrane
566	LG:041656.5:2001JUN22	24	24	forward 2	TM	Cytosolic
566	LG:041656.5:2001JUN22	25	42	forward 2	TM	Transmembrane
566	LG:041656.5:2001JUN22	43	357	forward 2	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	358	380	forward 2	TM	Transmembrane
566	LG:041656.5:2001JUN22	381	464	forward 2	TM	Cytosolic
566	LG:041656.5:2001JUN22	465	487	forward 2	TM	Transmembrane
566	LG:041656.5:2001JUN22	488	571	forward 2	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	572	594	forward 2	TM	Transmembrane
566	LG:041656.5:2001JUN22	595	813	forward 2	TM	Cytosolic
566	LG:041656.5:2001JUN22	814	833	forward 2	TM	Transmembrane
566	LG:041656.5:2001JUN22	834	842	forward 2	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	843	860	forward 2	TM	Transmembrane
566	LG:041656.5:2001JUN22	861	997	forward 2	TM	Cytosolic
566	LG:041656.5:2001JUN22	998	1020	forward 2	TM	Transmembrane
566	LG:041656.5:2001JUN22	1021	1030	forward 2	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	1	9	forward 3	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	10	32	forward 3	TM	Transmembrane
566	LG:041656.5:2001JUN22	33	391	forward 3	TM	Cytosolic
566	LG:041656.5:2001JUN22	392	414	forward 3	TM	Transmembrane
566	LG:041656.5:2001JUN22	415	475	forward 3	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	476	493	forward 3	TM	Transmembrane
566	LG:041656.5:2001JUN22	494	568	forward 3	TM	Cytosolic
566	LG:041656.5:2001JUN22	569	591	forward 3	TM	Transmembrane
566	LG:041656.5:2001JUN22	592	612	forward 3	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	613	635	forward 3	TM	Transmembrane

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
566	LG:041656.5:2001JUN22	636	655	forward 3	TM	Cytosolic
566	LG:041656.5:2001JUN22	656	675	forward 3	TM	Transmembrane
566	LG:041656.5:2001JUN22	676	689	forward 3	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	690	712	forward 3	TM	Transmembrane
566	LG:041656.5:2001JUN22	713	872	forward 3	TM	Cytosolic
566	LG:041656.5:2001JUN22	873	895	forward 3	TM	Transmembrane
566	LG:041656.5:2001JUN22	896	914	forward 3	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	915	937	forward 3	TM	Transmembrane
566	LG:041656.5:2001JUN22	938	948	forward 3	TM	Cytosolic
566	LG:041656.5:2001JUN22	949	971	forward 3	TM	Transmembrane
566	LG:041656.5:2001JUN22	972	996	forward 3	TM	Non-Cytosolic
566	LG:041656.5:2001JUN22	997	1019	forward 3	TM	Transmembrane
566	LG:041656.5:2001JUN22	1020	1030	forward 3	TM	Cytosolic
567	LI:2208837.4:2001MAY17	1	4	forward 3	TM	Cytosolic
567	LI:2208837.4:2001MAY17	5	27	forward 3	TM	Transmembrane
567	LI:2208837.4:2001MAY17	28	46	forward 3	TM	Non-Cytosolic
567	LI:2208837.4:2001MAY17	47	69	forward 3	TM	Transmembrane
567	LI:2208837.4:2001MAY17	70	88	forward 3	TM	Cytosolic
567	LI:2208837.4:2001MAY17	89	111	forward 3	TM	Transmembrane
567	LI:2208837.4:2001MAY17	112	658	forward 3	TM	Non-Cytosolic
569	LG:016760.1:2001MAR30	1	210	forward 2	TM	Non-Cytosolic
569	LG:016760.1:2001MAR30	211	233	forward 2	TM	Transmembrane
569	LG:016760.1:2001MAR30	234	307	forward 2	TM	Cytosolic
569	LG:016760.1:2001MAR30	308	330	forward 2	TM	Transmembrane
569	LG:016760.1:2001MAR30	331	344	forward 2	TM	Non-Cytosolic
569	LG:016760.1:2001MAR30	345	364	forward 2	TM	Transmembrane
569	LG:016760.1:2001MAR30	365	386	forward 2	TM	Cytosolic
569	LG:016760.1:2001MAR30	387	406	forward 2	TM	Transmembrane
569	LG:016760.1:2001MAR30	407	529	forward 2	TM	Non-Cytosolic
570	LG:1022858.1:2001MAR30	1	18	forward 2	TM	Cytosolic
570	LG:1022858.1:2001MAR30	19	36	forward 2	TM	Transmembrane
570	LG:1022858.1:2001MAR30	37	45	forward 2	TM	Non-Cytosolic
570	LG:1022858.1:2001MAR30	46	68	forward 2	TM	Transmembrane
570	LG:1022858.1:2001MAR30	69	184	forward 2	TM	Cytosolic
571	LG:1135406.15:2001MAR30	1	477	forward 1	TM	Non-Cytosolic
571	LG:1135406.15:2001MAR30	478	500	forward 1	TM	Transmembrane
571	LG:1135406.15:2001MAR30	501	581	forward 1	TM	Cytosolic
571	LG:1135406.15:2001MAR30	1	555	forward 2	TM	Non-Cytosolic
571	LG:1135406.15:2001MAR30	556	578	forward 2	TM	Transmembrane
571	LG:1135406.15:2001MAR30	579	580	forward 2	TM	Cytosolic
572	LG:1327517.37:2001MAR30	1	12	forward 3	TM	Cytosolic
572	LG:1327517.37:2001MAR30	13	32	forward 3	TM	Transmembrane
572	LG:1327517.37:2001MAR30	33	36	forward 3	TM	Non-Cytosolic
572	LG:1327517.37:2001MAR30	37	59	forward 3	TM	Transmembrane
572	LG:1327517.37:2001MAR30	60	407	forward 3	TM	Cytosolic
572	LG:1327517.37:2001MAR30	408	430	forward 3	TM	Transmembrane
572	LG:1327517.37:2001MAR30	431	490	forward 3	TM	Non-Cytosolic
572	LG:1327517.37:2001MAR30	491	508	forward 3	TM	Transmembrane
572	LG:1327517.37:2001MAR30	509	527	forward 3	TM	Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
572	LG:1327517.37:2001MAR30	528	547	forward 3	TM	Transmembrane
572	LG:1327517.37:2001MAR30	548	683	forward 3	TM	Non-Cytosolic
573	LG:1330214.34:2001MAR30	1	179	forward 2	TM	Cytosolic
573	LG:1330214.34:2001MAR30	180	202	forward 2	TM	Transmembrane
573	LG:1330214.34:2001MAR30	203	240	forward 2	TM	Non-Cytosolic
573	LG:1330214.34:2001MAR30	241	263	forward 2	TM	Transmembrane
573	LG:1330214.34:2001MAR30	264	275	forward 2	TM	Cytosolic
573	LG:1330214.34:2001MAR30	276	298	forward 2	TM	Transmembrane
573	LG:1330214.34:2001MAR30	299	737	forward 2	TM	Non-Cytosolic
576	LG:1452330.5:2001MAR30	1	1277	forward 2	TM	Non-Cytosolic
576	LG:1452330.5:2001MAR30	1278	1300	forward 2	TM	Transmembrane
576	LG:1452330.5:2001MAR30	1301	1430	forward 2	TM	Cytosolic
576	LG:1452330.5:2001MAR30	1431	1453	forward 2	TM	Transmembrane
576	LG:1452330.5:2001MAR30	1454	1704	forward 2	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	1	404	forward 1	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	405	427	forward 1	TM	Transmembrane
578	LG:215109.8:2001MAR30	428	431	forward 1	TM	Cytosolic
578	LG:215109.8:2001MAR30	432	454	forward 1	TM	Transmembrane
578	LG:215109.8:2001MAR30	455	562	forward 1	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	563	585	forward 1	TM	Transmembrane
578	LG:215109.8:2001MAR30	586	596	forward 1	TM	Cytosolic
578	LG:215109.8:2001MAR30	597	619	forward 1	TM	Transmembrane
578	LG:215109.8:2001MAR30	620	677	forward 1	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	678	700	forward 1	TM	Transmembrane
578	LG:215109.8:2001MAR30	701	792	forward 1	TM	Cytosolic
578	LG:215109.8:2001MAR30	793	815	forward 1	TM	Transmembrane
578	LG:215109.8:2001MAR30	816	829	forward 1	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	830	849	forward 1	TM	Transmembrane
578	LG:215109.8:2001MAR30	850	889	forward 1	TM	Cytosolic
578	LG:215109.8:2001MAR30	1	165	forward 2	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	166	188	forward 2	TM	Transmembrane
578	LG:215109.8:2001MAR30	189	404	forward 2	TM	Cytosolic
578	LG:215109.8:2001MAR30	405	427	forward 2	TM	Transmembrane
578	LG:215109.8:2001MAR30	428	460	forward 2	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	461	483	forward 2	TM	Transmembrane
578	LG:215109.8:2001MAR30	484	683	forward 2	TM	Cytosolic
578	LG:215109.8:2001MAR30	684	706	forward 2	TM	Transmembrane
578	LG:215109.8:2001MAR30	707	709	forward 2	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	710	732	forward 2	TM	Transmembrane
578	LG:215109.8:2001MAR30	733	780	forward 2	TM	Cytosolic
578	LG:215109.8:2001MAR30	781	803	forward 2	TM	Transmembrane
578	LG:215109.8:2001MAR30	804	822	forward 2	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	823	842	forward 2	TM	Transmembrane
578	LG:215109.8:2001MAR30	843	854	forward 2	TM	Cytosolic
578	LG:215109.8:2001MAR30	855	874	forward 2	TM	Transmembrane
578	LG:215109.8:2001MAR30	875	889	forward 2	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	1	376	forward 3	TM	Cytosolic
578	LG:215109.8:2001MAR30	377	399	forward 3	TM	Transmembrane
578	LG:215109.8:2001MAR30	400	413	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
578	LG:215109.8:2001MAR30	414	436	forward 3	TM	Transmembrane
578	LG:215109.8:2001MAR30	437	456	forward 3	TM	Cytosolic
578	LG:215109.8:2001MAR30	457	479	forward 3	TM	Transmembrane
578	LG:215109.8:2001MAR30	480	589	forward 3	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	590	612	forward 3	TM	Transmembrane
578	LG:215109.8:2001MAR30	613	616	forward 3	TM	Cytosolic
578	LG:215109.8:2001MAR30	617	639	forward 3	TM	Transmembrane
578	LG:215109.8:2001MAR30	640	674	forward 3	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	675	697	forward 3	TM	Transmembrane
578	LG:215109.8:2001MAR30	698	788	forward 3	TM	Cytosolic
578	LG:215109.8:2001MAR30	789	808	forward 3	TM	Transmembrane
578	LG:215109.8:2001MAR30	809	822	forward 3	TM	Non-Cytosolic
578	LG:215109.8:2001MAR30	823	845	forward 3	TM	Transmembrane
578	LG:215109.8:2001MAR30	846	888	forward 3	TM	Cytosolic
579	LG:279978.17:2001MAR30	1	547	forward 2	TM	Non-Cytosolic
579	LG:279978.17:2001MAR30	548	567	forward 2	TM	Transmembrane
579	LG:279978.17:2001MAR30	568	610	forward 2	TM	Cytosolic
582	LG:1454339.4:2001MAR30	1	180	forward 1	TM	Cytosolic
582	LG:1454339.4:2001MAR30	181	203	forward 1	TM	Transmembrane
582	LG:1454339.4:2001MAR30	204	1001	forward 1	TM	Non-Cytosolic
582	LG:1454339.4:2001MAR30	1	33	forward 2	TM	Cytosolic
582	LG:1454339.4:2001MAR30	34	56	forward 2	TM	Transmembrane
582	LG:1454339.4:2001MAR30	57	93	forward 2	TM	Non-Cytosolic
582	LG:1454339.4:2001MAR30	94	116	forward 2	TM	Transmembrane
582	LG:1454339.4:2001MAR30	117	180	forward 2	TM	Cytosolic
582	LG:1454339.4:2001MAR30	181	203	forward 2	TM	Transmembrane
582	LG:1454339.4:2001MAR30	204	206	forward 2	TM	Non-Cytosolic
582	LG:1454339.4:2001MAR30	207	226	forward 2	TM	Transmembrane
582	LG:1454339.4:2001MAR30	227	379	forward 2	TM	Cytosolic
582	LG:1454339.4:2001MAR30	380	402	forward 2	TM	Transmembrane
582	LG:1454339.4:2001MAR30	403	914	forward 2	TM	Non-Cytosolic
582	LG:1454339.4:2001MAR30	915	937	forward 2	TM	Transmembrane
582	LG:1454339.4:2001MAR30	938	1001	forward 2	TM	Cytosolic
582	LG:1454339.4:2001MAR30	1	180	forward 3	TM	Cytosolic
582	LG:1454339.4:2001MAR30	181	203	forward 3	TM	Transmembrane
582	LG:1454339.4:2001MAR30	204	925	forward 3	TM	Non-Cytosolic
582	LG:1454339.4:2001MAR30	926	948	forward 3	TM	Transmembrane
582	LG:1454339.4:2001MAR30	949	1001	forward 3	TM	Cytosolic
583	U:018342.1:2001MAY17	1	196	forward 2	TM	Non-Cytosolic
583	U:018342.1:2001MAY17	197	219	forward 2	TM	Transmembrane
583	U:018342.1:2001MAY17	220	306	forward 2	TM	Cytosolic
583	U:018342.1:2001MAY17	307	329	forward 2	TM	Transmembrane
583	U:018342.1:2001MAY17	330	342	forward 2	TM	Non-Cytosolic
583	U:018342.1:2001MAY17	1	76	forward 3	TM	Non-Cytosolic
583	U:018342.1:2001MAY17	77	99	forward 3	TM	Transmembrane
583	U:018342.1:2001MAY17	100	342	forward 3	TM	Cytosolic
584	U:1177772.36:2001MAY17	1	63	forward 1	TM	Cytosolic
584	U:1177772.36:2001MAY17	64	86	forward 1	TM	Transmembrane
584	U:1177772.36:2001MAY17	87	875	forward 1	TM	Non-Cytosolic

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TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
586	U:244159.24:2001MAY17	1	286	forward 1	TM	Cytosolic
586	U:244159.24:2001MAY17	287	309	forward 1	TM	Transmembrane
586	U:244159.24:2001MAY17	310	797	forward 1	TM	Non-Cytosolic
586	U:244159.24:2001MAY17	798	820	forward 1	TM	Transmembrane
586	U:244159.24:2001MAY17	821	831	forward 1	TM	Cytosolic
587	U:405244.8:2001MAY17	1	19	forward 2	TM	Non-Cytosolic
587	U:405244.8:2001MAY17	20	42	forward 2	TM	Transmembrane
587	U:405244.8:2001MAY17	43	48	forward 2	TM	Cytosolic
587	U:405244.8:2001MAY17	49	71	forward 2	TM	Transmembrane
587	U:405244.8:2001MAY17	72	1130	forward 2	TM	Non-Cytosolic
587	U:405244.8:2001MAY17	1	58	forward 3	TM	Cytosolic
587	U:405244.8:2001MAY17	59	81	forward 3	TM	Transmembrane
587	U:405244.8:2001MAY17	82	1130	forward 3	TM	Non-Cytosolic
588	U:270318.18:2001MAY17	1	576	forward 1	TM	Non-Cytosolic
588	U:270318.18:2001MAY17	577	599	forward 1	TM	Transmembrane
588	U:270318.18:2001MAY17	600	675	forward 1	TM	Cytosolic
588	U:270318.18:2001MAY17	676	698	forward 1	TM	Transmembrane
588	U:270318.18:2001MAY17	699	1203	forward 1	TM	Non-Cytosolic
589	U:154692.45:2001MAY17	1	49	forward 3	TM	Cytosolic
589	U:154692.45:2001MAY17	50	69	forward 3	TM	Transmembrane
589	U:154692.45:2001MAY17	70	675	forward 3	TM	Non-Cytosolic
591	U:814424.6:2001MAY17	1	43	forward 1	TM	Non-Cytosolic
591	U:814424.6:2001MAY17	44	66	forward 1	TM	Transmembrane
591	U:814424.6:2001MAY17	67	85	forward 1	TM	Cytosolic
591	U:814424.6:2001MAY17	86	108	forward 1	TM	Transmembrane
591	U:814424.6:2001MAY17	109	892	forward 1	TM	Non-Cytosolic
591	U:814424.6:2001MAY17	1	221	forward 2	TM	Non-Cytosolic
591	U:814424.6:2001MAY17	222	244	forward 2	TM	Transmembrane
591	U:814424.6:2001MAY17	245	263	forward 2	TM	Cytosolic
591	U:814424.6:2001MAY17	264	286	forward 2	TM	Transmembrane
591	U:814424.6:2001MAY17	287	892	forward 2	TM	Non-Cytosolic
591	U:814424.6:2001MAY17	1	189	forward 3	TM	Cytosolic
591	U:814424.6:2001MAY17	190	212	forward 3	TM	Transmembrane
591	U:814424.6:2001MAY17	213	226	forward 3	TM	Non-Cytosolic
591	U:814424.6:2001MAY17	227	249	forward 3	TM	Transmembrane
591	U:814424.6:2001MAY17	250	261	forward 3	TM	Cytosolic
591	U:814424.6:2001MAY17	262	284	forward 3	TM	Transmembrane
591	U:814424.6:2001MAY17	285	892	forward 3	TM	Non-Cytosolic
592	LG:1327517.25:2001JUN22	1	15	forward 3	TM	Cytosolic
592	LG:1327517.25:2001JUN22	16	38	forward 3	TM	Transmembrane
592	LG:1327517.25:2001JUN22	39	614	forward 3	TM	Non-Cytosolic
594	LG:413000.28:2001JUN22	1	14	forward 1	TM	Non-Cytosolic
594	LG:413000.28:2001JUN22	15	37	forward 1	TM	Transmembrane
594	LG:413000.28:2001JUN22	38	196	forward 1	TM	Cytosolic
594	LG:413000.28:2001JUN22	197	214	forward 1	TM	Transmembrane
594	LG:413000.28:2001JUN22	215	233	forward 1	TM	Non-Cytosolic
594	LG:413000.28:2001JUN22	234	256	forward 1	TM	Transmembrane
594	LG:413000.28:2001JUN22	257	262	forward 1	TM	Cytosolic
594	LG:413000.28:2001JUN22	263	280	forward 1	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
594	LG:413000.28:2001JUN22	281	350	forward 1	TM	Non-Cytosolic
594	LG:413000.28:2001JUN22	1	15	forward 3	TM	Cytosolic
594	LG:413000.28:2001JUN22	16	33	forward 3	TM	Transmembrane
594	LG:413000.28:2001JUN22	34	47	forward 3	TM	Non-Cytosolic
594	LG:413000.28:2001JUN22	48	70	forward 3	TM	Transmembrane
594	LG:413000.28:2001JUN22	71	203	forward 3	TM	Cytosolic
594	LG:413000.28:2001JUN22	204	226	forward 3	TM	Transmembrane
594	LG:413000.28:2001JUN22	227	350	forward 3	TM	Non-Cytosolic
595	LG:7692006.3:2001JUN22	1	69	forward 1	TM	Cytosolic
595	LG:7692006.3:2001JUN22	70	92	forward 1	TM	Transmembrane
595	LG:7692006.3:2001JUN22	93	106	forward 1	TM	Non-Cytosolic
595	LG:7692006.3:2001JUN22	107	126	forward 1	TM	Transmembrane
595	LG:7692006.3:2001JUN22	127	212	forward 1	TM	Cytosolic
595	LG:7692006.3:2001JUN22	213	235	forward 1	TM	Transmembrane
595	LG:7692006.3:2001JUN22	236	325	forward 1	TM	Non-Cytosolic
595	LG:7692006.3:2001JUN22	1	202	forward 2	TM	Cytosolic
595	LG:7692006.3:2001JUN22	203	225	forward 2	TM	Transmembrane
595	LG:7692006.3:2001JUN22	226	325	forward 2	TM	Non-Cytosolic
595	LG:7692006.3:2001JUN22	1	145	forward 3	TM	Cytosolic
595	LG:7692006.3:2001JUN22	146	168	forward 3	TM	Transmembrane
595	LG:7692006.3:2001JUN22	169	195	forward 3	TM	Non-Cytosolic
595	LG:7692006.3:2001JUN22	196	215	forward 3	TM	Transmembrane
595	LG:7692006.3:2001JUN22	216	219	forward 3	TM	Cytosolic
595	LG:7692006.3:2001JUN22	220	237	forward 3	TM	Transmembrane
595	LG:7692006.3:2001JUN22	238	246	forward 3	TM	Non-Cytosolic
595	LG:7692006.3:2001JUN22	247	269	forward 3	TM	Transmembrane
595	LG:7692006.3:2001JUN22	270	324	forward 3	TM	Cytosolic
596	LG:336953.5:2001JUN22	1	879	forward 1	TM	Non-Cytosolic
596	LG:336953.5:2001JUN22	880	902	forward 1	TM	Transmembrane
596	LG:336953.5:2001JUN22	903	922	forward 1	TM	Cytosolic
596	LG:336953.5:2001JUN22	923	945	forward 1	TM	Transmembrane
596	LG:336953.5:2001JUN22	946	1602	forward 1	TM	Non-Cytosolic
596	LG:336953.5:2001JUN22	1	710	forward 2	TM	Non-Cytosolic
596	LG:336953.5:2001JUN22	711	733	forward 2	TM	Transmembrane
596	LG:336953.5:2001JUN22	734	871	forward 2	TM	Cytosolic
596	LG:336953.5:2001JUN22	872	894	forward 2	TM	Transmembrane
596	LG:336953.5:2001JUN22	895	1601	forward 2	TM	Non-Cytosolic
596	LG:336953.5:2001JUN22	1	879	forward 3	TM	Non-Cytosolic
596	LG:336953.5:2001JUN22	880	902	forward 3	TM	Transmembrane
596	LG:336953.5:2001JUN22	903	1246	forward 3	TM	Cytosolic
596	LG:336953.5:2001JUN22	1247	1269	forward 3	TM	Transmembrane
596	LG:336953.5:2001JUN22	1270	1601	forward 3	TM	Non-Cytosolic
598	LG:425024.5:2001JUN22	1	6	forward 1	TM	Cytosolic
598	LG:425024.5:2001JUN22	7	25	forward 1	TM	Transmembrane
598	LG:425024.5:2001JUN22	26	29	forward 1	TM	Non-Cytosolic
598	LG:425024.5:2001JUN22	30	47	forward 1	TM	Transmembrane
598	LG:425024.5:2001JUN22	48	53	forward 1	TM	Cytosolic
598	LG:425024.5:2001JUN22	54	76	forward 1	TM	Transmembrane
598	LG:425024.5:2001JUN22	77	257	forward 1	TM	Non-Cytosolic



TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
598	LG:425024.5:2001JUN22	258	280	forward 1	TM	Transmembrane
598	LG:425024.5:2001JUN22	281	342	forward 1	TM	Cytosolic
598	LG:425024.5:2001JUN22	343	365	forward 1	TM	Transmembrane
598	LG:425024.5:2001JUN22	366	367	forward 1	TM	Non-Cytosolic
600	LG:978629.6:2001JUN22	1	425	forward 1	TM	Non-Cytosolic
600	LG:978629.6:2001JUN22	426	443	forward 1	TM	Transmembrane
600	LG:978629.6:2001JUN22	444	454	forward 1	TM	Cytosolic
600	LG:978629.6:2001JUN22	455	477	forward 1	TM	Transmembrane
600	LG:978629.6:2001JUN22	478	491	forward 1	TM	Non-Cytosolic
600	LG:978629.6:2001JUN22	492	514	forward 1	TM	Transmembrane
600	LG:978629.6:2001JUN22	515	526	forward 1	TM	Cytosolic
600	LG:978629.6:2001JUN22	527	549	forward 1	TM	Transmembrane
600	LG:978629.6:2001JUN22	550	814	forward 1	TM	Non-Cytosolic
600	LG:978629.6:2001JUN22	1	372	forward 2	TM	Non-Cytosolic
600	LG:978629.6:2001JUN22	373	395	forward 2	TM	Transmembrane
600	LG:978629.6:2001JUN22	396	424	forward 2	TM	Cytosolic
600	LG:978629.6:2001JUN22	425	447	forward 2	TM	Transmembrane
600	LG:978629.6:2001JUN22	448	450	forward 2	TM	Non-Cytosolic
600	LG:978629.6:2001JUN22	451	473	forward 2	TM	Transmembrane
600	LG:978629.6:2001JUN22	474	493	forward 2	TM	Cytosolic
600	LG:978629.6:2001JUN22	494	516	forward 2	TM	Transmembrane
600	LG:978629.6:2001JUN22	517	814	forward 2	TM	Non-Cytosolic
600	LG:978629.6:2001JUN22	1	370	forward 3	TM	Non-Cytosolic
600	LG:978629.6:2001JUN22	371	388	forward 3	TM	Transmembrane
600	LG:978629.6:2001JUN22	389	425	forward 3	TM	Cytosolic
600	LG:978629.6:2001JUN22	426	448	forward 3	TM	Transmembrane
600	LG:978629.6:2001JUN22	449	457	forward 3	TM	Non-Cytosolic
600	LG:978629.6:2001JUN22	458	480	forward 3	TM	Transmembrane
600	LG:978629.6:2001JUN22	481	486	forward 3	TM	Cytosolic
600	LG:978629.6:2001JUN22	487	509	forward 3	TM	Transmembrane
600	LG:978629.6:2001JUN22	510	813	forward 3	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	1	670	forward 1	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	671	693	forward 1	TM	Transmembrane
601	LG:005776.12:2001MAR30	694	712	forward 1	TM	Cytosolic
601	LG:005776.12:2001MAR30	713	735	forward 1	TM	Transmembrane
601	LG:005776.12:2001MAR30	736	1210	forward 1	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	1211	1228	forward 1	TM	Transmembrane
601	LG:005776.12:2001MAR30	1229	1276	forward 1	TM	Cytosolic
601	LG:005776.12:2001MAR30	1277	1299	forward 1	TM	Transmembrane
601	LG:005776.12:2001MAR30	1300	1318	forward 1	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	1319	1341	forward 1	TM	Transmembrane
601	LG:005776.12:2001MAR30	1342	1382	forward 1	TM	Cytosolic
601	LG:005776.12:2001MAR30	1383	1402	forward 1	TM	Transmembrane
601	LG:005776.12:2001MAR30	1403	1411	forward 1	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	1412	1434	forward 1	TM	Transmembrane
601	LG:005776.12:2001MAR30	1435	1505	forward 1	TM	Cytosolic
601	LG:005776.12:2001MAR30	1	647	forward 2	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	648	670	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	671	674	forward 2	TM	Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
601	LG:005776.12:2001MAR30	675	694	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	695	708	forward 2	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	709	731	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	732	788	forward 2	TM	Cytosolic
601	LG:005776.12:2001MAR30	789	806	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	807	951	forward 2	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	952	969	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	970	980	forward 2	TM	Cytosolic
601	LG:005776.12:2001MAR30	981	1000	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	1001	1004	forward 2	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	1005	1027	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	1028	1223	forward 2	TM	Cytosolic
601	LG:005776.12:2001MAR30	1224	1246	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	1247	1255	forward 2	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	1256	1278	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	1279	1326	forward 2	TM	Cytosolic
601	LG:005776.12:2001MAR30	1327	1344	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	1345	1383	forward 2	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	1384	1403	forward 2	TM	Transmembrane
601	LG:005776.12:2001MAR30	1404	1504	forward 2	TM	Cytosolic
601	LG:005776.12:2001MAR30	1	669	forward 3	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	670	692	forward 3	TM	Transmembrane
601	LG:005776.12:2001MAR30	693	698	forward 3	TM	Cytosolic
601	LG:005776.12:2001MAR30	699	721	forward 3	TM	Transmembrane
601	LG:005776.12:2001MAR30	722	1241	forward 3	TM	Non-Cytosolic
601	LG:005776.12:2001MAR30	1242	1264	forward 3	TM	Transmembrane
601	LG:005776.12:2001MAR30	1265	1318	forward 3	TM	Cytosolic
601	LG:005776.12:2001MAR30	1319	1341	forward 3	TM	Transmembrane
601	LG:005776.12:2001MAR30	1342	1504	forward 3	TM	Non-Cytosolic
602	LG:029219.1:2001MAR30	1	113	forward 1	TM	Cytosolic
602	LG:029219.1:2001MAR30	114	133	forward 1	TM	Transmembrane
602	LG:029219.1:2001MAR30	134	142	forward 1	TM	Non-Cytosolic
602	LG:029219.1:2001MAR30	1	111	forward 2	TM	Non-Cytosolic
602	LG:029219.1:2001MAR30	112	134	forward 2	TM	Transmembrane
602	LG:029219.1:2001MAR30	135	142	forward 2	TM	Cytosolic
604	LG:1397656.6:2001MAR30	1	318	forward 3	TM	Non-Cytosolic
604	LG:1397656.6:2001MAR30	319	341	forward 3	TM	Transmembrane
604	LG:1397656.6:2001MAR30	342	652	forward 3	TM	Cytosolic
604	LG:1397656.6:2001MAR30	653	675	forward 3	TM	Transmembrane
604	LG:1397656.6:2001MAR30	676	992	forward 3	TM	Non-Cytosolic
605	LG:1500866.5:2001MAR30	1	312	forward 2	TM	Non-Cytosolic
605	LG:1500866.5:2001MAR30	313	335	forward 2	TM	Transmembrane
605	LG:1500866.5:2001MAR30	336	472	forward 2	TM	Cytosolic
606	LG:1511332.1:2001MAR30	1	174	forward 3	TM	Cytosolic
606	LG:1511332.1:2001MAR30	175	197	forward 3	TM	Transmembrane
606	LG:1511332.1:2001MAR30	198	220	forward 3	TM	Non-Cytosolic
606	LG:1511332.1:2001MAR30	221	243	forward 3	TM	Transmembrane
606	LG:1511332.1:2001MAR30	244	263	forward 3	TM	Cytosolic
606	LG:1511332.1:2001MAR30	264	283	forward 3	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
606	LG:1511332.1:2001MAR30	284	326	forward 3	TM	Non-Cytosolic
609	LG:331581.5:2001MAR30	1	537	forward 2	TM	Non-Cytosolic
609	LG:331581.5:2001MAR30	538	560	forward 2	TM	Transmembrane
609	LG:331581.5:2001MAR30	561	670	forward 2	TM	Cytosolic
609	LG:331581.5:2001MAR30	671	688	forward 2	TM	Transmembrane
609	LG:331581.5:2001MAR30	689	702	forward 2	TM	Non-Cytosolic
609	LG:331581.5:2001MAR30	703	720	forward 2	TM	Transmembrane
609	LG:331581.5:2001MAR30	721	783	forward 2	TM	Cytosolic
609	LG:331581.5:2001MAR30	1	309	forward 3	TM	Non-Cytosolic
609	LG:331581.5:2001MAR30	310	332	forward 3	TM	Transmembrane
609	LG:331581.5:2001MAR30	333	460	forward 3	TM	Cytosolic
609	LG:331581.5:2001MAR30	461	483	forward 3	TM	Transmembrane
609	LG:331581.5:2001MAR30	484	537	forward 3	TM	Non-Cytosolic
609	LG:331581.5:2001MAR30	538	560	forward 3	TM	Transmembrane
609	LG:331581.5:2001MAR30	561	571	forward 3	TM	Cytosolic
609	LG:331581.5:2001MAR30	572	594	forward 3	TM	Transmembrane
609	LG:331581.5:2001MAR30	595	782	forward 3	TM	Non-Cytosolic
610	LG:481433.4:2001MAR30	1	669	forward 1	TM	Non-Cytosolic
610	LG:481433.4:2001MAR30	670	692	forward 1	TM	Transmembrane
610	LG:481433.4:2001MAR30	693	734	forward 1	TM	Cytosolic
610	LG:481433.4:2001MAR30	735	757	forward 1	TM	Transmembrane
610	LG:481433.4:2001MAR30	758	944	forward 1	TM	Non-Cytosolic
610	LG:481433.4:2001MAR30	945	962	forward 1	TM	Transmembrane
610	LG:481433.4:2001MAR30	963	982	forward 1	TM	Cytosolic
610	LG:481433.4:2001MAR30	983	1002	forward 1	TM	Transmembrane
610	LG:481433.4:2001MAR30	1003	1074	forward 1	TM	Non-Cytosolic
610	LG:481433.4:2001MAR30	1075	1097	forward 1	TM	Transmembrane
610	LG:481433.4:2001MAR30	1098	1101	forward 1	TM	Cytosolic
610	LG:481433.4:2001MAR30	1102	1124	forward 1	TM	Transmembrane
610	LG:481433.4:2001MAR30	1125	2094	forward 1	TM	Non-Cytosolic
610	LG:481433.4:2001MAR30	1	635	forward 2	TM	Non-Cytosolic
610	LG:481433.4:2001MAR30	636	655	forward 2	TM	Transmembrane
610	LG:481433.4:2001MAR30	656	666	forward 2	TM	Cytosolic
610	LG:481433.4:2001MAR30	667	689	forward 2	TM	Transmembrane
610	LG:481433.4:2001MAR30	690	1093	forward 2	TM	Non-Cytosolic
610	LG:481433.4:2001MAR30	1094	1116	forward 2	TM	Transmembrane
610	LG:481433.4:2001MAR30	1117	1127	forward 2	TM	Cytosolic
610	LG:481433.4:2001MAR30	1128	1150	forward 2	TM	Transmembrane
610	LG:481433.4:2001MAR30	1151	2094	forward 2	TM	Non-Cytosolic
610	LG:481433.4:2001MAR30	1	668	forward 3	TM	Cytosolic
610	LG:481433.4:2001MAR30	669	691	forward 3	TM	Transmembrane
610	LG:481433.4:2001MAR30	692	737	forward 3	TM	Non-Cytosolic
610	LG:481433.4:2001MAR30	738	760	forward 3	TM	Transmembrane
610	LG:481433.4:2001MAR30	761	914	forward 3	TM	Cytosolic
610	LG:481433.4:2001MAR30	915	937	forward 3	TM	Transmembrane
610	LG:481433.4:2001MAR30	938	2094	forward 3	TM	Non-Cytosolic
611	LG:246935.4:2001MAR30	1	96	forward 1	TM	Cytosolic
611	LG:246935.4:2001MAR30	97	119	forward 1	TM	Transmembrane
611	LG:246935.4:2001MAR30	120	592	forward 1	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
611	LG:246935.4:2001MAR30	1	495	forward 2	TM	Non-Cytosolic
611	LG:246935.4:2001MAR30	496	518	forward 2	TM	Transmembrane
611	LG:246935.4:2001MAR30	519	591	forward 2	TM	Cytosolic
611	LG:246935.4:2001MAR30	1	54	forward 3	TM	Cytosolic
611	LG:246935.4:2001MAR30	55	77	forward 3	TM	Transmembrane
611	LG:246935.4:2001MAR30	78	484	forward 3	TM	Non-Cytosolic
611	LG:246935.4:2001MAR30	485	507	forward 3	TM	Transmembrane
611	LG:246935.4:2001MAR30	508	591	forward 3	TM	Cytosolic
612	LG:475420.1:2001MAR30	1	1454	forward 1	TM	Non-Cytosolic
612	LG:475420.1:2001MAR30	1455	1477	forward 1	TM	Transmembrane
612	LG:475420.1:2001MAR30	1478	1488	forward 1	TM	Cytosolic
612	LG:475420.1:2001MAR30	1489	1511	forward 1	TM	Transmembrane
612	LG:475420.1:2001MAR30	1512	1553	forward 1	TM	Non-Cytosolic
612	LG:475420.1:2001MAR30	1554	1576	forward 1	TM	Transmembrane
612	LG:475420.1:2001MAR30	1577	1599	forward 1	TM	Cytosolic
612	LG:475420.1:2001MAR30	1600	1619	forward 1	TM	Transmembrane
612	LG:475420.1:2001MAR30	1620	1719	forward 1	TM	Non-Cytosolic
612	LG:475420.1:2001MAR30	1	1446	forward 2	TM	Non-Cytosolic
612	LG:475420.1:2001MAR30	1447	1469	forward 2	TM	Transmembrane
612	LG:475420.1:2001MAR30	1470	1489	forward 2	TM	Cytosolic
612	LG:475420.1:2001MAR30	1490	1512	forward 2	TM	Transmembrane
612	LG:475420.1:2001MAR30	1513	1719	forward 2	TM	Non-Cytosolic
612	LG:475420.1:2001MAR30	1	1447	forward 3	TM	Non-Cytosolic
612	LG:475420.1:2001MAR30	1448	1470	forward 3	TM	Transmembrane
612	LG:475420.1:2001MAR30	1471	1482	forward 3	TM	Cytosolic
612	LG:475420.1:2001MAR30	1483	1505	forward 3	TM	Transmembrane
612	LG:475420.1:2001MAR30	1506	1607	forward 3	TM	Non-Cytosolic
612	LG:475420.1:2001MAR30	1608	1630	forward 3	TM	Transmembrane
612	LG:475420.1:2001MAR30	1631	1719	forward 3	TM	Cytosolic
613	U:1073084.60:2001MAY17	1	1100	forward 1	TM	Non-Cytosolic
613	U:1073084.60:2001MAY17	1101	1123	forward 1	TM	Transmembrane
613	U:1073084.60:2001MAY17	1124	1142	forward 1	TM	Cytosolic
613	U:1073084.60:2001MAY17	1143	1162	forward 1	TM	Transmembrane
613	U:1073084.60:2001MAY17	1163	1163	forward 1	TM	Non-Cytosolic
613	U:1073084.60:2001MAY17	1	1043	forward 3	TM	Non-Cytosolic
613	U:1073084.60:2001MAY17	1044	1066	forward 3	TM	Transmembrane
613	U:1073084.60:2001MAY17	1067	1138	forward 3	TM	Cytosolic
613	U:1073084.60:2001MAY17	1139	1161	forward 3	TM	Transmembrane
613	U:1073084.60:2001MAY17	1162	1162	forward 3	TM	Non-Cytosolic
618	U:2208147.1:2001MAY17	1	38	forward 1	TM	Cytosolic
618	U:2208147.1:2001MAY17	39	61	forward 1	TM	Transmembrane
618	U:2208147.1:2001MAY17	62	195	forward 1	TM	Non-Cytosolic
621	U:759025.1:2001MAY17	1	206	forward 1	TM	Cytosolic
621	U:759025.1:2001MAY17	207	229	forward 1	TM	Transmembrane
621	U:759025.1:2001MAY17	230	237	forward 1	TM	Non-Cytosolic
621	U:759025.1:2001MAY17	1	140	forward 2	TM	Cytosolic
621	U:759025.1:2001MAY17	141	163	forward 2	TM	Transmembrane
621	U:759025.1:2001MAY17	164	200	forward 2	TM	Non-Cytosolic
621	U:759025.1:2001MAY17	201	223	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
621	U:759025.1:2001MAY17	224	236	forward 2	TM	Cytosolic
622	U:765589.1:2001MAY17	1	335	forward 1	TM	Non-Cytosolic
622	U:765589.1:2001MAY17	336	353	forward 1	TM	Transmembrane
622	U:765589.1:2001MAY17	354	373	forward 1	TM	Cytosolic
622	U:765589.1:2001MAY17	374	396	forward 1	TM	Transmembrane
622	U:765589.1:2001MAY17	397	423	forward 1	TM	Non-Cytosolic
622	U:765589.1:2001MAY17	424	446	forward 1	TM	Transmembrane
622	U:765589.1:2001MAY17	447	458	forward 1	TM	Cytosolic
622	U:765589.1:2001MAY17	459	476	forward 1	TM	Transmembrane
622	U:765589.1:2001MAY17	477	507	forward 1	TM	Non-Cytosolic
622	U:765589.1:2001MAY17	1	277	forward 2	TM	Non-Cytosolic
622	U:765589.1:2001MAY17	278	300	forward 2	TM	Transmembrane
622	U:765589.1:2001MAY17	301	380	forward 2	TM	Cytosolic
622	U:765589.1:2001MAY17	381	403	forward 2	TM	Transmembrane
622	U:765589.1:2001MAY17	404	417	forward 2	TM	Non-Cytosolic
622	U:765589.1:2001MAY17	418	440	forward 2	TM	Transmembrane
622	U:765589.1:2001MAY17	441	507	forward 2	TM	Cytosolic
622	U:765589.1:2001MAY17	1	288	forward 3	TM	Non-Cytosolic
622	U:765589.1:2001MAY17	289	311	forward 3	TM	Transmembrane
622	U:765589.1:2001MAY17	312	377	forward 3	TM	Cytosolic
622	U:765589.1:2001MAY17	378	400	forward 3	TM	Transmembrane
622	U:765589.1:2001MAY17	401	403	forward 3	TM	Non-Cytosolic
622	U:765589.1:2001MAY17	404	421	forward 3	TM	Transmembrane
622	U:765589.1:2001MAY17	422	427	forward 3	TM	Cytosolic
622	U:765589.1:2001MAY17	428	450	forward 3	TM	Transmembrane
622	U:765589.1:2001MAY17	451	455	forward 3	TM	Non-Cytosolic
622	U:765589.1:2001MAY17	456	478	forward 3	TM	Transmembrane
622	U:765589.1:2001MAY17	479	507	forward 3	TM	Cytosolic
623	U:902535.3:2001MAY17	1	184	forward 1	TM	Cytosolic
624	U:257592.5:2001MAY17	1	607	forward 1	TM	Non-Cytosolic
624	U:257592.5:2001MAY17	608	630	forward 1	TM	Transmembrane
624	U:257592.5:2001MAY17	631	636	forward 1	TM	Cytosolic
624	U:257592.5:2001MAY17	637	659	forward 1	TM	Transmembrane
624	U:257592.5:2001MAY17	660	1385	forward 1	TM	Non-Cytosolic
626	LG:1382838.272:2001JUN22	1	19	forward 3	TM	Non-Cytosolic
626	LG:1382838.272:2001JUN22	20	42	forward 3	TM	Transmembrane
626	LG:1382838.272:2001JUN22	43	90	forward 3	TM	Cytosolic
626	LG:1382838.272:2001JUN22	91	110	forward 3	TM	Transmembrane
626	LG:1382838.272:2001JUN22	111	769	forward 3	TM	Non-Cytosolic
630	LG:7693136.5:2001JUN22	1	199	forward 2	TM	Non-Cytosolic
630	LG:7693136.5:2001JUN22	200	222	forward 2	TM	Transmembrane
630	LG:7693136.5:2001JUN22	223	276	forward 2	TM	Cytosolic
630	LG:7693136.5:2001JUN22	277	294	forward 2	TM	Transmembrane
630	LG:7693136.5:2001JUN22	295	388	forward 2	TM	Non-Cytosolic
631	LG:001505.13:2001MAR30	1	214	forward 3	TM	Non-Cytosolic
631	LG:001505.13:2001MAR30	215	237	forward 3	TM	Transmembrane
631	LG:001505.13:2001MAR30	238	338	forward 3	TM	Cytosolic
631	LG:001505.13:2001MAR30	339	358	forward 3	TM	Transmembrane
631	LG:001505.13:2001MAR30	359	413	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
632	LG:1051541.1:2001MAR30	1	101	forward 1	TM	Cytosolic
632	LG:1051541.1:2001MAR30	102	124	forward 1	TM	Transmembrane
632	LG:1051541.1:2001MAR30	125	138	forward 1	TM	Non-Cytosolic
632	LG:1051541.1:2001MAR30	139	161	forward 1	TM	Transmembrane
632	LG:1051541.1:2001MAR30	162	302	forward 1	TM	Cytosolic
632	LG:1051541.1:2001MAR30	1	94	forward 3	TM	Cytosolic
632	LG:1051541.1:2001MAR30	95	117	forward 3	TM	Transmembrane
632	LG:1051541.1:2001MAR30	118	121	forward 3	TM	Non-Cytosolic
632	LG:1051541.1:2001MAR30	122	144	forward 3	TM	Transmembrane
632	LG:1051541.1:2001MAR30	145	301	forward 3	TM	Cytosolic
633	LG:1090140.1:2001MAR30	1	550	forward 2	TM	Non-Cytosolic
633	LG:1090140.1:2001MAR30	551	573	forward 2	TM	Transmembrane
633	LG:1090140.1:2001MAR30	574	593	forward 2	TM	Cytosolic
633	LG:1090140.1:2001MAR30	594	613	forward 2	TM	Transmembrane
633	LG:1090140.1:2001MAR30	614	958	forward 2	TM	Non-Cytosolic
633	LG:1090140.1:2001MAR30	1	548	forward 3	TM	Non-Cytosolic
633	LG:1090140.1:2001MAR30	549	571	forward 3	TM	Transmembrane
633	LG:1090140.1:2001MAR30	572	591	forward 3	TM	Cytosolic
633	LG:1090140.1:2001MAR30	592	614	forward 3	TM	Transmembrane
633	LG:1090140.1:2001MAR30	615	957	forward 3	TM	Non-Cytosolic
635	LG:1500340.1:2001MAR30	1	32	forward 2	TM	Non-Cytosolic
635	LG:1500340.1:2001MAR30	33	55	forward 2	TM	Transmembrane
635	LG:1500340.1:2001MAR30	56	61	forward 2	TM	Cytosolic
635	LG:1500340.1:2001MAR30	62	84	forward 2	TM	Transmembrane
635	LG:1500340.1:2001MAR30	85	103	forward 2	TM	Non-Cytosolic
635	LG:1500340.1:2001MAR30	104	126	forward 2	TM	Transmembrane
635	LG:1500340.1:2001MAR30	127	208	forward 2	TM	Cytosolic
636	LG:1502353.1:2001MAR30	1	112	forward 1	TM	Cytosolic
636	LG:1502353.1:2001MAR30	113	135	forward 1	TM	Transmembrane
636	LG:1502353.1:2001MAR30	136	140	forward 1	TM	Non-Cytosolic
638	LG:231372.4:2001MAR30	1	410	forward 2	TM	Non-Cytosolic
638	LG:231372.4:2001MAR30	411	433	forward 2	TM	Transmembrane
638	LG:231372.4:2001MAR30	434	439	forward 2	TM	Cytosolic
638	LG:231372.4:2001MAR30	440	457	forward 2	TM	Transmembrane
638	LG:231372.4:2001MAR30	458	625	forward 2	TM	Non-Cytosolic
639	LG:234855.6:2001MAR30	1	636	forward 2	TM	Non-Cytosolic
639	LG:234855.6:2001MAR30	637	659	forward 2	TM	Transmembrane
639	LG:234855.6:2001MAR30	660	668	forward 2	TM	Cytosolic
640	LG:242157.8:2001MAR30	1	536	forward 1	TM	Non-Cytosolic
640	LG:242157.8:2001MAR30	537	559	forward 1	TM	Transmembrane
640	LG:242157.8:2001MAR30	560	643	forward 1	TM	Cytosolic
640	LG:242157.8:2001MAR30	1	539	forward 2	TM	Non-Cytosolic
640	LG:242157.8:2001MAR30	540	559	forward 2	TM	Transmembrane
640	LG:242157.8:2001MAR30	560	643	forward 2	TM	Cytosolic
640	LG:242157.8:2001MAR30	1	537	forward 3	TM	Non-Cytosolic
640	LG:242157.8:2001MAR30	538	560	forward 3	TM	Transmembrane
640	LG:242157.8:2001MAR30	561	566	forward 3	TM	Cytosolic
640	LG:242157.8:2001MAR30	567	589	forward 3	TM	Transmembrane
640	LG:242157.8:2001MAR30	590	643	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
641	LG:477127.6:2001MAR30	1	659	forward 1	TM	Non-Cytosolic
641	LG:477127.6:2001MAR30	660	682	forward 1	TM	Transmembrane
641	LG:477127.6:2001MAR30	683	752	forward 1	TM	Cytosolic
641	LG:477127.6:2001MAR30	753	775	forward 1	TM	Transmembrane
641	LG:477127.6:2001MAR30	776	859	forward 1	TM	Non-Cytosolic
641	LG:477127.6:2001MAR30	1	664	forward 2	TM	Non-Cytosolic
641	LG:477127.6:2001MAR30	665	687	forward 2	TM	Transmembrane
641	LG:477127.6:2001MAR30	688	858	forward 2	TM	Cytosolic
641	LG:477127.6:2001MAR30	1	135	forward 3	TM	Cytosolic
641	LG:477127.6:2001MAR30	136	158	forward 3	TM	Transmembrane
641	LG:477127.6:2001MAR30	159	743	forward 3	TM	Non-Cytosolic
641	LG:477127.6:2001MAR30	744	766	forward 3	TM	Transmembrane
641	LG:477127.6:2001MAR30	767	858	forward 3	TM	Cytosolic
643	LG:474937.20:2001MAR30	1	146	forward 1	TM	Cytosolic
643	LG:474937.20:2001MAR30	147	169	forward 1	TM	Transmembrane
643	LG:474937.20:2001MAR30	170	842	forward 1	TM	Non-Cytosolic
643	LG:474937.20:2001MAR30	1	779	forward 2	TM	Non-Cytosolic
643	LG:474937.20:2001MAR30	780	802	forward 2	TM	Transmembrane
643	LG:474937.20:2001MAR30	803	813	forward 2	TM	Cytosolic
643	LG:474937.20:2001MAR30	814	833	forward 2	TM	Transmembrane
643	LG:474937.20:2001MAR30	834	842	forward 2	TM	Non-Cytosolic
643	LG:474937.20:2001MAR30	1	145	forward 3	TM	Cytosolic
643	LG:474937.20:2001MAR30	146	168	forward 3	TM	Transmembrane
643	LG:474937.20:2001MAR30	169	406	forward 3	TM	Non-Cytosolic
643	LG:474937.20:2001MAR30	407	429	forward 3	TM	Transmembrane
643	LG:474937.20:2001MAR30	430	770	forward 3	TM	Cytosolic
643	LG:474937.20:2001MAR30	771	793	forward 3	TM	Transmembrane
643	LG:474937.20:2001MAR30	794	841	forward 3	TM	Non-Cytosolic
647	U:015309.1:2001MAY17	1	171	forward 3	TM	Cytosolic
647	U:015309.1:2001MAY17	172	194	forward 3	TM	Transmembrane
647	U:015309.1:2001MAY17	195	235	forward 3	TM	Non-Cytosolic
648	U:030502.2:2001MAY17	1	261	forward 2	TM	Non-Cytosolic
648	U:030502.2:2001MAY17	262	284	forward 2	TM	Transmembrane
648	U:030502.2:2001MAY17	285	426	forward 2	TM	Cytosolic
648	U:030502.2:2001MAY17	427	446	forward 2	TM	Transmembrane
648	U:030502.2:2001MAY17	447	460	forward 2	TM	Non-Cytosolic
648	U:030502.2:2001MAY17	461	483	forward 2	TM	Transmembrane
648	U:030502.2:2001MAY17	484	494	forward 2	TM	Cytosolic
648	U:030502.2:2001MAY17	1	464	forward 3	TM	Non-Cytosolic
648	U:030502.2:2001MAY17	465	487	forward 3	TM	Transmembrane
648	U:030502.2:2001MAY17	488	493	forward 3	TM	Cytosolic
650	U:1011706.2:2001MAY17	1	793	forward 1	TM	Non-Cytosolic
650	U:1011706.2:2001MAY17	794	816	forward 1	TM	Transmembrane
650	U:1011706.2:2001MAY17	817	903	forward 1	TM	Cytosolic
650	U:1011706.2:2001MAY17	1	81	forward 2	TM	Cytosolic
650	U:1011706.2:2001MAY17	82	104	forward 2	TM	Transmembrane
650	U:1011706.2:2001MAY17	105	134	forward 2	TM	Non-Cytosolic
650	U:1011706.2:2001MAY17	135	157	forward 2	TM	Transmembrane
650	U:1011706.2:2001MAY17	158	169	forward 2	TM	Cytosolic

TABLE 4

SEQ ID	Template ID	Start	Stop	Frame	Domain Type	Topology
NO:						
650	U:1011706.2:2001MAY17	170	189	forward 2	TM	Transmembrane
650	U:1011706.2:2001MAY17	190	198	forward 2	TM	Non-Cytosolic
650	U:1011706.2:2001MAY17	199	218	forward 2	TM	Transmembrane
650	U:1011706.2:2001MAY17	219	238	forward 2	TM	Cytosolic
650	U:1011706.2:2001MAY17	239	261	forward 2	TM	Transmembrane
650	U:1011706.2:2001MAY17	262	275	forward 2	TM	Non-Cytosolic
650	U:1011706.2:2001MAY17	276	298	forward 2	TM	Transmembrane
650	U:1011706.2:2001MAY17	299	304	forward 2	TM	Cytosolic
650	U:1011706.2:2001MAY17	305	324	forward 2	TM	Transmembrane
650	U:1011706.2:2001MAY17	325	356	forward 2	TM	Non-Cytosolic
650	U:1011706.2:2001MAY17	357	376	forward 2	TM	Transmembrane
650	U:1011706.2:2001MAY17	377	431	forward 2	TM	Cytosolic
650	U:1011706.2:2001MAY17	432	454	forward 2	TM	Transmembrane
650	U:1011706.2:2001MAY17	455	903	forward 2	TM	Non-Cytosolic
651	U:1171752.20:2001MAY17	1	369	forward 3	TM	Non-Cytosolic
651	U:1171752.20:2001MAY17	370	392	forward 3	TM	Transmembrane
651	U:1171752.20:2001MAY17	393	725	forward 3	TM	Cytosolic
652	U:2049713.6:2001MAY17	1	31	forward 2	TM	Cytosolic
652	U:2049713.6:2001MAY17	32	54	forward 2	TM	Transmembrane
652	U:2049713.6:2001MAY17	55	343	forward 2	TM	Non-Cytosolic
653	U:397393.2:2001MAY17	1	16	forward 3	TM	Cytosolic
653	U:397393.2:2001MAY17	17	39	forward 3	TM	Transmembrane
653	U:397393.2:2001MAY17	40	62	forward 3	TM	Non-Cytosolic
653	U:397393.2:2001MAY17	63	82	forward 3	TM	Transmembrane
653	U:397393.2:2001MAY17	83	285	forward 3	TM	Cytosolic
653	U:397393.2:2001MAY17	286	303	forward 3	TM	Transmembrane
653	U:397393.2:2001MAY17	304	747	forward 3	TM	Non-Cytosolic
656	U:903956.35:2001MAY17	1	1026	forward 1	TM	Non-Cytosolic
656	U:903956.35:2001MAY17	1027	1044	forward 1	TM	Transmembrane
656	U:903956.35:2001MAY17	1045	1056	forward 1	TM	Cytosolic
656	U:903956.35:2001MAY17	1057	1079	forward 1	TM	Transmembrane
656	U:903956.35:2001MAY17	1080	1156	forward 1	TM	Non-Cytosolic
656	U:903956.35:2001MAY17	1	1020	forward 2	TM	Non-Cytosolic
656	U:903956.35:2001MAY17	1021	1040	forward 2	TM	Transmembrane
656	U:903956.35:2001MAY17	1041	1065	forward 2	TM	Cytosolic
656	U:903956.35:2001MAY17	1066	1088	forward 2	TM	Transmembrane
656	U:903956.35:2001MAY17	1089	1119	forward 2	TM	Non-Cytosolic
656	U:903956.35:2001MAY17	1120	1142	forward 2	TM	Transmembrane
656	U:903956.35:2001MAY17	1143	1156	forward 2	TM	Cytosolic
656	U:903956.35:2001MAY17	1	1025	forward 3	TM	Non-Cytosolic
656	U:903956.35:2001MAY17	1026	1045	forward 3	TM	Transmembrane
656	U:903956.35:2001MAY17	1046	1057	forward 3	TM	Cytosolic
656	U:903956.35:2001MAY17	1058	1080	forward 3	TM	Transmembrane
656	U:903956.35:2001MAY17	1081	1122	forward 3	TM	Non-Cytosolic
656	U:903956.35:2001MAY17	1123	1142	forward 3	TM	Transmembrane
656	U:903956.35:2001MAY17	1143	1156	forward 3	TM	Cytosolic
657	U:055784.15:2001MAY17	1326	1391	forward 3	SP	
657	U:055784.15:2001MAY17	1	2943	forward 1	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	2944	2966	forward 1	TM	Transmembrane



TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
657	U:055784.15:2001MAY17	2967	2996	forward 1	TM	Cytosolic
657	U:055784.15:2001MAY17	2997	3019	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	3020	3042	forward 1	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3043	3060	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	3061	3157	forward 1	TM	Cytosolic
657	U:055784.15:2001MAY17	3158	3180	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	3181	3580	forward 1	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3581	3603	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	3604	3726	forward 1	TM	Cytosolic
657	U:055784.15:2001MAY17	3727	3749	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	3750	3841	forward 1	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3842	3864	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	3865	3884	forward 1	TM	Cytosolic
657	U:055784.15:2001MAY17	3885	3907	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	3908	3916	forward 1	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3917	3934	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	3935	3940	forward 1	TM	Cytosolic
657	U:055784.15:2001MAY17	3941	3963	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	3964	4147	forward 1	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	4148	4167	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	4168	4214	forward 1	TM	Cytosolic
657	U:055784.15:2001MAY17	4215	4237	forward 1	TM	Transmembrane
657	U:055784.15:2001MAY17	4238	4242	forward 1	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	1	2903	forward 2	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	2904	2926	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	2927	2946	forward 2	TM	Cytosolic
657	U:055784.15:2001MAY17	2947	2969	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	2970	3006	forward 2	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3007	3029	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	3030	3112	forward 2	TM	Cytosolic
657	U:055784.15:2001MAY17	3113	3132	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	3133	3141	forward 2	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3142	3164	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	3165	3168	forward 2	TM	Cytosolic
657	U:055784.15:2001MAY17	3169	3191	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	3192	3243	forward 2	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3244	3266	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	3267	3300	forward 2	TM	Cytosolic
657	U:055784.15:2001MAY17	3301	3323	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	3324	3579	forward 2	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3580	3602	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	3603	3846	forward 2	TM	Cytosolic
657	U:055784.15:2001MAY17	3847	3869	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	3870	3915	forward 2	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3916	3935	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	3936	3998	forward 2	TM	Cytosolic
657	U:055784.15:2001MAY17	3999	4021	forward 2	TM	Transmembrane
657	U:055784.15:2001MAY17	4022	4242	forward 2	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	1	114	forward 3	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
657	U:055784.15:2001MAY17	115	137	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	138	202	forward 3	TM	Cytosolic
657	U:055784.15:2001MAY17	203	225	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	226	234	forward 3	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	235	257	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	258	400	forward 3	TM	Cytosolic
657	U:055784.15:2001MAY17	401	423	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	424	437	forward 3	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	438	460	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	461	617	forward 3	TM	Cytosolic
657	U:055784.15:2001MAY17	618	637	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	638	1535	forward 3	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	1536	1558	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	1559	1638	forward 3	TM	Cytosolic
657	U:055784.15:2001MAY17	1639	1661	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	1662	3140	forward 3	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3141	3163	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	3164	3174	forward 3	TM	Cytosolic
657	U:055784.15:2001MAY17	3175	3197	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	3198	3229	forward 3	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3230	3252	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	3253	3291	forward 3	TM	Cytosolic
657	U:055784.15:2001MAY17	3292	3314	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	3315	3415	forward 3	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	3416	3438	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	3439	3579	forward 3	TM	Cytosolic
657	U:055784.15:2001MAY17	3580	3602	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	3603	4212	forward 3	TM	Non-Cytosolic
657	U:055784.15:2001MAY17	4213	4235	forward 3	TM	Transmembrane
657	U:055784.15:2001MAY17	4236	4242	forward 3	TM	Cytosolic
659	U:2207923.8:2001MAY17	1	136	forward 2	TM	Non-Cytosolic
659	U:2207923.8:2001MAY17	137	159	forward 2	TM	Transmembrane
659	U:2207923.8:2001MAY17	160	195	forward 2	TM	Cytosolic
659	U:2207923.8:2001MAY17	196	213	forward 2	TM	Transmembrane
659	U:2207923.8:2001MAY17	214	266	forward 2	TM	Non-Cytosolic
659	U:2207923.8:2001MAY17	267	289	forward 2	TM	Transmembrane
659	U:2207923.8:2001MAY17	290	301	forward 2	TM	Cytosolic
659	U:2207923.8:2001MAY17	302	319	forward 2	TM	Transmembrane
659	U:2207923.8:2001MAY17	320	644	forward 2	TM	Non-Cytosolic
661	U:764674.1:2001MAY17	1	360	forward 1	TM	Non-Cytosolic
661	U:764674.1:2001MAY17	361	383	forward 1	TM	Transmembrane
661	U:764674.1:2001MAY17	384	568	forward 1	TM	Cytosolic
661	U:764674.1:2001MAY17	569	591	forward 1	TM	Transmembrane
661	U:764674.1:2001MAY17	592	593	forward 1	TM	Non-Cytosolic
661	U:764674.1:2001MAY17	1	55	forward 2	TM	Non-Cytosolic
661	U:764674.1:2001MAY17	56	78	forward 2	TM	Transmembrane
661	U:764674.1:2001MAY17	79	84	forward 2	TM	Cytosolic
661	U:764674.1:2001MAY17	85	107	forward 2	TM	Transmembrane
661	U:764674.1:2001MAY17	108	293	forward 2	TM	Non-Cytosolic

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
661	U:764674.1:2001MAY17	294	316	forward 2	TM	Transmembrane
661	U:764674.1:2001MAY17	317	328	forward 2	TM	Cytosolic
661	U:764674.1:2001MAY17	329	346	forward 2	TM	Transmembrane
661	U:764674.1:2001MAY17	347	360	forward 2	TM	Non-Cytosolic
661	U:764674.1:2001MAY17	361	383	forward 2	TM	Transmembrane
661	U:764674.1:2001MAY17	384	475	forward 2	TM	Cytosolic
661	U:764674.1:2001MAY17	476	493	forward 2	TM	Transmembrane
661	U:764674.1:2001MAY17	494	497	forward 2	TM	Non-Cytosolic
661	U:764674.1:2001MAY17	498	520	forward 2	TM	Transmembrane
661	U:764674.1:2001MAY17	521	526	forward 2	TM	Cytosolic
661	U:764674.1:2001MAY17	527	549	forward 2	TM	Transmembrane
661	U:764674.1:2001MAY17	550	568	forward 2	TM	Non-Cytosolic
661	U:764674.1:2001MAY17	569	591	forward 2	TM	Transmembrane
661	U:764674.1:2001MAY17	592	592	forward 2	TM	Cytosolic
661	U:764674.1:2001MAY17	1	6	forward 3	TM	Cytosolic
661	U:764674.1:2001MAY17	7	29	forward 3	TM	Transmembrane
661	U:764674.1:2001MAY17	30	51	forward 3	TM	Non-Cytosolic
661	U:764674.1:2001MAY17	52	74	forward 3	TM	Transmembrane
661	U:764674.1:2001MAY17	75	85	forward 3	TM	Cytosolic
661	U:764674.1:2001MAY17	86	108	forward 3	TM	Transmembrane
661	U:764674.1:2001MAY17	109	161	forward 3	TM	Non-Cytosolic
661	U:764674.1:2001MAY17	162	184	forward 3	TM	Transmembrane
661	U:764674.1:2001MAY17	185	290	forward 3	TM	Cytosolic
661	U:764674.1:2001MAY17	291	313	forward 3	TM	Transmembrane
661	U:764674.1:2001MAY17	314	327	forward 3	TM	Non-Cytosolic
661	U:764674.1:2001MAY17	328	346	forward 3	TM	Transmembrane
661	U:764674.1:2001MAY17	347	358	forward 3	TM	Cytosolic
661	U:764674.1:2001MAY17	359	381	forward 3	TM	Transmembrane
661	U:764674.1:2001MAY17	382	592	forward 3	TM	Non-Cytosolic
662	U:893532.747:2001MAY17	1	19	forward 1	TM	Cytosolic
662	U:893532.747:2001MAY17	20	39	forward 1	TM	Transmembrane
662	U:893532.747:2001MAY17	40	495	forward 1	TM	Non-Cytosolic
662	U:893532.747:2001MAY17	1	27	forward 2	TM	Cytosolic
662	U:893532.747:2001MAY17	28	50	forward 2	TM	Transmembrane
662	U:893532.747:2001MAY17	51	495	forward 2	TM	Non-Cytosolic
662	U:893532.747:2001MAY17	1	23	forward 3	TM	Cytosolic
662	U:893532.747:2001MAY17	24	46	forward 3	TM	Transmembrane
662	U:893532.747:2001MAY17	47	129	forward 3	TM	Non-Cytosolic
662	U:893532.747:2001MAY17	130	152	forward 3	TM	Transmembrane
662	U:893532.747:2001MAY17	153	163	forward 3	TM	Cytosolic
662	U:893532.747:2001MAY17	164	186	forward 3	TM	Transmembrane
662	U:893532.747:2001MAY17	187	494	forward 3	TM	Non-Cytosolic
663	LG:1121446.8:2001JUN22	1	171	forward 1	TM	Cytosolic
663	LG:1121446.8:2001JUN22	172	194	forward 1	TM	Transmembrane
663	LG:1121446.8:2001JUN22	195	635	forward 1	TM	Non-Cytosolic
663	LG:1121446.8:2001JUN22	1	433	forward 2	TM	Non-Cytosolic
663	LG:1121446.8:2001JUN22	434	456	forward 2	TM	Transmembrane
663	LG:1121446.8:2001JUN22	457	468	forward 2	TM	Cytosolic
663	LG:1121446.8:2001JUN22	469	491	forward 2	TM	Transmembrane

TABLE 4

SEQ ID NO:	Template ID	Start	Stop	Frame	Domain Type	Topology
663	LG:1121446.8:2001JUN22	492	635	forward 2	TM	Non-Cytosolic
663	LG:1121446.8:2001JUN22	1	435	forward 3	TM	Non-Cytosolic
663	LG:1121446.8:2001JUN22	436	458	forward 3	TM	Transmembrane
663	LG:1121446.8:2001JUN22	459	478	forward 3	TM	Cytosolic
663	LG:1121446.8:2001JUN22	479	501	forward 3	TM	Transmembrane
663	LG:1121446.8:2001JUN22	502	515	forward 3	TM	Non-Cytosolic
663	LG:1121446.8:2001JUN22	516	535	forward 3	TM	Transmembrane
663	LG:1121446.8:2001JUN22	536	599	forward 3	TM	Cytosolic
663	LG:1121446.8:2001JUN22	600	622	forward 3	TM	Transmembrane
663	LG:1121446.8:2001JUN22	623	635	forward 3	TM	Non-Cytosolic
668	LG:7697332.3:2001JUN22	1	632	forward 2	TM	Non-Cytosolic
668	LG:7697332.3:2001JUN22	633	655	forward 2	TM	Transmembrane
668	LG:7697332.3:2001JUN22	656	681	forward 2	TM	Cytosolic

Table 5

1/LG:1040626.1:2001MAR30 || 1-96; 1-302; 91-651; 91-477; 95-639; 416-978;  
 421-781; 723-1314; 762-1314; 817-885; 874-1342; 879-1435; 879-994; 886-1076  
 2/LG:1041136.7:2001MAR30 || 1-176; 12-572; 146-652; 146-342; 152-377; 164-  
 435; 169-794; 178-463; 178-462; 182-283; 211-496; 227-475; 227-686; 236-483;  
 595-726; 625-1253; 674-944; 809-1228; 831-1253; 832-1253; 962-1253; 983-1252;  
 984-1621; 1037-1529; 1075-1726; 1088-1710; 1371-1888; 1444-1843; 1434-1932;  
 1437-1971; 1437-1865; 1438-1971; 1437-1867; 1456-1855; 1456-1572; 1447-1920;  
 1451-1732; 1455-1584; 1456-1871; 1456-1911; 1456-1899; 1456-1866; 1456-1848;  
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 1462-1698; 1465-1951; 1465-1971; 1466-1927; 1466-1919; 1468-1785; 1480-1970;  
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 1609-1971; 1615-1973; 1612-1967; 1612-1970; 1616-1972; 1618-1971; 1618-1982;  
 1623-1931; 1628-1875; 1631-1972; 1681-1971; 1687-1844; 1690-1943; 1693-1962;  
 1738-1977; 1713-1854; 1741-1971; 1744-1971; 1749-1972; 1787-1971; 1821-1973;  
 1847-1939; 1868-1941; 1896-1971  
 3/LG:1043848.1:2001MAR30 || 1-577; 399-944; 399-780; 445-889; 576-1007; 644-  
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 4/LG:1097673.1:2001MAR30 || 1-514; 114-7084; 405-847; 1445-1871; 1445-1648;  
 1504-1967; 1935-2329; 1989-2597; 2083-2618; 2312-2867; 2459-2985; 2487-2784;  
 3178-3678; 3496-4094; 3496-4117; 3629-4121; 3632-3901; 3963-4422; 3981-4449;  
 3986-4247; 3986-4223; 4016-4546; 4066-4490; 4153-4740; 4155-4869; 4198-4590;  
 4243-4666; 4287-4438; 4519-5094; 4614-4992; 4616-4892; 4623-4865; 4672-5231;  
 4687-4944; 4721-4844; 4718-5263; 4786-7084; 4830-5057; 4835-5100; 4853-5401;  
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 850; 1040-1623; 1125-1598; 1154-1332; 1156-1457; 1226-1700; 1381-1686  
 6/LG:1397110.7:2001MAR30 || 1-128; 25-187; 25-177; 25-277; 25-291; 96-238;  
 119-285; 208-777; 473-761; 499-825; 535-663; 539-802; 587-825; 587-822; 650-  
 825; 698-865; 727-825; 730-839; 754-824; 759-825; 760-1182; 762-829; 1097-  
 1354; 1122-1556; 1125-1525; 1124-1380; 1125-1573; 1134-1392; 1144-1514; 1173-  
 1716; 1250-1633; 1286-1636; 1311-1615; 1367-1637; 1386-1622; 1465-1620; 1468-  
 1620; 1524-1620; 1530-1620; 1583-1857  
 7/LG:1512094.1:2001MAR30 || 1-551; 249-884

Table 5

8/LG:230734.53:2001MAR30 || 1-329; 1-52; 132-367; 139-444; 145-370; 145-306; 145-288; 145-237; 145-222; 150-428; 151-642; 151-391; 197-713; 216-422; 262-534; 262-500; 263-519; 333-588; 372-586; 374-624; 374-621; 383-628; 387-553; 399-644; 402-555; 422-649; 422-623; 426-652; 582-811  
9/LG:240154.9:2001MAR30 || 1-223; 8-581; 169-411; 181-414; 197-553; 198-406; 209-438; 210-649; 300-406; 302-534; 450-708; 471-701; 473-667; 518-722; 519-1216; 523-668; 527-693; 531-693; 549-720; 581-704; 633-696; 846-1446; 858-1095; 858-1118; 858-1337; 860-1104; 860-1387; 873-1273; 864-1150; 869-1272; 872-1116; 872-1109; 874-1051; 874-1273; 874-1094; 874-1109; 874-1111; 874-1071; 876-1206; 887-1143; 899-1157; 911-1069; 911-1202; 950-1208; 967-1458; 992-1456; 1021-1220; 1037-1498; 1046-1253; 1063-1503; 1079-1316; 1167-1496; 1187-1454; 1188-1412; 1271-1339; 1271-1665; 1271-1493; 1271-1582; 1271-1699; 1273-1496; 1275-1556; 1275-1394; 1275-1456; 1275-1689; 1275-1357; 1275-1437; 1282-1483; 1297-1519; 1318-1521; 1359-1819; 1418-1749; 1576-1818; 1640-1749  
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11/LG:257151.4:2001MAR30 || 1-442; 12-442; 116-309; 153-512; 281-377; 292-512; 309-512; 411-492; 424-512; 424-918; 827-1124; 827-1097; 827-1075; 849-1203; 990-1272; 992-1238; 1057-1336; 1143-1681; 1193-1457; 1237-1566; 1251-1426; 1258-1379; 1275-1402; 1277-1468; 1291-1564; 1310-1821; 1324-1726; 1402-1516; 1416-1678; 1426-1656; 1442-1982; 1460-2038; 1488-2083; 1478-1815; 1515-2001; 1538-1828; 1603-1820; 1621-1823; 1645-2044; 1709-2069; 1715-1890  
12/LG:334053.8:2001MAR30 || 1-304; 22-298; 28-300; 28-302; 37-275; 47-347; 49-248; 54-302; 54-264; 54-307; 54-304; 54-305; 69-303; 77-323; 77-306; 95-750; 101-305; 155-322; 183-306; 185-305; 183-890; 190-824; 223-306; 233-306; 237-306; 266-321; 417-877; 449-877; 455-750; 551-859; 574-871; 582-730; 585-797; 587-874; 593-859; 593-863; 593-742; 598-697; 608-877; 608-871; 608-737; 611-1078; 613-875; 613-747; 615-871; 616-744; 616-1075; 616-922; 616-698; 616-714; 616-871; 616-894; 616-811; 616-745; 616-924; 616-826; 616-702; 616-711; 616-697; 616-756; 619-859; 618-871; 620-871; 624-871; 628-871; 631-1079; 632-1077; 632-871; 632-1078; 635-1080; 636-1080; 637-1072; 643-1072; 648-1081; 650-871; 655-1079; 656-864; 663-871; 667-904; 673-932; 673-1078; 678-1072; 683-884; 683-871; 686-872; 688-859; 707-1078; 711-859; 715-1078; 720-871; 721-1072; 729-859; 732-871; 736-1078; 742-859; 741-1072; 742-1081; 747-871; 753-871; 753-1212; 764-1078; 764-872; 765-871; 772-1078; 809-859; 849-1507; 996-1248; 1003-1294; 1011-1080; 1027-1078; 1063-1313; 1099-1619; 1087-1338; 1097-1153; 1097-1359; 1097-1356; 1098-1244; 1098-1569; 1098-1711; 1102-1671; 1104-1267; 1108-1279; 1109-1279; 1118-1359; 1144-1508; 1144-1477; 1144-1279; 1162-1620; 1165-1500; 1191-1305; 1167-1499; 1203-1455; 1204-1458; 1211-1589; 1211-1479; 1210-1709; 1245-1450; 1272-1391; 1253-1347; 1256-1717; 1321-1489; 1335-1420; 1316-1715; 1339-1507; 1322-1722; 1335-1587; 1335-1609; 1323-1588; 1324-1720; 1336-1500; 1338-1607; 1346-1720; 1360-1715; 1366-1636; 1378-1715; 1385-1715; 1402-1500; 1395-1719; 1396-1713; 1396-1715; 1402-1576; 1408-1713; 1414-1715; 1418-1715; 1426-1710; 1432-1507; 1441-1720; 1462-1714; 1467-1699; 1490-1718; 1499-1702; 1510-1715; 1523-1714; 1531-1691; 1577-1669; 1665-1722  
13/LG:392033.1:2001MAR30 || 1-237; 1-364; 203-720; 206-529; 648-1196  
14/LG:401748.16:2001MAR30 || 1-341; 263-814; 263-835; 327-586; 462-631; 465-835; 531-1035; 591-769; 492-674; 595-814; 541-818; 542-794; 604-803; 620-749; 565-846; 568-818; 657-937; 578-1053; 584-815; 586-838; 598-1049; 603-1177; 606-968; 618-1238; 621-902; 680-812; 699-956  
15/LG:476084.1:2001MAR30 || 1-3696; 38-570; 38-645; 38-610; 39-2266; 96-731; 463-1067; 462-944; 461-1060; 736-1022; 736-1190; 736-1153; 813-1082; 862-1035; 882-1474; 1008-1140; 1135-1729; 1357-1872; 1359-1629; 1399-1744; 1581-1670; 1594-2028; 1632-1882; 1702-1959; 1710-2227; 1717-2249; 1730-2179; 1810-2091; 1810-2258; 1821-2270; 1856-2271; 1867-2266; 1870-2266; 1878-2267; 1878-

Table 5

2256; 1881-2266; 1886-2148; 1886-2266; 1896-2266; 1901-2269; 1904-2177; 1909-2178; 1927-2266; 1940-2178; 1980-2266; 1982-2266; 1986-2266; 2021-2266; 2049-2264; 2101-2368; 2103-2266; 2107-2264; 2156-2264; 2169-2264; 2247-2829; 2247-2569; 2247-2517; 2252-2798; 2289-2442; 2377-2584; 2377-2610; 2377-2794; 2439-2962; 2443-2602; 2462-2602; 2490-2602; 2536-2602; 2589-2839; 2604-2869; 2615-2721; 2669-2950; 2670-2930; 2692-2895; 2706-2860; 2706-3031; 2716-2946; 2718-3297; 2753-3025; 2764-2956; 2764-2951; 2765-3002; 2764-2979; 2765-3111; 2765-3145; 2765-3110; 2779-3025; 2808-2998; 2808-3025; 2827-3101; 2833-3084; 2842-2957; 2846-2928; 2870-2981; 2884-2957; 2938-3025; 2941-3183; 2943-3025; 2960-3571; 2969-3025; 3181-3418; 3197-3506; 3199-3496; 3199-3509; 3199-3698; 3199-3467; 3201-3518; 3201-3349; 3204-3311; 3241-3620; 3241-3658; 3241-3598; 3251-3698; 3266-3708; 3269-3619; 3267-3708; 3278-3708; 3320-3428; 3326-3553; 3336-3709; 3350-3708; 3359-3708; 3362-3708; 3366-3698; 3374-3588; 3375-3708; 3381-3708; 3384-3708; 3406-3708; 3415-3708; 3414-3673; 3421-3708; 3423-3619; 3425-3708; 3430-3806; 3432-3567; 3490-3708; 3493-3708; 3505-3808; 3504-3708; 3524-3808; 3517-3727; 3535-3708; 3538-3708; 3550-3709; 3556-3708; 3558-3658; 3560-3698; 3572-3808; 3569-3708; 3586-3697; 3596-3696; 3614-3708; 3620-3808; 3622-3708; 3627-3696; 3627-3708; 3627-3698; 3627-3709; 3642-3802  
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79/LG:300009.1:2001MAR30 || 1-168; 32-296; 116-296; 116-914; 132-296; 586-  
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80/LG:333886.2:2001MAR30 || 1-592; 188-629; 243-629; 256-826; 431-765; 434-  
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83/LG:250170.3:2001MAR30 || 3-702; 1-673; 434-1013; 565-847; 653-971; 662-906; 817-1060; 995-1414; 995-1241; 1113-1715; 1115-1579; 1115-1338; 1226-1508; 1236-1559; 1239-1338; 1260-1508; 1285-1514; 1316-1594; 1356-1681; 1369-1657; 1430-1677; 1435-1751; 1494-1775; 1505-1770; 1549-2004; 1555-1665; 1555-1769; 1555-2004; 1555-1905; 1682-1790; 1682-2142; 1695-2169; 1733-1927; 1752-1995; 1759-1936; 1835-2085; 1857-2093; 1883-2006; 1910-2339; 1912-2134; 1943-2161; 1943-2174; 1944-2339; 1955-2174; 1970-2134; 1972-2135; 2007-2337; 2006-2339; 2015-2337; 2026-2305; 2061-2350; 2067-2337; 2188-2337; 2188-2261; 2188-2350; 2207-2337; 2235-2337; 2263-2339

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243/LG:1400447.1:2001MAR30 || 1-344; 1-322; 1-379; 1-222; 1-361; 1-240; 11-314; 41-577; 139-525; 370-584; 512-1035; 926-1468; 952-1022; 952-1023

244/LG:1500260.1:2001MAR30 || 1-569; 202-699; 204-457; 256-695; 405-698; 428-695

245/LG:1500873.3:2001MAR30 || 1-6094; 1093-1716; 1204-1418; 1286-1634; 1554-2251; 1575-1649; 1575-2101; 1903-2380; 2435-2988; 2747-3039; 3250-3549; 3303-3753; 3432-3755; 3608-3843; 3715-4149; 3872-4384; 3899-4362; 4012-4297; 4052-4220; 4101-4381; 4356-4943; 4356-4946; 4365-4935; 4542-4915; 4542-4764; 4543-4693; 4604-4830; 4737-5445; 5179-5320; 5196-5320; 5209-5319; 5220-5412; 5220-5320; 5220-5636; 5262-5469; 5332-5465; 5375-5610; 5375-5617; 5375-5856; 5375-5618; 5443-5695; 5531-5809; 5528-6115; 5577-6152; 5579-6063; 5580-6069; 5589-6055; 5599-6219; 5627-5813; 5633-5816; 5632-6093; 5640-6094; 5675-6094; 5689-6156; 5722-6148; 5730-6087; 5733-5935; 5737-6078; 5744-6090; 5758-6093; 5793-6152; 5795-6050; 5816-6062; 5841-6097; 5847-6094; 5903-6100

246/LG:1505341.1:2001MAR30 || 279-832; 188-471; 1-256

247/LG:169863.4:2001MAR30 || 672-1115; 348-907; 391-722; 323-685; 267-684; 212-683; 391-681; 279-617; 1-603; 338-598; 1-452

248/LG:208637.1:2001MAR30 || 1-632; 246-922; 405-877; 404-520; 405-959; 411-937; 414-895; 571-1157; 710-1196; 747-859; 792-1089; 802-1366; 804-1312; 810-1048; 1081-1714; 1116-1649; 1211-1454; 1426-1732; 1425-1967; 1458-1995; 1465-1991; 1515-1602; 1658-2072; 1755-2093; 1900-2169; 1916-2431; 1917-2512; 2024-2271; 2026-2281; 2164-2309; 2167-2395; 2329-2574; 2474-2848; 2474-2653; 2502-2820; 2521-2904; 2580-2704; 2590-3115; 2596-2836; 2604-2891; 2639-2999; 2643-2907; 2663-2907; 2675-3000; 2679-3060; 2719-3002; 2733-2981; 2762-3043; 2768-2974; 2773-3010; 2773-3059; 2773-3057; 2792-3057; 2794-3030; 2828-3089; 2875-3155; 2897-3130; 2921-3158; 2928-3236; 2930-3154; 2970-3053; 3003-3211; 3005-3546; 3008-3242; 3014-3193; 3029-3267; 3049-3350; 3049-3269; 3052-3265; 3052-3534; 3057-3266; 3057-3360; 3057-3279; 3058-3297; 3078-3814; 3079-3335; 3086-3350; 3088-3359; 3089-3215; 3104-3328; 3104-3358; 3104-3340; 3105-3274; 3137-3260; 3137-3356; 3148-3389; 3154-3399; 3155-3545; 3155-3437; 3156-3397; 3212-3510; 3230-3662; 3259-3500; 3268-3664; 3269-3748; 3271-3483; 3282-3520; 3287-

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249/LG:234936.67:2001MAR30 || 1-471; 242-496; 244-472; 244-490; 258-485; 279-717; 279-518; 340-558; 334-532; 496-1091; 544-806; 626-1210; 655-896; 836-1150; 1106-1350; 1140-1687; 1532-1785; 1548-1785; 1601-1982; 1666-1911; 1703-1957; 1799-2037

250/LG:243305.3:2001MAR30 || 1-175; 1-385; 288-857; 288-836; 291-1069; 367-623; 503-587; 561-1061; 561-913; 584-837; 599-1006; 671-837; 713-837; 743-837; 743-1179

251/LG:334645.20:2001MAR30 || 1-541; 369-929; 371-632; 390-693; 390-1037; 683-1062; 704-1305; 757-976; 891-1365; 891-1093; 916-1023; 917-1119; 917-1188; 941-1402; 944-1402; 950-1408; 962-1407; 971-1407; 1016-1233; 1054-1410; 1076-1407; 1085-1411; 1124-1364; 1173-1365; 1180-1407; 1188-1407; 1332-1407

252/LG:349468.13:2001MAR30 || 1-272; 1-486; 19-505; 97-373; 130-662; 130-399; 250-521; 251-431; 262-450; 394-709; 412-657; 463-632; 487-709; 513-965; 543-709; 646-795; 647-696

253/LG:385145.1:2001MAR30 || 1-747; 1-546; 17-198; 35-237; 37-295; 160-689; 338-567; 369-527; 571-1201; 873-1506; 1071-1513; 1191-1346; 1195-1371; 1438-1773; 1438-2017; 1441-1656; 1896-2180

254/LG:391807.1:2001MAR30 || 166-635; 159-610; 494-619; 494-612; 1-593

255/LG:399287.10:2001MAR30 || 1409-1756; 1688-1747; 1273-1747; 1269-1741; 1351-1741; 1258-1741; 1277-1741; 975-1555; 949-1454; 826-1399; 727-1378; 743-969; 603-896; 146-737; 551-730; 548-645; 1-537; 1-217

256/LG:404157.1:2001MAR30 || 1-772; 183-769; 301-969; 454-877; 457-752; 498-788; 581-838; 867-1050; 931-1526; 931-1319; 942-1084; 1052-1514; 1091-1619; 1201-1663; 1247-1666; 1259-1660; 1265-1669; 1354-1516; 1369-1663; 1468-1821; 1601-2102; 1608-1664; 1635-1917; 1675-1928; 1795-2069; 1808-2269; 1811-2124; 1835-2177; 2186-2788; 2250-2746; 2358-2787; 2367-2589; 2409-2657; 2425-2796; 2452-2602; 2478-2788; 2515-2788; 2528-2943; 2598-2789

257/LG:979390.2:2001MAR30 || 1116-1394; 1012-1393; 1138-1382; 1124-1371; 1103-1267; 1208-1267; 486-1117; 797-1092; 454-971; 288-875; 672-841; 310-798; 243-733; 109-483; 1-400; 84-386; 84-327

258/LG:981962.1:2001MAR30 || 1266-1922; 1555-1857; 1556-1859; 1410-1820; 1370-1643; 1293-1597; 981-1529; 1014-1493; 989-1490; 1032-1489; 1029-1489; 1057-1454; 1324-1443; 950-1430; 1164-1425; 1022-1303; 786-1296; 786-1274; 1021-1228; 989-1221; 535-1108; 545-1102; 409-877; 373-875; 1-616; 366-596; 334-593; 238-420

259/LG:982976.2:2001MAR30 || 1-461; 222-768; 222-984; 389-625; 505-761; 512-880; 723-1540; 739-1490; 820-1402; 820-1403; 833-1355; 869-1300; 923-1648; 942-1372; 1043-1330; 1050-1344; 1147-1394; 1275-1903; 1311-1699; 1418-1804; 1487-1712; 1546-1961; 1583-2009; 1790-1997; 1790-2115; 1900-2459; 2083-2545; 2128-2530; 2132-2499; 2247-2530; 2294-2499; 2299-2544; 2318-2499; 2333-2576; 2380-2545; 2387-2576

260/LG:1448087.1:2001MAR30 || 1-235; 18-308; 18-188; 18-226; 76-273

261/LG:1449021.1:2001MAR30 || 120-721; 228-639; 230-635; 244-618; 307-604; 147-604; 146-593; 1-578; 34-465

262/LG:144920.1:2001MAR30 || 1-591; 1-613; 79-714; 352-956; 461-911; 471-911; 516-695; 561-1130; 650-1280; 675-1279; 1045-1305; 1048-1299; 1156-1448; 1156-1567; 1267-1750; 1398-1829; 1399-1654; 1697-1935; 1793-1973; 1848-2380; 1872-2378; 1905-2465; 1931-2251; 2024-2364; 2024-2446; 2029-2242; 2116-2271; 2136-2368; 2272-2322

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263/LG:474725.1:2001MAR30 || 1-534; 1-612; 200-728; 449-1077; 514-1077; 588-842; 588-921; 632-879; 866-1360; 866-1075; 936-1177; 938-1531; 1101-1401; 1136-1379; 1368-1979; 1418-1965; 1443-2091; 1446-1765; 1451-1965; 1478-1918; 1579-1999; 1614-2006; 1624-2003; 1633-1998; 1663-1895; 1668-2004; 1690-2179; 1736-2001; 1875-2004; 1902-2003; 1902-2071

264/LG:1085952.14:2001MAR30 || 1-157; 1-376; 1-234; 7-288; 12-235; 17-354; 33-290; 42-238; 43-519; 45-592; 45-612; 49-606; 49-154; 49-474; 50-169; 50-542; 78-290; 81-665; 87-337; 88-462; 99-563; 103-766; 107-234; 120-563; 120-366; 158-285; 184-438; 172-394; 175-316; 184-707; 213-668; 221-657; 247-706; 250-689; 285-668; 294-708; 303-704; 305-570; 310-473; 336-684; 358-558; 400-704; 421-706; 436-706; 458-694; 458-706; 458-564; 479-706; 479-704; 500-675; 551-706; 576-706

265/LI:011009.2:2001MAY17 || 1-610; 1079-1771; 1141-1638; 1224-1699; 186-543; 212-852; 220-714; 225-732; 240-880; 240-831; 248-773; 251-804; 268-901; 273-899; 280-955; 282-903; 301-800; 304-900; 304-663; 306-826; 311-900; 312-1034; 337-1101; 347-826; 352-1070; 359-915; 371-885; 387-599; 409-974; 522-968; 521-1231; 536-1204; 541-1119; 546-893; 551-656; 558-845; 564-1000; 571-1179; 575-1036; 581-1297; 623-1149; 642-1161; 646-1178; 660-1353; 685-1377; 704-1439; 739-1256; 742-1204; 766-1284; 782-1502; 786-1410; 815-1324; 820-1477; 834-1318; 835-1434; 844-1429; 852-1473; 864-1551; 868-1485; 869-1485; 895-1460; 898-1547; 899-1553; 900-1342; 900-1367; 906-1491; 908-1447; 909-1374; 907-1407; 907-1386; 922-1454; 946-1444; 976-1466; 1013-1718; 1012-1591; 1025-1544; 1039-1714; 1039-1481; 1052-1539; 1072-1721; 1105-1292; 1115-1700; 1114-1303; 1128-1769; 1128-1314; 1147-1587; 1149-1710; 1156-1264; 1210-1827; 1228-1745; 1246-1729; 1270-1748; 1309-1862; 1361-1504; 1387-1934; 1430-1705; 1454-2033; 1454-1689; 1455-1930; 1469-2001; 1510-1679; 1564-2012; 1626-1806; 1622-2268; 1662-2263; 1690-2266; 1696-2267; 1697-2290; 1708-1811; 1758-1928; 1779-2275; 1811-2264; 1875-2290; 1914-2009; 1915-2015; 2105-2249; 1225-1699; 1-466; 120-634; 170-517

266/LI:016933.2:2001MAY17 || 75-499; 115-586; 147-496; 162-496; 186-390; 195-494; 200-501; 209-496; 260-516; 266-322; 331-888; 355-490; 358-490; 442-879; 395-744; 645-892; 578-833; 580-1087; 24-120; 662-895; 594-892; 1165-1257; 752-1207; 783-1163; 798-1209; 808-1201; 809-1236; 809-1157; 809-1091; 809-987; 809-1000; 809-977; 809-959; 809-947; 809-895; 825-985; 825-1240; 825-983; 825-948; 836-1204; 910-1116; 951-1236; 1007-1164; 1007-1140; 1096-1249; 1-373; 186-386; 331-508; 419-721; 809-992; 873-1123

267/LI:1072014.6:2001MAY17 || 1733-2015; 1759-2190; 1771-2024; 1769-1978; 1789-2045; 1797-2005; 2409-2634; 2428-2634; 1800-2303; 1854-2743; 1822-1888; 1827-2194; 1854-2155; 1859-2137; 1906-2194; 2429-2634; 1938-2199; 2449-2684; 2474-2622; 1942-2578; 2009-2250; 2011-2280; 2013-2753; 2032-2575; 2072-2291; 2476-2717; 2080-2528; 2120-2551; 2131-2603; 2159-2398; 2518-2789; 2567-2633; 2659-2797; 2159-2348; 2170-2634; 2175-2633; 2185-2595; 2186-2634; 2189-2634; 2188-2633; 2195-2455; 2196-2638; 2197-2431; 2200-2634; 2208-2638; 2213-2648; 2219-2532; 2225-2630; 2232-2634; 2233-2635; 2239-2518; 2239-2634; 2250-2634; 2258-2637; 2264-2634; 2267-2634; 2268-2641; 2292-2561; 2298-2634; 2300-2634; 2311-2634; 2316-2635; 2336-2632; 2338-2637; 2346-2632; 2342-2634; 2348-2563; 2367-2634; 2371-2634; 2369-2636; 2375-2627; 2395-2635; 2404-2635; 2408-2617; 1461-1732; 1450-2321; 1487-1707; 1526-1775; 1530-1995; 1538-2294; 1559-1752; 1565-2059; 1576-1950; 1596-2220; 1587-1990; 1589-2051; 1663-1906; 1665-1941; 1-447; 52-628; 54-137; 129-320; 153-764; 155-395; 190-261; 300-783; 300-915; 375-926; 409-905; 409-593; 613-687; 612-878; 618-2660; 658-947; 658-1043; 746-984; 753-1034; 770-1302; 835-974; 1017-1350; 1027-1233; 1083-1531; 1116-1704; 1115-1505; 1171-1435; 1184-1423; 1168-2058; 1201-1420; 1193-2093; 1237-1531; 1255-1498; 1288-1812; 1298-1674; 1298-1566; 1298-1530; 1303-1420; 1289-2012; 1309-1479; 1328-1626; 1345-1589; 1413-2061; 1406-1681; 1414-2089; 1446-1907; 1671-1979; 1696-2400

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268/LI:1165280.4:2001MAY17 || 1340-1901; 1596-1865; 1915-2172; 2026-2292;  
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 269/LI:1167958.4:2001MAY17 || 292-527; 828-1337; 924-1517; 995-1496; 1093-  
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 270/LI:1168073.15:2001MAY17 || 1-521; 345-745; 675-1290; 1054-1238; 1514-  
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 271/LI:1170154.12:2001MAY17 || 1197-1577; 1365-1564; 1885-2412; 2273-2415;  
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 272/LI:1173769.2:2001MAY17 || 1-599; 1-255; 1-622; 11-117; 29-593; 167-356;  
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 273/LI:1174292.18:2001MAY17 || 1472-2054; 2046-2423; 2059-2338; 2097-2336;  
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274/LI:1177989.1:2001MAY17 || 2436-2917; 2301-2834; 2440-2778; 2436-2770;  
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 275/LI:1179173.3:2001MAY17 || 1-2015; 1-388; 11-529; 27-189; 34-302; 96-556;  
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 565/LG:249518.11:2001JUN22 || 1-431; 1-340  
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TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
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2	LG:1041136.7:2001MAR30	Stomatognathic System - 18%
3	LG:1043848.1:2001MAR30	Liver - 95%
4	LG:1097673.1:2001MAR30	Connective Tissue - 17%, Unclassified/Mixed - 11%, Exocrine Glands - 11%
5	LG:133991.1:2001MAR30	Liver - 31%, Pancreas - 31%, Unclassified/Mixed - 24%
6	LG:1397110.7:2001MAR30	Germ Cells - 22%, Skin - 14%, Female Genitalia - 11%
7	LG:1512094.1:2001MAR30	Liver - 100%
8	LG:230734.53:2001MAR30	Endocrine System - 20%, Skin - 17%, Digestive System - 14%
9	LG:240154.9:2001MAR30	Embryonic Structures - 12%, Liver - 12%, Hemic and Immune System - 10%
10	LG:245863.31:2001MAR30	Female Genitalia - 24%, Connective Tissue - 18%, Digestive System - 16%
11	LG:257151.4:2001MAR30	Connective Tissue - 21%, Pancreas - 19%, Musculoskeletal System - 13%
12	LG:334053.8:2001MAR30	Embryonic Structures - 17%, Sense Organs - 15%
13	LG:392033.1:2001MAR30	Unclassified/Mixed - 93%
14	LG:401748.16:2001MAR30	Nervous System - 15%, Cardiovascular System - 15%, Female Genitalia - 15%, Hemic and Immune System - 15%, Connective Tissue - 15%
15	LG:476084.1:2001MAR30	Germ Cells - 21%, Unclassified/Mixed - 12%
16	LG:068514.1:2001MAR30	Germ Cells - 52%, Unclassified/Mixed - 16%, Liver - 11%
17	U:010505.1:2001MAY17	Hemic and Immune System - 55%, Unclassified/Mixed - 45%
18	U:011664.1:2001MAY17	Endocrine System - 50%, Respiratory System - 18%, Female Genitalia - 18%
19	U:021459.66:2001MAY17	Pancreas - 19%, Skin - 12%
20	U:1047290.8:2001MAY17	Hemic and Immune System - 100%
21	U:1071608.1:2001MAY17	Pancreas - 40%, Liver - 36%, Cardiovascular System - 16%
22	U:1077079.4:2001MAY17	Nervous System - 100%
23	U:1173294.9:2001MAY17	Embryonic Structures - 13%, Liver - 11%
24	U:148565.7:2001MAY17	Nervous System - 100%
25	U:2052562.23:2001MAY17	Liver - 76%, Urinary Tract - 16%
26	U:2119354.20:2001MAY17	Skin - 24%, Liver - 11%
27	U:2209329.1:2001MAY17	Sense Organs - 33%, Unclassified/Mixed - 28%
28	U:240143.12:2001MAY17	Stomatognathic System - 14%, Musculoskeletal System - 12%
29	U:250855.6:2001MAY17	Germ Cells - 31%, Female Genitalia - 12%, Skin - 11%
30	U:293078.2:2001MAY17	Hemic and Immune System - 50%, Cardiovascular System - 40%, Nervous System - 10%
31	U:351818.62:2001MAY17	Skin - 23%, Urinary Tract - 20%, Male Genitalia - 18%
32	U:409990.1:2001MAY17	Stomatognathic System - 20%, Germ Cells - 12%
33	U:474832.7:2001MAY17	Embryonic Structures - 13%
34	U:814696.11:2001MAY17	Sense Organs - 24%, Connective Tissue - 21%
35	U:818488.31:2001MAY17	Liver - 14%, Exocrine Glands - 13%, Endocrine System - 12%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
36	U:2049834.12:2001MAY17	Unclassified/Mixed - 14%, Exocrine Glands - 12%, Urinary Tract - 11%
37	U:338956.8:2001MAY17	Embryonic Structures - 56%, Urinary Tract - 44%
38	U:1175083.15:2001MAY17	Germ Cells - 96%
39	U:1189311.14:2001MAY17	Pancreas - 12%, Germ Cells - 10%
40	U:330984.6:2001MAY17	Germ Cells - 21%, Sense Organs - 15%
41	LG:1093461.22:2001JUN22	Unclassified/Mixed - 52%, Endocrine System - 16%, Urinary Tract - 12%
42	LG:1138554.48:2001JUN22	Musculoskeletal System - 67%, Urinary Tract - 33%
43	LG:1377369.20:2001JUN22	Embryonic Structures - 14%, Connective Tissue - 14%, Liver - 11%
44	LG:200050.17:2001JUN22	Nervous System - 13%, Sense Organs - 10%
45	LG:437008.4:2001JUN22	Female Genitalia - 36%, Nervous System - 36%, Hemic and Immune System - 27%
46	LG:7684119.1:2001JUN22	Stomatognathic System - 29%, Sense Organs - 25%
47	LG:7690376.8:2001JUN22	Nervous System - 100%
48	LG:068514.3:2001JUN22	Germ Cells - 67%
49	LG:270209.1:2001JUN22	Endocrine System - 40%, Digestive System - 20%, Respiratory System - 20%, Female Genitalia - 20%
50	LG:1400575.1:2001MAR30	Male Genitalia - 37%, Respiratory System - 26%, Endocrine System - 21%
51	LG:242968.4:2001MAR30	widely distributed
52	LG:344741.17:2001MAR30	Musculoskeletal System - 24%, Embryonic Structures - 15%
53	LG:443203.7:2001MAR30	Skin - 30%, Exocrine Glands - 26%, Unclassified/Mixed - 15%
54	LG:481492.6:2001MAR30	Exocrine Glands - 37%, Embryonic Structures - 14%, Endocrine System - 14%
55	U:035870.26:2001MAY17	Germ Cells - 13%, Respiratory System - 12%
56	U:2121852.1:2001MAY17	Hemic and Immune System - 50%, Nervous System - 50%
57	U:2164765.1:2001MAY17	Endocrine System - 100%
58	U:2167150.1:2001MAY17	Digestive System - 100%
59	U:230062.10:2001MAY17	Unclassified/Mixed - 15%, Cardiovascular System - 13%, Connective Tissue - 13%
60	U:351749.1:2001MAY17	Urinary Tract - 57%, Hemic and Immune System - 29%, Nervous System - 14%
61	U:399808.27:2001MAY17	Skin - 84%, Male Genitalia - 11%
62	U:401269.13:2001MAY17	Hemic and Immune System - 51%, Connective Tissue - 10%
63	U:481492.3:2001MAY17	Stomatognathic System - 39%, Exocrine Glands - 37%
64	U:1186340.9:2001MAY17	Embryonic Structures - 22%, Skin - 10%
65	LG:1324237.7:2001JUN22	Digestive System - 31%, Unclassified/Mixed - 27%, Respiratory System - 21%
66	LG:142131.16:2001JUN22	Hemic and Immune System - 51%, Connective Tissue - 10%
67	LG:407723.12:2001JUN22	Liver - 57%, Urinary Tract - 21%, Unclassified/Mixed - 12%
68	LG:7685000.6:2001JUN22	Respiratory System - 67%, Nervous System - 33%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
69	LG:1395921.6:2001JUN22	Endocrine System - 82%, Liver - 12%
70	LG:230062.16:2001JUN22	Unclassified/Mixed - 19%, Connective Tissue - 13%, Cardiovascular System - 11%
71	LG:7690036.1:2001JUN22	Musculoskeletal System - 38%, Male Genitalia - 19%, Digestive System - 13%
72	LG:044276.1:2001JUN22	Germ Cells - 84%
73	LG:1091967.34:2001JUN22	Nervous System - 46%, Male Genitalia - 31%, Hemic and Immune System - 23%
74	LG:242968.17:2001JUN22	widely distributed
75	LG:081174.1:2001MAR30	Nervous System - 100%
76	LG:1385255.10:2001MAR30	Unclassified/Mixed - 13%, Skin - 11%
77	LG:1397492.21:2001MAR30	Skin - 44%, Respiratory System - 16%, Hemic and Immune System - 11%, Connective Tissue - 11%
78	LG:1512330.2:2001MAR30	Sense Organs - 78%, Respiratory System - 10%
79	LG:300009.1:2001MAR30	Liver - 43%, Pancreas - 21%, Connective Tissue - 17%
80	LG:333886.2:2001MAR30	Sense Organs - 16%, Stomatognathic System - 14%
81	LG:349438.18:2001MAR30	Female Genitalia - 52%, Exocrine Glands - 20%
82	LG:358239.46:2001MAR30	Stomatognathic System - 34%, Respiratory System - 11%
83	LG:250170.3:2001MAR30	Hemic and Immune System - 24%, Exocrine Glands - 18%, Respiratory System - 15%
84	LG:1383159.5:2001MAR30	Male Genitalia - 47%, Germ Cells - 35%
85	LI:044888.1:2001MAY17	Germ Cells - 47%, Endocrine System - 19%, Digestive System - 13%
86	LI:101277.1:2001MAY17	Urinary Tract - 70%, Exocrine Glands - 15%
88	LI:1072004.14:2001MAY17	Skin - 15%
90	LI:1183158.1:2001MAY17	Urinary Tract - 67%, Nervous System - 33%
91	LI:1188807.9:2001MAY17	Stomatognathic System - 25%, Liver - 23%
92	LI:206576.15:2001MAY17	Germ Cells - 21%
93	LI:2120427.4:2001MAY17	Respiratory System - 60%, Male Genitalia - 40%
94	LI:2196074.2:2001MAY17	Digestive System - 100%
96	LI:237723.23:2001MAY17	Sense Organs - 15%
97	LI:817560.12:2001MAY17	Hemic and Immune System - 100%
99	LI:235333.5:2001MAY17	Digestive System - 12%, Respiratory System - 12%
100	LI:373808.8:2001MAY17	Germ Cells - 50%, Unclassified/Mixed - 34%, Male Genitalia - 16%
101	LI:424554.1:2001MAY17	Stomatognathic System - 80%, Musculoskeletal System - 15%
102	LG:028634.1:2001JUN22	Female Genitalia - 58%, Hemic and Immune System - 25%, Nervous System - 17%
103	LG:087230.3:2001JUN22	Liver - 45%, Exocrine Glands - 20%, Female Genitalia - 10%, Male Genitalia - 10%, Nervous System - 10%
104	LG:1397520.8:2001JUN22	Female Genitalia - 100%
105	LG:213947.1:2001JUN22	Liver - 60%, Hemic and Immune System - 27%, Respiratory System - 13%
106	LG:218029.8:2001JUN22	Unclassified/Mixed - 30%, Respiratory System - 25%, Hemic and Immune System - 15%
107	LG:300009.1:2001JUN22	Liver - 41%, Pancreas - 22%, Connective Tissue - 17%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
108	LG:411188.1:2001JUN22	Sense Organs - 34%, Nervous System - 28%, Germ Cells - 18%
109	LG:481295.21:2001JUN22	Unclassified/Mixed - 16%, Skin - 12%
110	LG:7684165.8:2001JUN22	Cardiovascular System - 18%, Connective Tissue - 18%, Unclassified/Mixed - 16%
111	LG:7690928.6:2001JUN22	Musculoskeletal System - 50%, Hemic and Immune System - 25%, Urinary Tract - 25%
112	LG:990040.8:2001JUN22	Stomatognathic System - 10%
113	LG:126510.8:2001JUN22	Hemic and Immune System - 33%, Respiratory System - 16%, Liver - 14%
114	LG:7692710.8:2001JUN22	Sense Organs - 30%, Unclassified/Mixed - 15%
115	LG:044888.1:2001JUN22	Germ Cells - 53%, Endocrine System - 23%, Digestive System - 15%
116	LG:1447083.2:2001JUN22	Germ Cells - 31%
117	LG:7672289.1:2001JUN22	Endocrine System - 100%
118	LG:1013021.3:2001MAR30	Respiratory System - 63%, Digestive System - 25%, Hemic and Immune System - 13%
119	LG:1096667.17:2001MAR30	Germ Cells - 17%
120	LG:1270681.12:2001MAR30	Connective Tissue - 19%, Skin - 12%
121	LG:1328242.1:2001MAR30	Germ Cells - 19%, Liver - 16%, Male Genitalia - 11%
122	LG:1396586.4:2001MAR30	Pancreas - 35%, Digestive System - 15%, Exocrine Glands - 15%
123	LG:1396919.6:2001MAR30	Cardiovascular System - 100%
124	LG:1397751.10:2001MAR30	Germ Cells - 16%, Nervous System - 11%
125	LG:1450059.4:2001MAR30	widely distributed
126	LG:1503615.8:2001MAR30	Unclassified/Mixed - 35%, Nervous System - 26%
127	LG:1507027.3:2001MAR30	Unclassified/Mixed - 16%, Nervous System - 16%, Embryonic Structures - 11%, Pancreas - 11%
128	LG:202892.1:2001MAR30	Sense Organs - 41%, Unclassified/Mixed - 14%, Hemic and Immune System - 11%
129	LG:220407.3:2001MAR30	Sense Organs - 30%
130	LG:242234.11:2001MAR30	widely distributed
131	LG:245181.20:2001MAR30	Germ Cells - 10%
132	LG:320165.7:2001MAR30	Nervous System - 20%, Germ Cells - 16%, Digestive System - 15%
133	LG:333965.2:2001MAR30	Liver - 31%, Pancreas - 15%, Digestive System - 14%
134	LG:402431.16:2001MAR30	Stomatognathic System - 11%
135	LG:404400.4:2001MAR30	Unclassified/Mixed - 25%, Musculoskeletal System - 23%, Female Genitalia - 14%
136	LG:406860.73:2001MAR30	Sense Organs - 19%, Liver - 17%, Unclassified/Mixed - 13%
137	LG:413797.14:2001MAR30	Nervous System - 23%, Male Genitalia - 17%, Sense Organs - 14%
138	LG:420527.51:2001MAR30	Connective Tissue - 12%
139	LG:277227.1:2001MAR30	Skin - 11%
140	LG:373260.30:2001MAR30	Musculoskeletal System - 34%, Unclassified/Mixed - 20%, Nervous System - 20%
141	LG:418805.7:2001MAR30	Cardiovascular System - 15%, Urinary Tract - 11%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
142	LG:1398946.18:2001MAR30	Respiratory System - 17%, Hemic and Immune System - 11%, Germ Cells - 11%
143	LG:382911.1:2001MAR30	Sense Organs - 19%
144	U:028146.27:2001MAY17	Skin - 23%, Nervous System - 12%, Cardiovascular System - 12%, Digestive System - 12%
145	U:1072703.6:2001MAY17	Liver - 24%, Respiratory System - 14%, Digestive System - 13%
146	U:1073062.138:2001MAY17	Female Genitalia - 63%, Hemic and Immune System - 25%, Nervous System - 13%
147	U:1084954.7:2001MAY17	Urinary Tract - 11%
148	U:202892.5:2001MAY17	Hemic and Immune System - 19%, Unclassified/Mixed - 16%, Pancreas - 16%
149	U:2030686.1:2001MAY17	Connective Tissue - 48%, Female Genitalia - 17%, Digestive System - 14%
151	U:2118426.12:2001MAY17	Sense Organs - 25%, Male Genitalia - 22%, Respiratory System - 13%
154	U:2155821.1:2001MAY17	Cardiovascular System - 100%
155	U:2201523.6:2001MAY17	widely distributed
156	U:235867.27:2001MAY17	Digestive System - 70%, Pancreas - 21%
157	U:238414.1:2001MAY17	Connective Tissue - 16%, Sense Organs - 10%
158	U:242234.6:2001MAY17	widely distributed
159	U:245181.22:2001MAY17	widely distributed
160	U:245474.13:2001MAY17	Unclassified/Mixed - 16%
161	U:311661.1:2001MAY17	Urinary Tract - 48%, Musculoskeletal System - 28%
162	U:320165.21:2001MAY17	Nervous System - 20%, Germ Cells - 18%, Urinary Tract - 13%
163	U:337026.1:2001MAY17	Exocrine Glands - 21%, Digestive System - 11%, Urinary Tract - 10%
164	U:347977.10:2001MAY17	widely distributed
165	U:413040.39:2001MAY17	Pancreas - 38%, Female Genitalia - 19%, Urinary Tract - 15%
166	U:467422.1:2001MAY17	Respiratory System - 36%, Urinary Tract - 20%, Musculoskeletal System - 11%
167	U:474596.53:2001MAY17	Germ Cells - 15%
168	U:481144.22:2001MAY17	widely distributed
169	U:725220.1:2001MAY17	Digestive System - 67%, Nervous System - 33%
170	U:804636.17:2001MAY17	Hemic and Immune System - 17%, Cardiovascular System - 16%, Liver - 11%
171	U:815194.23:2001MAY17	Nervous System - 20%
172	U:817950.6:2001MAY17	Sense Organs - 14%, Cardiovascular System - 11%, Exocrine Glands - 10%
173	U:903485.6:2001MAY17	Embryonic Structures - 25%, Musculoskeletal System - 15%
174	U:220407.8:2001MAY17	Endocrine System - 13%
175	U:413606.59:2001MAY17	Unclassified/Mixed - 41%
176	U:202971.33:2001MAY17	Pancreas - 27%, Skin - 21%, Endocrine System - 12%, Liver - 12%
177	U:2209219.4:2001MAY17	Cardiovascular System - 100%
178	LG:1100586.2:2001JUN22	Endocrine System - 100%



TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
179	LG:113410.1:2001JUN22	Cardiovascular System - 37%, Female Genitalia - 26%, Exocrine Glands - 15%
180	LG:1500938.10:2001JUN22	Urinary Tract - 22%, Respiratory System - 15%, Pancreas - 14%
181	LG:303607.15:2001JUN22	Germ Cells - 24%
182	LG:411148.11:2001JUN22	Embryonic Structures - 16%
183	LG:435726.8:2001JUN22	Unclassified/Mixed - 55%, Endocrine System - 36%
184	LG:475378.4:2001JUN22	Endocrine System - 50%, Musculoskeletal System - 33%, Male Genitalia - 11%
185	LG:7692134.1:2001JUN22	Hemic and Immune System - 32%, Musculoskeletal System - 32%, Respiratory System - 26%
186	LG:985139.2:2001JUN22	Hemic and Immune System - 35%, Digestive System - 24%, Nervous System - 18%
187	LG:149419.8:2001JUN22	Stomatognathic System - 21%, Germ Cells - 13%
188	LG:199172.17:2001JUN22	Liver - 28%, Musculoskeletal System - 20%, Female Genitalia - 19%
189	LG:256101.6:2001JUN22	Nervous System - 100%
190	LG:220407.3:2001JUN22	Sense Organs - 30%
191	LG:331677.12:2001JUN22	Stomatognathic System - 23%, Embryonic Structures - 13%, Cardiovascular System - 12%
192	LG:367128.7:2001JUN22	Unclassified/Mixed - 58%, Female Genitalia - 14%, Urinary Tract - 11%
193	LG:403176.4:2001JUN22	Endocrine System - 43%, Liver - 11%, Female Genitalia - 11%
194	LG:985230.9:2001JUN22	Unclassified/Mixed - 18%
195	LG:005580.6:2001MAR30	Embryonic Structures - 16%, Exocrine Glands - 10%
196	LG:100653.5:2001MAR30	Unclassified/Mixed - 14%, Sense Organs - 12%
197	LG:1099240.25:2001MAR30	Unclassified/Mixed - 10%
198	LG:1117947.1:2001MAR30	Exocrine Glands - 15%, Respiratory System - 12%
199	LG:1327967.11:2001MAR30	Liver - 25%, Stomatognathic System - 24%
200	LG:1395721.9:2001MAR30	Unclassified/Mixed - 16%, Hemic and Immune System - 12%
201	LG:210508.1:2001MAR30	Germ Cells - 76%, Female Genitalia - 14%, Hemic and Immune System - 10%
202	LG:232313.46:2001MAR30	Liver - 17%, Skin - 13%, Digestive System - 11%
203	LG:349746.22:2001MAR30	Nervous System - 17%, Germ Cells - 15%, Musculoskeletal System - 12%
204	LG:350526.1:2001MAR30	Nervous System - 67%, Male Genitalia - 33%
205	LG:385569.1:2001MAR30	Germ Cells - 95%
206	LG:440659.1:2001MAR30	Cardiovascular System - 13%, Germ Cells - 12%
207	LG:1081135.1:2001MAR30	Germ Cells - 28%
208	LG:1387341.2:2001MAR30	Male Genitalia - 10%
209	LG:197915.17:2001MAR30	Germ Cells - 16%, Unclassified/Mixed - 11%
210	LI:071874.1:2001MAY17	Urinary Tract - 67%, Hemic and Immune System - 33%
211	LI:1076016.1:2001MAY17	Sense Organs - 53%, Pancreas - 17%, Liver - 16%
212	LI:2050098.6:2001MAY17	Germ Cells - 27%, Male Genitalia - 12%
213	LI:233360.4:2001MAY17	Cardiovascular System - 23%, Endocrine System - 15%, Respiratory System - 12%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
214	LI:365343.34:2001MAY17	Pancreas - 21%, Digestive System - 19%, Exocrine Glands - 10%
215	LI:757755.14:2001MAY17	Nervous System - 17%
216	LI:1086645.2:2001MAY17	Skin - 41%, Liver - 23%, Digestive System - 10%
217	LG:1015174.1:2001JUN22	Embryonic Structures - 13%
218	LG:1135945.19:2001JUN22	Endocrine System - 33%, Hemic and Immune System - 25%, Respiratory System - 17%, Female Genitalia - 17%
219	LG:1382836.16:2001JUN22	Female Genitalia - 54%, Musculoskeletal System - 46%
220	LG:228817.5:2001JUN22	Stomatognathic System - 31%, Respiratory System - 11%
221	LG:253987.9:2001JUN22	widely distributed
222	LG:7683993.20:2001JUN22	Unclassified/Mixed - 34%, Endocrine System - 12%, Embryonic Structures - 12%
223	LG:7691137.1:2001JUN22	Connective Tissue - 30%, Unclassified/Mixed - 14%, Male Genitalia - 14%
224	LG:977849.6:2001JUN22	Nervous System - 17%, Liver - 11%
225	LG:1088040.17:2001JUN22	Stomatognathic System - 13%, Unclassified/Mixed - 11%
226	LG:1096582.2:2001JUN22	Germ Cells - 19%, Connective Tissue - 13%
227	LG:002095.19:2001JUN22	Exocrine Glands - 12%, Nervous System - 11%, Urinary Tract - 11%
228	LG:227596.1:2001JUN22	Connective Tissue - 52%, Female Genitalia - 22%, Unclassified/Mixed - 12%
229	LG:276154.23:2001JUN22	Germ Cells - 23%, Skin - 15%
230	LG:332254.1:2001JUN22	Skin - 50%, Hemic and Immune System - 14%, Endocrine System - 14%
231	LG:1052984.26:2001MAR30	Embryonic Structures - 43%, Male Genitalia - 30%, Exocrine Glands - 18%
232	LG:1064250.5:2001MAR30	Sense Organs - 23%
233	LG:1065609.1:2001MAR30	Cardiovascular System - 50%, Female Genitalia - 25%, Hemic and Immune System - 13%, Nervous System - 13%
234	LG:1076162.1:2001MAR30	Male Genitalia - 57%, Digestive System - 29%, Nervous System - 14%
235	LG:1079476.6:2001MAR30	Sense Organs - 20%, Embryonic Structures - 12%
236	LG:1080579.9:2001MAR30	Exocrine Glands - 32%, Digestive System - 16%, Endocrine System - 16%
237	LG:1082253.1:2001MAR30	Digestive System - 17%, Unclassified/Mixed - 12%, Musculoskeletal System - 11%
238	LG:1082263.10:2001MAR30	Respiratory System - 14%, Liver - 12%, Endocrine System - 12%, Embryonic Structures - 12%
239	LG:1092343.1:2001MAR30	Germ Cells - 49%, Hemic and Immune System - 10%
240	LG:1094967.1:2001MAR30	Digestive System - 13%, Female Genitalia - 12%, Hemic and Immune System - 12%, Embryonic Structures - 12%
241	LG:1384132.9:2001MAR30	Exocrine Glands - 57%, Nervous System - 21%, Digestive System - 14%
242	LG:1384676.4:2001MAR30	Male Genitalia - 44%, Digestive System - 22%, Nervous System - 22%
243	LG:1400447.1:2001MAR30	Respiratory System - 45%, Nervous System - 27%, Digestive System - 18%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
244	LG:1500260.1:2001MAR30	Endocrine System - 76%, Digestive System - 12%, Female Genitalia - 12%
245	LG:1500873.3:2001MAR30	Unclassified/Mixed - 23%, Germ Cells - 13%, Embryonic Structures - 11%
246	LG:1505341.1:2001MAR30	Respiratory System - 71%, Male Genitalia - 29%
247	LG:169863.4:2001MAR30	Sense Organs - 57%, Endocrine System - 13%, Unclassified/Mixed - 10%
248	LG:208637.1:2001MAR30	Stomatognathic System - 18%
249	LG:234936.67:2001MAR30	Liver - 30%, Skin - 23%, Male Genitalia - 11%
250	LG:243305.3:2001MAR30	Embryonic Structures - 30%, Unclassified/Mixed - 23%, Digestive System - 13%, Endocrine System - 13%
251	LG:334645.20:2001MAR30	Germ Cells - 24%, Urinary Tract - 15%, Endocrine System - 14%, Unclassified/Mixed - 14%
252	LG:349468.13:2001MAR30	Nervous System - 34%, Pancreas - 31%, Musculoskeletal System - 21%
253	LG:385145.1:2001MAR30	Embryonic Structures - 54%, Digestive System - 11%, Endocrine System - 11%
254	LG:391807.1:2001MAR30	Germ Cells - 65%, Urinary Tract - 29%
255	LG:399287.10:2001MAR30	Germ Cells - 84%
256	LG:404157.1:2001MAR30	Unclassified/Mixed - 33%, Skin - 17%, Hemic and Immune System - 11%
257	LG:979390.2:2001MAR30	Liver - 23%, Pancreas - 23%, Connective Tissue - 18%
258	LG:981962.1:2001MAR30	Skin - 20%, Musculoskeletal System - 17%, Respiratory System - 14%
259	LG:982976.2:2001MAR30	Sense Organs - 54%, Cardiovascular System - 10%
260	LG:1448087.1:2001MAR30	Male Genitalia - 100%
261	LG:1449021.1:2001MAR30	Germ Cells - 67%, Unclassified/Mixed - 20%
262	LG:144920.1:2001MAR30	Liver - 26%, Unclassified/Mixed - 19%, Respiratory System - 15%
263	LG:474725.1:2001MAR30	Unclassified/Mixed - 35%, Endocrine System - 17%, Exocrine Glands - 15%
264	LG:1085952.14:2001MAR30	Embryonic Structures - 29%, Nervous System - 15%, Urinary Tract - 10%
265	U:011009.2:2001MAY17	Sense Organs - 78%, Nervous System - 13%, Urinary Tract - 10%
266	U:016933.2:2001MAY17	Connective Tissue - 23%, Exocrine Glands - 15%, Urinary Tract - 13%
267	U:1072014.6:2001MAY17	Embryonic Structures - 15%, Sense Organs - 13%, Unclassified/Mixed - 12%
268	U:1165280.4:2001MAY17	Nervous System - 18%, Respiratory System - 15%, Unclassified/Mixed - 14%, Male Genitalia - 14%
269	U:1167958.4:2001MAY17	Embryonic Structures - 77%, Digestive System - 10%
270	U:1168073.15:2001MAY17	Connective Tissue - 33%, Endocrine System - 21%, Musculoskeletal System - 17%
271	U:1170154.12:2001MAY17	Sense Organs - 27%, Connective Tissue - 12%, Female Genitalia - 10%
272	U:1173769.2:2001MAY17	Embryonic Structures - 27%, Liver - 26%, Musculoskeletal System - 19%
273	U:1174292.18:2001MAY17	widely distributed

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
274	U:1177989.1:2001MAY17	Exocrine Glands - 28%, Embryonic Structures - 16%, Urinary Tract - 13%
275	U:1179173.3:2001MAY17	Musculoskeletal System - 24%, Pancreas - 17%
276	U:1180137.1:2001MAY17	Connective Tissue - 54%, Respiratory System - 23%, Digestive System - 15%
277	U:1181458.2:2001MAY17	Sense Organs - 36%, Liver - 11%
278	U:1182817.8:2001MAY17	Sense Organs - 18%
279	U:1182838.4:2001MAY17	Sense Organs - 16%, Embryonic Structures - 12%
280	U:2053637.1:2001MAY17	Female Genitalia - 16%, Exocrine Glands - 15%, Embryonic Structures - 11%, Male Genitalia - 11%
281	U:2119713.6:2001MAY17	Liver - 24%, Unclassified/Mixed - 13%, Skin - 10%
282	U:2121833.1:2001MAY17	Respiratory System - 71%, Male Genitalia - 29%
283	U:2121863.1:2001MAY17	Sense Organs - 48%, Cardiovascular System - 13%, Skin - 12%
284	U:2121899.1:2001MAY17	Pancreas - 17%, Digestive System - 15%, Musculoskeletal System - 11%
285	U:2122035.5:2001MAY17	Respiratory System - 43%, Female Genitalia - 29%, Male Genitalia - 29%
286	U:2122507.3:2001MAY17	Female Genitalia - 33%, Cardiovascular System - 27%, Urinary Tract - 27%
287	U:2190152.1:2001MAY17	Exocrine Glands - 43%, Endocrine System - 24%, Cardiovascular System - 19%
288	U:2195736.1:2001MAY17	Hemic and Immune System - 43%, Exocrine Glands - 36%, Digestive System - 14%
289	U:2195745.2:2001MAY17	Cardiovascular System - 67%, Hemic and Immune System - 33%
290	U:2196327.1:2001MAY17	Unclassified/Mixed - 13%, Embryonic Structures - 13%, Male Genitalia - 13%, Pancreas - 13%
291	U:2197842.1:2001MAY17	Embryonic Structures - 36%, Musculoskeletal System - 25%, Respiratory System - 18%
292	U:2202913.1:2001MAY17	Female Genitalia - 21%, Respiratory System - 21%, Endocrine System - 21%, Male Genitalia - 21%
293	U:2206159.1:2001MAY17	Sense Organs - 30%, Exocrine Glands - 14%, Cardiovascular System - 13%
294	U:2208960.3:2001MAY17	Unclassified/Mixed - 15%, Embryonic Structures - 15%, Female Genitalia - 11%
295	U:2209149.1:2001MAY17	Nervous System - 100%
296	U:223050.2:2001MAY17	Embryonic Structures - 60%, Endocrine System - 18%
297	U:393468.1:2001MAY17	Unclassified/Mixed - 54%, Urinary Tract - 33%
298	U:480324.48:2001MAY17	Male Genitalia - 18%, Cardiovascular System - 16%, Nervous System - 16%
299	U:722634.7:2001MAY17	Pancreas - 63%, Urinary Tract - 25%, Nervous System - 13%
300	U:796992.1:2001MAY17	Unclassified/Mixed - 26%, Skin - 20%, Hemic and Immune System - 11%
301	U:093337.1:2001MAY17	Cardiovascular System - 38%, Endocrine System - 24%, Hemic and Immune System - 14%
302	U:1081130.3:2001MAY17	Hemic and Immune System - 50%, Nervous System - 50%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
303	U:1170908.4:2001MAY17	Embryonic Structures - 14%, Skin - 11%, Female Genitalia - 11%
304	U:1177451.1:2001MAY17	Sense Organs - 58%
305	U:1180303.18:2001MAY17	Sense Organs - 43%, Skin - 11%
306	U:1182999.3:2001MAY17	Germ Cells - 31%, Unclassified/Mixed - 21%, Urinary Tract - 11%, Cardiovascular System - 11%
307	U:1183525.1:2001MAY17	Urinary Tract - 33%, Digestive System - 33%, Female Genitalia - 17%, Nervous System - 17%
308	U:2121675.1:2001MAY17	Unclassified/Mixed - 38%, Respiratory System - 19%, Exocrine Glands - 19%
309	U:2121766.11:2001MAY17	Female Genitalia - 15%, Musculoskeletal System - 14%, Urinary Tract - 12%
310	U:2188633.1:2001MAY17	Embryonic Structures - 71%, Cardiovascular System - 29%
311	U:2188820.2:2001MAY17	Unclassified/Mixed - 29%, Cardiovascular System - 24%, Urinary Tract - 24%
312	U:2191871.1:2001MAY17	Exocrine Glands - 56%, Unclassified/Mixed - 20%, Urinary Tract - 16%
313	U:2196157.2:2001MAY17	Hemic and Immune System - 60%, Male Genitalia - 40%
314	U:230109.4:2001MAY17	Embryonic Structures - 18%, Hemic and Immune System - 16%, Skin - 15%
315	U:790409.4:2001MAY17	Stomatognathic System - 86%
316	LG:084399.1:2001JUN22	Exocrine Glands - 67%, Nervous System - 33%
317	LG:1079456.3:2001JUN22	Nervous System - 100%
318	LG:1080406.7:2001JUN22	Endocrine System - 13%, Exocrine Glands - 12%, Male Genitalia - 11%
319	LG:1505015.1:2001JUN22	Cardiovascular System - 44%, Female Genitalia - 22%, Male Genitalia - 22%
320	LG:208637.1:2001JUN22	Stomatognathic System - 17%, Liver - 11%
321	LG:233311.5:2001JUN22	Female Genitalia - 13%
322	LG:385145.1:2001JUN22	Embryonic Structures - 53%, Digestive System - 12%, Endocrine System - 12%
323	LG:404157.1:2001JUN22	Unclassified/Mixed - 30%, Skin - 17%, Respiratory System - 12%
324	LG:7684505.1:2001JUN22	Hemic and Immune System - 44%, Exocrine Glands - 25%, Urinary Tract - 19%
325	LG:7687730.1:2001JUN22	Female Genitalia - 11%, Digestive System - 11%, Urinary Tract - 10%, Respiratory System - 10%
326	LG:7687809.2:2001JUN22	Unclassified/Mixed - 22%, Embryonic Structures - 15%, Male Genitalia - 15%
327	LG:7690098.1:2001JUN22	Unclassified/Mixed - 33%, Embryonic Structures - 23%, Connective Tissue - 18%
328	LG:7690113.1:2001JUN22	Cardiovascular System - 22%, Embryonic Structures - 18%, Exocrine Glands - 16%
329	LG:7690362.3:2001JUN22	Female Genitalia - 50%, Nervous System - 50%
330	LG:7691200.3:2001JUN22	Pancreas - 19%, Connective Tissue - 15%, Hemic and Immune System - 13%
331	LG:7691277.3:2001JUN22	Female Genitalia - 100%
332	LG:7691280.4:2001JUN22	Female Genitalia - 67%, Nervous System - 33%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
333	LG:7691562.2:2001JUN22	Germ Cells - 26%, Exocrine Glands - 19%, Endocrine System - 16%
334	LG:7691685.3:2001JUN22	Male Genitalia - 100%
335	LG:7693155.4:2001JUN22	Sense Organs - 95%
336	LG:981962.1:2001JUN22	Skin - 19%, Musculoskeletal System - 17%, Respiratory System - 14%
337	LG:1449021.1:2001JUN22	Germ Cells - 69%, Unclassified/Mixed - 14%
338	LG:481631.22:2001JUN22	Unclassified/Mixed - 29%
339	LG:7690406.2:2001JUN22	Connective Tissue - 29%, Unclassified/Mixed - 25%, Exocrine Glands - 17%, Nervous System - 17%
340	LG:7690773.2:2001JUN22	Pancreas - 20%, Cardiovascular System - 15%, Unclassified/Mixed - 13%
341	LG:1347119.1:2001JUN22	Embryonic Structures - 16%, Germ Cells - 15%, Stomatognathic System - 10%
342	LG:7691570.2:2001JUN22	Digestive System - 100%
343	LG:023518.3:2001MAR30	Urinary Tract - 41%, Musculoskeletal System - 35%, Hemic and Immune System - 18%
344	LG:1100502.1:2001MAR30	Liver - 90%, Nervous System - 10%
345	LG:235076.6:2001MAR30	widely distributed
346	LG:270582.4:2001MAR30	Exocrine Glands - 33%, Nervous System - 31%, Endocrine System - 25%
347	LG:334752.12:2001MAR30	Urinary Tract - 64%, Hemic and Immune System - 17%
348	LG:425641.11:2001MAR30	Germ Cells - 18%, Skin - 15%
349	LG:980241.4:2001MAR30	Sense Organs - 18%, Embryonic Structures - 13%
351	LI:1072888.10:2001MAY17	Sense Organs - 35%, Germ Cells - 25%, Musculoskeletal System - 16%
352	LI:2048255.1:2001MAY17	Pancreas - 71%, Digestive System - 29%
353	LI:330658.1:2001MAY17	Endocrine System - 100%
354	LI:410188.4:2001MAY17	Cardiovascular System - 61%, Unclassified/Mixed - 12%
355	LI:902565.38:2001MAY17	Nervous System - 58%, Hemic and Immune System - 25%, Digestive System - 17%
356	LI:2032241.1:2001MAY17	Sense Organs - 60%, Unclassified/Mixed - 23%
357	LI:2192055.1:2001MAY17	Skin - 94%
358	LG:133851.16:2001JUN22	Female Genitalia - 27%, Musculoskeletal System - 23%, Male Genitalia - 15%
359	LG:1398822.1:2001JUN22	Urinary Tract - 61%, Male Genitalia - 21%
360	LG:1502274.17:2001JUN22	Germ Cells - 31%, Liver - 13%, Cardiovascular System - 10%
361	LG:166400.33:2001JUN22	Sense Organs - 52%
362	LG:235076.15:2001JUN22	widely distributed
363	LG:7689943.1:2001JUN22	Skin - 82%, Male Genitalia - 12%
364	LG:7693319.3:2001JUN22	Sense Organs - 60%, Cardiovascular System - 11%, Nervous System - 11%
365	LG:980241.4:2001JUN22	Sense Organs - 14%, Embryonic Structures - 13%
366	LG:226475.15:2001JUN22	Urinary Tract - 17%, Female Genitalia - 12%
367	LG:422564.11:2001JUN22	Female Genitalia - 11%, Urinary Tract - 11%, Digestive System - 11%
368	LG:026384.13:2001MAR30	Digestive System - 25%, Germ Cells - 22%, Exocrine Glands - 20%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
369	LG:1087811.6:2001MAR30	Hemic and Immune System - 19%, Unclassified/Mixed - 11%
370	LG:208877.7:2001MAR30	Skin - 43%, Female Genitalia - 13%
371	LG:232959.49:2001MAR30	Liver - 22%, Endocrine System - 22%, Urinary Tract - 17%
372	LG:331078.21:2001MAR30	Liver - 38%, Urinary Tract - 16%, Male Genitalia - 10%
373	LG:334345.5:2001MAR30	Male Genitalia - 67%, Unclassified/Mixed - 23%, Urinary Tract - 10%
374	LG:345279.19:2001MAR30	Sense Organs - 19%, Germ Cells - 15%
375	LG:400109.5:2001MAR30	Embryonic Structures - 12%
376	LG:001294.11:2001MAR30	Sense Organs - 13%
377	LG:230895.5:2001MAR30	Respiratory System - 29%, Nervous System - 29%, Female Genitalia - 24%
379	U:1072276.1:2001MAY17	Germ Cells - 42%, Exocrine Glands - 17%, Urinary Tract - 15%
380	U:1072654.40:2001MAY17	Unclassified/Mixed - 71%, Digestive System - 29%
381	U:123815.12:2001MAY17	Urinary Tract - 100%
382	U:198705.6:2001MAY17	Digestive System - 67%, Nervous System - 33%
383	U:2032264.3:2001MAY17	Liver - 82%, Hemic and Immune System - 18%
384	U:2070168.1:2001MAY17	Unclassified/Mixed - 45%, Cardiovascular System - 36%, Nervous System - 18%
385	U:2077540.1:2001MAY17	Respiratory System - 75%, Nervous System - 25%
387	U:2120273.5:2001MAY17	Male Genitalia - 53%, Digestive System - 25%, Exocrine Glands - 16%
388	U:237520.26:2001MAY17	Male Genitalia - 16%, Germ Cells - 11%
389	U:243892.46:2001MAY17	Pancreas - 96%
390	U:400590.4:2001MAY17	Digestive System - 92%
392	U:2052211.9:2001MAY17	Pancreas - 63%, Hemic and Immune System - 13%, Digestive System - 13%, Male Genitalia - 13%
393	U:407291.5:2001MAY17	Liver - 95%
394	U:2167560.1:2001MAY17	Unclassified/Mixed - 100%
395	U:401586.1:2001MAY17	Respiratory System - 44%, Embryonic Structures - 28%, Exocrine Glands - 14%
396	LG:1093982.21:2001JUN22	Cardiovascular System - 14%, Exocrine Glands - 13%, Liver - 11%
397	LG:1383133.102:2001JUN22	Male Genitalia - 98%
398	LG:199121.19:2001JUN22	Cardiovascular System - 13%, Connective Tissue - 10%
399	LG:482411.11:2001JUN22	Stomatognathic System - 23%, Unclassified/Mixed - 15%
400	LG:991986.23:2001JUN22	Urinary Tract - 21%, Connective Tissue - 21%, Unclassified/Mixed - 18%
401	LG:1500347.6:2001JUN22	Embryonic Structures - 21%, Liver - 15%, Connective Tissue - 11%
402	LG:7670971.1:2001JUN22	Urinary Tract - 100%
403	LG:010761.6:2001MAR30	Connective Tissue - 19%, Pancreas - 17%, Endocrine System - 12%
404	LG:104970.6:2001MAR30	Pancreas - 14%, Germ Cells - 11%
405	LG:1078420.1:2001MAR30	Endocrine System - 33%, Female Genitalia - 18%, Cardiovascular System - 10%, Exocrine Glands - 10%
406	LG:1094182.9:2001MAR30	Germ Cells - 10%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
407	LG:1399075.18:2001MAR30	Unclassified/Mixed - 13%, Germ Cells - 12%
408	LG:1501344.7:2001MAR30	Nervous System - 100%
409	LI:1144484.3:2001MAY17	Endocrine System - 26%, Cardiovascular System - 24%, Male Genitalia - 15%
410	LI:337388.11:2001MAY17	Exocrine Glands - 63%, Hemic and Immune System - 25%, Nervous System - 13%
411	LI:347709.101:2001MAY17	widely distributed
412	LI:480238.8:2001MAY17	Germ Cells - 23%, Embryonic Structures - 11%, Liver - 10%
413	LI:2121656.1:2001MAY17	Embryonic Structures - 21%, Unclassified/Mixed - 14%, Digestive System - 12%
414	LG:1328038.5:2001JUN22	Digestive System - 100%
415	LG:437443.21:2001JUN22	Sense Organs - 21%, Connective Tissue - 18%
416	LG:474165.24:2001JUN22	Endocrine System - 44%, Hemic and Immune System - 33%, Nervous System - 22%
417	LG:7689014.1:2001JUN22	Digestive System - 86%, Hemic and Immune System - 14%
418	LG:984007.4:2001JUN22	Pancreas - 16%, Nervous System - 13%, Urinary Tract - 12%
419	LG:008606.21:2001JUN22	Skin - 17%, Nervous System - 10%
420	LG:240680.1:2001JUN22	Female Genitalia - 33%, Digestive System - 33%, Nervous System - 33%
421	LG:160481.1:2001MAR30	Hemic and Immune System - 50%, Female Genitalia - 33%, Nervous System - 17%
422	LG:292275.1:2001MAR30	Nervous System - 43%, Cardiovascular System - 29%, Respiratory System - 14%, Male Genitalia - 14%
423	LG:407582.21:2001MAR30	Stomatognathic System - 40%, Unclassified/Mixed - 19%, Respiratory System - 12%
424	LI:2051428.9:2001MAY17	Nervous System - 23%, Sense Organs - 19%, Germ Cells - 13%
425	LI:355644.50:2001MAY17	Digestive System - 24%, Nervous System - 21%, Female Genitalia - 15%, Exocrine Glands - 15%
426	LI:375954.18:2001MAY17	Nervous System - 30%, Hemic and Immune System - 11%, Endocrine System - 11%
427	LI:480115.132:2001MAY17	Respiratory System - 89%
428	LG:1383554.10:2001JUN22	Sense Organs - 64%, Liver - 15%
429	LG:1135060.33:2001MAR30	Respiratory System - 50%, Hemic and Immune System - 30%, Digestive System - 20%
430	LG:1351716.96:2001MAR30	Digestive System - 50%, Respiratory System - 50%
431	LG:1400811.225:2001MAR30	Urinary Tract - 60%, Digestive System - 40%
432	LG:1401132.92:2001MAR30	Musculoskeletal System - 86%, Digestive System - 14%
433	LG:1401165.155:2001MAR30	Digestive System - 50%, Respiratory System - 50%
434	LG:1452363.23:2001MAR30	Pancreas - 47%, Male Genitalia - 21%, Nervous System - 16%
435	LG:1503254.1:2001MAR30	Unclassified/Mixed - 70%, Urinary Tract - 30%
436	LG:411364.13:2001MAR30	Sense Organs - 18%, Embryonic Structures - 16%, Germ Cells - 10%
437	LG:238631.16:2001MAR30	Endocrine System - 18%, Male Genitalia - 13%, Liver - 11%



TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
438	LG:235157.34:2001MAR30	Liver - 16%, Embryonic Structures - 12%, Pancreas - 12%
439	LI:1027765.6:2001MAY17	Nervous System - 100%
441	LI:1073108.49:2001MAY17	Hemic and Immune System - 18%, Pancreas - 16%, Urinary Tract - 13%, Digestive System - 13%
442	LI:1189828.21:2001MAY17	Nervous System - 15%, Unclassified/Mixed - 14%, Liver - 12%, Hemic and Immune System - 12%
443	LI:2191073.14:2001MAY17	Respiratory System - 100%
444	LI:2191348.6:2001MAY17	Hemic and Immune System - 100%
445	LI:2191424.12:2001MAY17	Urinary Tract - 100%
446	LI:2206792.26:2001MAY17	Pancreas - 42%, Endocrine System - 21%, Hemic and Immune System - 21%
447	LI:255510.1264:2001MAY17	Digestive System - 100%
448	LI:392902.48:2001MAY17	Stomatognathic System - 38%
449	LI:411364.14:2001MAY17	Embryonic Structures - 18%
450	LI:417464.1:2001MAY17	Urinary Tract - 64%, Digestive System - 11%
451	LI:439077.1:2001MAY17	Digestive System - 100%
453	LG:1225513.19:2001JUN22	Exocrine Glands - 19%, Urinary Tract - 16%, Hemic and Immune System - 13%, Digestive System - 13%
454	LG:1447752.2:2001JUN22	Respiratory System - 100%
455	LG:239410.21:2001JUN22	Digestive System - 34%, Male Genitalia - 30%
456	LG:7683955.1:2001JUN22	Musculoskeletal System - 46%, Exocrine Glands - 31%, Respiratory System - 15%
457	LG:7691296.7:2001JUN22	Digestive System - 100%
458	LG:7696542.11:2001JUN22	Musculoskeletal System - 21%, Exocrine Glands - 21%, Digestive System - 17%
459	LG:7696552.2:2001JUN22	Musculoskeletal System - 20%, Digestive System - 15%, Exocrine Glands - 13%
460	LG:7696586.3:2001JUN22	Respiratory System - 100%
461	LI:1072102.34:2001MAY17	Urinary Tract - 46%, Endocrine System - 45%
462	LI:2119925.1:2001MAY17	Endocrine System - 41%, Stomatognathic System - 20%, Liver - 15%
463	LI:2173928.1:2001MAY17	Unclassified/Mixed - 100%
464	LI:2193503.1:2001MAY17	Cardiovascular System - 50%, Hemic and Immune System - 25%, Nervous System - 25%
465	LI:368098.26:2001MAY17	Pancreas - 42%, Liver - 38%
466	LI:455378.1:2001MAY17	Urinary Tract - 80%, Nervous System - 20%
467	LI:480845.50:2001MAY17	Liver - 17%, Cardiovascular System - 11%, Endocrine System - 11%
468	LI:2205863.1:2001MAY17	Germ Cells - 24%, Connective Tissue - 23%, Endocrine System - 10%
469	LG:201188.2:2001JUN22	Sense Organs - 42%, Respiratory System - 12%, Germ Cells - 11%
470	LG:1272496.28:2001MAR30	Liver - 26%, Female Genitalia - 20%, Musculoskeletal System - 17%
471	LG:1500367.1:2001MAR30	Exocrine Glands - 35%, Stomatognathic System - 20%, Nervous System - 13%
472	LG:952182.4:2001MAR30	Male Genitalia - 100%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
473	LI:197195.10:2001MAY17	Germ Cells - 17%, Male Genitalia - 13%, Unclassified/Mixed - 12%
474	LI:2031121.1:2001MAY17	Germ Cells - 99%
475	LI:2198279.3:2001MAY17	Respiratory System - 38%, Hemic and Immune System - 38%, Digestive System - 25%
476	LI:2201248.1:2001MAY17	Digestive System - 43%, Endocrine System - 23%, Respiratory System - 13%, Exocrine Glands - 13%
477	LI:234507.10:2001MAY17	Musculoskeletal System - 14%
478	LI:237999.48:2001MAY17	Musculoskeletal System - 54%, Connective Tissue - 23%
479	LI:244935.47:2001MAY17	Connective Tissue - 21%, Musculoskeletal System - 14%
480	LI:257664.143:2001MAY17	Stomatognathic System - 23%, Pancreas - 14%, Endocrine System - 12%
481	LI:261900.1:2001MAY17	Musculoskeletal System - 32%, Unclassified/Mixed - 23%, Cardiovascular System - 18%
482	LI:346724.22:2001MAY17	Unclassified/Mixed - 11%, Embryonic Structures - 11%
483	LI:815333.1:2001MAY17	Liver - 20%, Nervous System - 16%, Connective Tissue - 15%
484	LI:889399.7:2001MAY17	Skin - 100%
485	LI:1088907.2:2001MAY17	Unclassified/Mixed - 71%, Male Genitalia - 29%
486	LI:218680.7:2001MAY17	Embryonic Structures - 31%, Hemic and Immune System - 18%, Connective Tissue - 11%
487	LG:081189.8:2001JUN22	Female Genitalia - 26%, Connective Tissue - 19%, Liver - 13%, Embryonic Structures - 13%
488	LG:315445.21:2001JUN22	Connective Tissue - 14%, Unclassified/Mixed - 14%
489	LG:900035.56:2001JUN22	Musculoskeletal System - 18%, Sense Organs - 15%, Connective Tissue - 13%
490	LG:008513.80:2001MAR30	Skin - 74%
491	LG:1384720.130:2001MAR30	Pancreas - 29%, Germ Cells - 12%, Female Genitalia - 11%
492	LG:1453611.1:2001MAR30	Cardiovascular System - 47%, Musculoskeletal System - 40%, Digestive System - 13%
493	LG:1500258.1:2001MAR30	Sense Organs - 36%, Cardiovascular System - 13%
494	LG:1501754.5:2001MAR30	Liver - 78%
495	LG:1502796.1:2001MAR30	Liver - 50%, Female Genitalia - 19%, Unclassified/Mixed - 19%
496	LG:348973.11:2001MAR30	Skin - 23%, Liver - 21%, Nervous System - 14%
497	LG:362757.1:2001MAR30	Connective Tissue - 88%, Nervous System - 13%
498	LG:401322.6:2001MAR30	Sense Organs - 46%, Liver - 21%, Skin - 16%
499	LG:897867.1:2001MAR30	Skin - 53%, Unclassified/Mixed - 38%
500	LI:1947939.1:2001MAY17	Unclassified/Mixed - 83%, Hemic and Immune System - 17%
501	LI:245487.16:2001MAY17	widely distributed
502	LI:257715.58:2001MAY17	Male Genitalia - 17%, Digestive System - 14%, Female Genitalia - 13%
503	LI:333453.9:2001MAY17	Embryonic Structures - 20%, Germ Cells - 12%, Exocrine Glands - 11%
504	LI:412658.111:2001MAY17	Pancreas - 16%, Connective Tissue - 11%, Male Genitalia - 11%
505	LI:720054.1:2001MAY17	Digestive System - 100%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
506	LI:765245.9:2001MAY17	Sense Organs - 13%, Female Genitalia - 12%, Connective Tissue - 12%
507	LI:814445.58:2001MAY17	Skin - 59%, Stomatognathic System - 13%
508	LI:897867.1:2001MAY17	Skin - 70%, Unclassified/Mixed - 22%
509	LI:311318.6:2001MAY17	Liver - 56%, Musculoskeletal System - 17%
510	LI:401605.12:2001MAY17	Urinary Tract - 16%, Exocrine Glands - 14%, Cardiovascular System - 13%
511	LG:1088618.90:2001JUN22	Pancreas - 11%
512	LG:1446318.6:2001JUN22	Unclassified/Mixed - 17%, Stomatognathic System - 13%, Musculoskeletal System - 12%
513	LG:229284.37:2001JUN22	Exocrine Glands - 11%, Hemic and Immune System - 11%, Liver - 10%, Male Genitalia - 10%
514	LG:7683471.8:2001JUN22	Respiratory System - 100%
515	LG:7697194.7:2001JUN22	Cardiovascular System - 40%, Musculoskeletal System - 24%, Stomatognathic System - 16%
516	LG:952407.1:2001JUN22	Digestive System - 100%
517	LG:248005.17:2001JUN22	Germ Cells - 12%
518	LG:025007.3:2001MAR30	Urinary Tract - 24%, Embryonic Structures - 15%, Endocrine System - 15%
519	LG:1510893.1:2001MAR30	Liver - 100%
520	LG:297070.1:2001MAR30	Embryonic Structures - 38%, Urinary Tract - 29%, Cardiovascular System - 17%
521	LG:363612.2:2001MAR30	Nervous System - 62%, Unclassified/Mixed - 24%
522	LG:468481.1:2001MAR30	Germ Cells - 33%, Sense Organs - 20%, Nervous System - 18%
523	LG:966475.1:2001MAR30	Unclassified/Mixed - 78%, Hemic and Immune System - 11%, Nervous System - 11%
524	LG:1135422.1:2001MAR30	Germ Cells - 61%, Liver - 39%
525	LI:1010121.1:2001MAY17	Digestive System - 100%
526	LI:1072416.19:2001MAY17	Stomatognathic System - 12%, Cardiovascular System - 11%, Pancreas - 10%
527	LI:1188564.7:2001MAY17	Sense Organs - 69%, Connective Tissue - 16%
528	LI:2118902.5:2001MAY17	Embryonic Structures - 19%, Endocrine System - 17%, Connective Tissue - 13%, Musculoskeletal System - 13%
529	LI:2206501.1:2001MAY17	Male Genitalia - 70%, Female Genitalia - 20%, Nervous System - 10%
530	LI:337830.1:2001MAY17	Endocrine System - 38%, Nervous System - 16%, Connective Tissue - 11%, Male Genitalia - 11%
531	LI:347853.17:2001MAY17	widely distributed
532	LI:253580.4:2001MAY17	widely distributed
533	LG:330850.3:2001JUN22	Embryonic Structures - 16%, Germ Cells - 10%, Skin - 10%
534	LG:464722.13:2001JUN22	Germ Cells - 10%
535	LG:7686119.1:2001JUN22	Hemic and Immune System - 100%
536	LG:903691.14:2001JUN22	Sense Organs - 12%, Connective Tissue - 10%
537	LG:1096385.3:2001MAR30	Female Genitalia - 40%, Digestive System - 40%, Nervous System - 20%
538	LG:1101445.1:2001MAR30	Liver - 43%, Connective Tissue - 33%, Cardiovascular System - 19%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
539	LG:1138457.20:2001MAR30	Liver - 45%, Urinary Tract - 35%, Digestive System - 10%, Respiratory System - 10%
540	LG:1440118.1:2001MAR30	Liver - 90%, Hemic and Immune System - 10%
541	LG:1443997.1:2001MAR30	Liver - 50%, Pancreas - 50%
542	LG:1497707.1:2001MAR30	Exocrine Glands - 24%, Unclassified/Mixed - 21%, Hemic and Immune System - 18%
543	LG:1501729.1:2001MAR30	Liver - 60%, Cardiovascular System - 27%, Male Genitalia - 13%
544	LG:1502186.1:2001MAR30	Liver - 100%
545	LG:223142.1:2001MAR30	Germ Cells - 66%
546	LG:255713.1:2001MAR30	Male Genitalia - 32%, Musculoskeletal System - 27%, Respiratory System - 23%
547	LG:420283.38:2001MAR30	widely distributed
548	LG:449413.3:2001MAR30	Nervous System - 100%
549	LG:997599.1:2001MAR30	Male Genitalia - 88%, Digestive System - 12%
550	LG:232776.8:2001MAR30	Germ Cells - 22%, Respiratory System - 10%, Connective Tissue - 10%
551	LI:1045207.1:2001MAY17	Pancreas - 43%, Unclassified/Mixed - 22%, Digestive System - 17%, Urinary Tract - 17%
552	LI:1086565.6:2001MAY17	Hemic and Immune System - 29%, Exocrine Glands - 24%, Urinary Tract - 19%, Digestive System - 19%
553	LI:1142855.1:2001MAY17	Exocrine Glands - 36%, Digestive System - 29%, Nervous System - 21%
554	LI:2188689.1:2001MAY17	Respiratory System - 33%, Unclassified/Mixed - 21%, Urinary Tract - 17%, Cardiovascular System - 17%
555	LI:2193411.1:2001MAY17	Nervous System - 100%
556	LI:2198244.1:2001MAY17	Exocrine Glands - 100%
557	LI:2198795.4:2001MAY17	Musculoskeletal System - 30%, Unclassified/Mixed - 22%, Female Genitalia - 22%
558	LI:2199688.3:2001MAY17	Unclassified/Mixed - 83%, Female Genitalia - 17%
559	LI:790138.64:2001MAY17	Digestive System - 19%, Exocrine Glands - 14%, Connective Tissue - 14%
560	LI:757871.10:2001MAY17	Germ Cells - 18%
561	LG:1096385.2:2001JUN22	Digestive System - 40%, Respiratory System - 40%, Nervous System - 20%
562	LG:1100878.1:2001JUN22	Embryonic Structures - 75%, Unclassified/Mixed - 25%
563	LG:1447560.1:2001JUN22	Cardiovascular System - 35%, Unclassified/Mixed - 30%, Urinary Tract - 15%
564	LG:1453540.34:2001JUN22	Hemic and Immune System - 50%, Nervous System - 50%
565	LG:249518.11:2001JUN22	Digestive System - 100%
566	LG:041656.5:2001JUN22	Germ Cells - 22%, Respiratory System - 13%
567	LI:2208837.4:2001MAY17	Connective Tissue - 25%, Nervous System - 16%, Cardiovascular System - 14%
568	LG:7694341.2:2001JUN22	Sense Organs - 17%, Embryonic Structures - 16%
569	LG:016760.1:2001MAR30	Germ Cells - 41%, Connective Tissue - 13%, Unclassified/Mixed - 13%
570	LG:1022858.1:2001MAR30	Nervous System - 100%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
571	LG:1135406.15:2001MAR30	Exocrine Glands - 12%, Cardiovascular System - 11%, Male Genitalia - 11%
572	LG:1327517.37:2001MAR30	Connective Tissue - 15%, Endocrine System - 14%, Female Genitalia - 12%
573	LG:1330214.34:2001MAR30	widely distributed
574	LG:1384735.5:2001MAR30	Sense Organs - 75%, Unclassified/Mixed - 13%
575	LG:1449837.4:2001MAR30	widely distributed
576	LG:1452330.5:2001MAR30	Nervous System - 12%, Connective Tissue - 12%
577	LG:1510248.1:2001MAR30	Liver - 100%
578	LG:215109.8:2001MAR30	Embryonic Structures - 10%
579	LG:279978.17:2001MAR30	Urinary Tract - 57%, Liver - 37%
580	LG:414732.1:2001MAR30	Endocrine System - 82%, Nervous System - 18%
581	LG:1132208.1:2001MAR30	Exocrine Glands - 36%, Unclassified/Mixed - 32%, Hemic and Immune System - 14%
582	LG:1454339.4:2001MAR30	Nervous System - 31%, Embryonic Structures - 18%, Musculoskeletal System - 16%
583	U:018342.1:2001MAY17	Endocrine System - 58%, Unclassified/Mixed - 42%
584	U:1177772.36:2001MAY17	Female Genitalia - 30%, Nervous System - 20%, Male Genitalia - 14%
585	U:2207152.6:2001MAY17	Male Genitalia - 100%
586	U:244159.24:2001MAY17	Musculoskeletal System - 15%, Connective Tissue - 12%, Exocrine Glands - 11%
587	U:405244.8:2001MAY17	Pancreas - 13%, Digestive System - 11%
588	U:270318.18:2001MAY17	Liver - 20%
589	U:154692.45:2001MAY17	Connective Tissue - 21%, Digestive System - 15%, Exocrine Glands - 14%
590	U:411238.31:2001MAY17	Respiratory System - 40%, Pancreas - 21%, Cardiovascular System - 17%
591	U:814424.6:2001MAY17	Musculoskeletal System - 11%
592	LG:1327517.25:2001JUN22	Cardiovascular System - 22%, Liver - 18%, Musculoskeletal System - 12%
593	LG:343949.3:2001JUN22	Pancreas - 61%
594	LG:413000.28:2001JUN22	Connective Tissue - 43%, Musculoskeletal System - 13%, Respiratory System - 11%
595	LG:7692006.3:2001JUN22	Nervous System - 100%
596	LG:336953.5:2001JUN22	Connective Tissue - 17%, Sense Organs - 11%
597	LG:1399785.1:2001JUN22	Embryonic Structures - 11%
598	LG:425024.5:2001JUN22	Skin - 41%, Exocrine Glands - 24%, Nervous System - 15%
599	LG:482494.10:2001JUN22	Stomatognathic System - 17%, Germ Cells - 15%
600	LG:978629.6:2001JUN22	Liver - 16%, Endocrine System - 13%
601	LG:005776.12:2001MAR30	Germ Cells - 17%
602	LG:029219.1:2001MAR30	Digestive System - 80%, Hemic and Immune System - 20%
603	LG:091743.1:2001MAR30	Respiratory System - 100%
604	LG:1397656.6:2001MAR30	Digestive System - 10%, Pancreas - 10%
605	LG:1500866.5:2001MAR30	Skin - 20%, Pancreas - 10%
606	LG:1511332.1:2001MAR30	Stomatognathic System - 96%
607	LG:233288.31:2001MAR30	widely distributed

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
608	LG:269269.24:2001MAR30	widely distributed
609	LG:331581.5:2001MAR30	Skin - 12%, Unclassified/Mixed - 11%
610	LG:481433.4:2001MAR30	Stomatognathic System - 14%, Germ Cells - 10%
611	LG:246935.4:2001MAR30	Germ Cells - 35%
612	LG:475420.1:2001MAR30	Sense Organs - 85%, Endocrine System - 13%
613	LI:1073084.60:2001MAY17	Cardiovascular System - 26%, Connective Tissue - 18%
614	LI:2040379.1:2001MAY17	Female Genitalia - 41%, Connective Tissue - 41%, Hemic and Immune System - 18%
615	LI:2119526.4:2001MAY17	Liver - 27%, Sense Organs - 22%, Connective Tissue - 15%
616	LI:213228.1:2001MAY17	Sense Organs - 42%, Embryonic Structures - 41%
617	LI:2179709.1:2001MAY17	Nervous System - 100%
618	LI:2208147.1:2001MAY17	Liver - 75%, Female Genitalia - 17%
619	LI:235487.10:2001MAY17	Urinary Tract - 14%, Endocrine System - 11%
620	LI:476342.4:2001MAY17	Connective Tissue - 78%, Nervous System - 22%
621	LI:759025.1:2001MAY17	Male Genitalia - 88%, Respiratory System - 12%
622	LI:765589.1:2001MAY17	Liver - 25%, Digestive System - 13%, Respiratory System - 11%
623	LI:902535.3:2001MAY17	Endocrine System - 100%
624	LI:257592.5:2001MAY17	Stomatognathic System - 28%, Urinary Tract - 18%
625	LI:471684.65:2001MAY17	Embryonic Structures - 17%, Cardiovascular System - 12%
626	LG:1382838.272:2001JUN22	Musculoskeletal System - 13%, Exocrine Glands - 12%, Cardiovascular System - 11%
627	LG:142736.1:2001JUN22	Connective Tissue - 78%, Nervous System - 22%
628	LG:221707.43:2001JUN22	Respiratory System - 100%
629	LG:7689247.1:2001JUN22	Female Genitalia - 67%, Nervous System - 33%
630	LG:7693136.5:2001JUN22	Embryonic Structures - 26%, Connective Tissue - 20%, Unclassified/Mixed - 17%
631	LG:001505.13:2001MAR30	Germ Cells - 64%, Skin - 14%
632	LG:1051541.1:2001MAR30	Female Genitalia - 54%, Cardiovascular System - 31%
633	LG:1090140.1:2001MAR30	widely distributed
634	LG:1094595.2:2001MAR30	Stomatognathic System - 19%
635	LG:1500340.1:2001MAR30	Liver - 100%
636	LG:1502353.1:2001MAR30	Sense Organs - 39%, Germ Cells - 22%
637	LG:1511710.6:2001MAR30	Unclassified/Mixed - 29%, Hemic and Immune System - 17%, Endocrine System - 17%, Exocrine Glands - 17%
638	LG:231372.4:2001MAR30	Stomatognathic System - 15%, Skin - 11%, Respiratory System - 10%
639	LG:234855.6:2001MAR30	Germ Cells - 10%
640	LG:242157.8:2001MAR30	Sense Organs - 13%, Unclassified/Mixed - 11%
641	LG:477127.6:2001MAR30	Hemic and Immune System - 14%, Embryonic Structures - 11%
642	LG:412684.17:2001MAR30	Sense Organs - 14%, Nervous System - 14%, Urinary Tract - 10%, Embryonic Structures - 10%
643	LG:474937.20:2001MAR30	Sense Organs - 12%
644	LG:1452698.8:2001MAR30	Pancreas - 16%, Unclassified/Mixed - 13%, Cardiovascular System - 11%
645	LG:1503673.1:2001MAR30	Liver - 53%, Musculoskeletal System - 35%

TABLE 6

SEQ ID NO:	Template ID	Tissue Distribution
646	LG:213092.14:2001MAR30	Nervous System - 32%, Liver - 21%, Connective Tissue - 16%
647	LI:015309.1:2001MAY17	Exocrine Glands - 71%, Nervous System - 29%
648	LI:030502.2:2001MAY17	Germ Cells - 77%, Liver - 16%
649	LI:100501.1:2001MAY17	Nervous System - 100%
650	LI:1011706.2:2001MAY17	Unclassified/Mixed - 18%, Female Genitalia - 15%, Endocrine System - 12%
651	LI:1171752.20:2001MAY17	Urinary Tract - 22%, Male Genitalia - 18%, Nervous System - 16%
652	LI:2049713.6:2001MAY17	Hemic and Immune System - 73%, Digestive System - 18%
653	LI:397393.2:2001MAY17	Exocrine Glands - 36%, Urinary Tract - 29%, Respiratory System - 21%
654	LI:401697.25:2001MAY17	Respiratory System - 16%, Endocrine System - 16%, Digestive System - 12%
655	LI:903668.7:2001MAY17	Hemic and Immune System - 40%, Skin - 32%, Liver - 18%
656	LI:903956.35:2001MAY17	Stomatognathic System - 50%, Pancreas - 14%
657	LI:055784.15:2001MAY17	Sense Organs - 21%
658	LI:2195792.2:2001MAY17	Liver - 36%, Endocrine System - 20%, Cardiovascular System - 16%
659	LI:2207923.8:2001MAY17	Embryonic Structures - 19%, Musculoskeletal System - 13%
660	LI:232953.31:2001MAY17	Embryonic Structures - 15%, Nervous System - 12%, Hemic and Immune System - 12%
661	LI:764674.1:2001MAY17	Germ Cells - 22%, Liver - 19%, Respiratory System - 19%
662	LI:893532.747:2001MAY17	Respiratory System - 27%, Connective Tissue - 23%, Endocrine System - 17%, Exocrine Glands - 17%
663	LG:1121446.8:2001JUN22	Embryonic Structures - 15%, Skin - 10%
664	LG:1440335.2:2001JUN22	Connective Tissue - 65%, Female Genitalia - 20%, Male Genitalia - 10%
665	LG:370271.9:2001JUN22	Endocrine System - 57%, Respiratory System - 29%, Hemic and Immune System - 14%
666	LG:414048.16:2001JUN22	Female Genitalia - 100%
667	LG:7683385.1:2001JUN22	Liver - 100%
668	LG:7697332.3:2001JUN22	Skin - 33%, Sense Organs - 32%
669	LG:1047075.1:2001JUN22	Female Genitalia - 60%, Urinary Tract - 40%
670	LG:331171.2:2001JUN22	Germ Cells - 14%, Endocrine System - 11%, Exocrine Glands - 10%

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
671	3	182	159	704	g9802302	1.00E-47	glyceraldehyde-3-phosphate dehydrogenase
671	3	182	159	704	g35053	1.00E-47	uracil DNA glycosylase
671	3	182	159	704	g31645	1.00E-47	glyceraldehyde-3-phosphate dehydrogenase
672	3	205	189	803	g17902308	1.00E-104	unnamed protein product
672	3	205	189	803	g13436260	1.00E-104	3 beta-hydroxy-delta 5-C27-steroid oxidoreductase
672	3	205	189	803	g11545403	1.00E-104	3 beta-hydroxy-delta 5-C27-steroid oxidoreductase
673	3	128	309	692	g12851208	1.00E-67	data source:MGD, source key:MG1:103149, evidence:ISS-putative-ubiquitin carboxy-terminal hydrolase L1
673	3	128	309	692	g5834486	1.00E-67	PGP9.5
673	3	128	309	692	g5759213	4.00E-67	ubiquitin carboxy-terminal hydrolase PGP9.5
674	1	499	502	1998	g4115404	0	chondroitin 6-sulfotransferase
674	1	499	502	1998	g3510308	0	chondroitin 6-sulfotransferase
674	1	499	502	1998	g12585682	0	chondroitin 6-sulfotransferase
677	3	179	138	674	g387502	2.00E-86	orotidine-5'-monophosphate decarboxylase
677	3	179	138	674	g13278066	2.00E-86	Similar to uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase)
677	3	179	138	674	g5262523	6.00E-81	hypothetical protein
678	1	193	232	810	g2707824	4.00E-91	aldehyde reductase
678	1	193	232	810	g178481	4.00E-91	aldehyde reductase (EC 1.1.1.2)
678	1	193	232	810	g13529278	4.00E-91	aldo-keto reductase family 1, member A1 (aldehyde reductase)
679	2	134	680	1081	g18490306	3.00E-07	Similar to RIKEN cDNA 4930519N16 gene
679	2	134	680	1081	g16552119	1.00E-05	unnamed protein product
679	2	134	680	1081	g348245	1.00E-05	protein serine/threonine kinase
680	3	234	603	1304	g15928817	1.00E-126	Similar to pyroline 5-carboxylate reductase isoform
680	3	234	603	1304	g18089016	1.00E-126	Unknown (protein for MGC:21444)
680	3	234	603	1304	g13905180	1.00E-120	Similar to pyroline 5-carboxylate reductase isoform
682	1	77	301	531	g9929935	1.00E-14	hypothetical protein
682	1	77	301	531	g7959267	1.00E-14	KIAA1503 protein
682	1	77	301	531	g16549456	1.00E-10	unnamed protein product
683	1	179	1	537	g474388	4.00E-72	Inhibitor 2
683	1	179	1	537	g4704218	4.00E-72	Inhibitor 2 of protein phosphatase 1



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
683	1	179	1	537	g1932771	4.00E-72	protein phosphatase inhibitor 2
684	3	96	720	1007	g524869	3.00E-45	δ-pyruvoyl-tetrahydropterin synthase
684	3	96	720	1007	g451208	3.00E-45	δ-pyruvoyl-tetrahydropterin synthase
684	3	96	720	1007	g3142325	3.00E-45	δ-pyruvoyl-tetrahydropterin synthase
685	2	633	98	1996	g9651727	0	CIP synthetase isoform
685	2	633	98	1996	g10436355	0	unnamed protein product
685	2	633	98	1996	g10435517	0	unnamed protein product
686	2	655	2	1966	g17644260	0	b820621.1 (ATPase, Class VI, type 11C)
686	2	655	2	1966	g5689373	0	KIAA1021 protein
686	2	655	2	1966	g6457274	0	putative E1-E2 ATPase
689	3	778	1155	3488	g9837517	0	cysteinyl-tRNA synthetase
689	3	778	1155	3488	g12804055	0	cysteinyl-tRNA synthetase
689	3	778	1155	3488	g9837515	0	cytoplasmic cysteinyl-tRNA synthetase
690	2	227	86	766	g204495	1.00E-123	glutathione S-transferase Ya subunit
690	2	227	86	766	g204508	1.00E-119	glutathione S-transferase
690	2	227	86	766	g204493	1.00E-119	glutathione S-transferase
692	2	71	257	469	g1468969	2.00E-21	brain acyl-CoA synthetase II
692	2	71	257	469	g12848615	2.00E-21	data source:MGI, source key:MGI:1921455, evidence:ISS-fatty acid Coenzyme A ligase, long chain 3-putative
692	2	71	257	469	g4165018	2.00E-20	Acyl-CoA synthetase 3
693	1	406	1	1218	g18044066	0	RIKEN cDNA 5033406L14 gene
693	1	406	1	1218	g12856270	0	data source:SPTR, source key:g9JUL5, evidence:ISS-homolog to REC PROTEIN-putative
693	1	406	1	1218	g6682873	1.00E-136	reduced expression in cancer
694	2	172	2	517	g312179	7.00E-90	glyceraldehyde 3-phosphate dehydrogenase (phosphorylating)
694	2	172	2	517	g1184772	7.00E-90	cytosolic glyceraldehyde-3-phosphate dehydrogenase GAPC2
694	2	172	2	517	g1185554	7.00E-90	glyceraldehyde-3-phosphate dehydrogenase
695	3	187	3	563	g12406973	1.00E-105	alanine-glyoxylate aminotransferase 2
695	3	187	3	563	g17901292	1.00E-102	unnamed protein product
695	3	187	3	563	g1944136	7.00E-77	beta-alanine-pyruvate aminotransferase
696	1	434	718	2019	g4186038	0	glucose 1-dehydrogenase

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
696	1	434	718	2019	g7242608	0	dU510D1.1 (hexose-6-phosphate dehydrogenase (glucose 1-glucose-6-phosphate dehydrogenase isozyme
696	1	434	718	2019	g1651209	2.00E-31	3 beta-hydroxy-delta 5-C27-steroid oxidoreductase
698	2	390	227	1396	g13436260	0	unnamed protein product
698	2	390	227	1396	g17902306	0	unnamed protein product
698	2	390	227	1396	g17902308	0	unnamed protein product
700	3	488	249	1712	g17644260	0	b8206121.1 (ATPase, Class VI, type 11C)
700	3	488	249	1712	g6457274	1.00E-178	putative E1-E2 ATPase
700	3	488	249	1712	g18086549	1.00E-118	putative amphipath transporter
701	3	142	1197	1622	g306812	8.00E-75	glutathione transferase M1
701	3	142	1197	1622	g31924	4.00E-74	glutathione S-transferase (AA 1-218)
701	3	142	1197	1622	g31935	2.00E-61	glutathione S-transferase
702	1	183	982	1530	g14189960	2.00E-21	PRO0764
702	1	183	982	1530	g15214765	4.00E-21	Similar to hypothetical protein
702	1	183	982	1530	g299471	2.00E-20	X-linked retinopathy protein
703	2	413	2	1240	g11323192	0	dJ1022E24.4 (continues in bA476115 (AL137028))
703	2	413	2	1240	g7023200	0	unnamed protein product
703	2	413	2	1240	g16552496	1.00E-138	unnamed protein product
704	2	361	539	1621	g3191969	0	dJ337O18.2.1 (Lysosomal Protective Protein precursor (EC 3.4.16.5, Cathepsin A, Carboxypeptidase C) (isoform 1))
704	2	361	539	1621	g13929457	0	dJ337O18.2.2 (Lysosomal Protective Protein precursor (EC 3.4.16.5, Cathepsin A, Carboxypeptidase C) (isoform 2))
704	2	361	539	1621	g12653639	0	Similar to protective protein for beta-galactosidase (galactosialidosis)
705	1	456	433	1800	g450271	0	epoxide hydrolase
705	1	456	433	1800	g34543	0	epoxide hydrolase (AA 1-455)
705	1	456	433	1800	g340390	0	epoxide hydrolase
706	3	277	1806	2636	g14161726	1.00E-150	putative 1-aminocyclopropane-1-carboxylate synthase
706	3	277	1806	2636	g16553410	1.00E-149	unnamed protein product
706	3	277	1806	2636	g18044197	1.00E-149	1-aminocyclopropane-1-carboxylate synthase
707	3	331	87	1079	g1754714	3.00E-71	oviductin
707	3	331	87	1079	g15277254	5.00E-68	oviductin
707	3	331	87	1079	g2981641	1.00E-63	polyprotein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
708	3	201	96	698	g1847416	4.00E-19	RE15159p
708	3	201	96	698	g14026730	2.00E-12	homoserine kinase
708	3	201	96	698	g17984501	3.00E-12	membrane protein related to metalloendopeptidase
710	3	203	3	611	g6453472	1.00E-115	hypothetical protein
710	3	203	3	611	g6331206	2.00E-10	KIAA1267 protein
710	3	203	3	611	g6807806	2.00E-10	hypothetical protein
711	3	120	3	362	g34192	7.00E-27	KUP protein
711	3	120	3	362	g15126609	3.00E-14	Similar to heat shock 70kD protein 2
711	3	120	3	362	g4589638	3.00E-14	KIAA0997 protein
713	1	109	232	558	g12005726	4.00E-26	DC21
713	1	109	232	558	g338336	3.00E-22	spermidine/spermine N1-acetyltransferase
713	1	109	232	558	g14250050	3.00E-22	spermidine/spermine N1-acetyltransferase
714	3	370	75	1184	g16924333	1.00E-175	cytosolic acyl coenzyme A thioester hydrolase
714	3	370	75	1184	g2780414	1.00E-175	brain acyl-CoA hydrolase
714	3	370	75	1184	g15488731	1.00E-170	Unknown (protein for MGC:19175)
715	2	82	410	655	g7023029	2.00E-11	unnamed protein product
715	2	82	410	655	g14388428	5.00E-09	hypothetical protein
716	3	198	45	638	g202842	5.00E-94	aldolase C
716	3	198	45	638	g4519576	5.00E-94	aldolase C
716	3	198	45	638	g14198249	1.00E-93	aldolase 3, C isoform
718	2	642	2	1927	g17644260	0	BB20621.1 (ATPase, Class VI, type 11C)
718	2	642	2	1927	g5689373	0	KIAA1021 protein
718	2	642	2	1927	g457274	0	putative E1-E2 ATPase
719	1	82	211	456	g12698182	5.00E-12	hypothetical protein
719	1	82	211	456	g16552221	7.00E-11	unnamed protein product
719	1	82	211	456	g18089169	1.00E-10	Similar to hypothetical protein FLJ21394
720	2	278	131	964	g6467206	1.00E-101	gonadotropin inducible transcription repressor-4
720	2	278	131	964	g13623354	4.00E-95	Similar to zinc finger protein 136 (clone pHZ-20)
720	2	278	131	964	g6330394	2.00E-93	KIAA1198 protein
721	1	639	1	1917	g15797278	0	unnamed protein product
721	1	639	1	1917	g15797260	0	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
721	1	639	1	1917	g15797254	0	unnamed protein product
722	2	457	164	1534	g5441939	0	inhibin beta-A chain precursor
722	2	457	164	1534	g307069	0	beta-A inhibin
722	2	457	164	1534	g181947	0	erythroid differentiation protein precursor
723	2	247	101	841	g12052983	3.00E-97	hypothetical protein
723	2	247	101	841	g14042293	4.00E-96	unnamed protein product
723	2	247	101	841	g6467206	1.00E-94	gonadotropin inducible transcription repressor-4
724	2	139	2	418	g12002127	9.00E-61	CCK1 protein
724	2	139	2	418	g10312152	9.00E-61	mucosae-associated epithelial chemokine
724	2	139	2	418	g9392591	9.00E-61	CC chemokine CCL28
725	3	326	2547	3524	g189701	1.00E-145	endothelial cell growth factor
725	3	326	2547	3524	g6862560	1.00E-145	endothelial cell growth factor 1
725	3	326	2547	3524	g17390355	1.00E-145	endothelial cell growth factor 1 (platelet-derived)
729	2	265	11	805	g459811	3.00E-93	basic fibroblast growth factor (ctg start codon); putative
729	2	265	11	805	g183084	9.00E-93	21 kd basic fibroblast growth factor (ctg start codon; putative)
729	2	265	11	805	g183087	9.00E-89	basic fibroblast growth factor
731	3	50	3	152	g3411161	7.00E-12	mitogen- and stress-activated protein kinase-2
731	3	50	3	152	g3452409	7.00E-12	Ribosomal protein kinase B (RSK-B)
732	3	66	351	548	g6624117	1.00E-10	mitogen- and stress-activated protein kinase-2
732	3	66	351	548	g18089095	4.00E-21	pre-B cell enhancing factor
732	3	66	351	548	g404013	4.00E-21	Similar to pre-B-cell colony-enhancing factor
733	3	174	3	524	g12002127	7.00E-72	pre-B cell enhancing factor
733	3	174	3	524	g10312152	7.00E-72	CCK1 protein
733	3	174	3	524	g9392591	7.00E-72	mucosae-associated epithelial chemokine
736	3	66	351	548	g6624117	4.00E-21	CC chemokine CCL28
736	3	66	351	548	g18089095	4.00E-21	pre-B cell enhancing factor
736	3	66	351	548	g404013	4.00E-21	Similar to pre-B-cell colony-enhancing factor
737	3	357	3	1073	g386852	0	pre-B cell enhancing factor
737	3	357	3	1073	g494	1.00E-137	kininogen
737	3	357	3	1073	g492	1.00E-136	kininogen
737	3	357	3	1073	g492	1.00E-136	prekininogen

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
739	1	423	1	1269	g5834566	0	cd927N21.1.1 (chromogranin B (secretogranin 1, SCG1) (isoform 1))
739	1	423	1	1269	g12653215	0	chromogranin B (secretogranin 1)
739	1	423	1	1269	g36439	0	precursor polypeptide (AA-20 to 657)
740	2	265	11	805	g459811	3.00E-93	basic fibroblast growth factor (ctg start codon); putative
740	2	265	11	805	g183084	9.00E-93	21 kd basic fibroblast growth factor (ctg start codon; put.); putative
740	2	265	11	805	g183087	9.00E-89	basic fibroblast growth factor
741	2	197	695	1285	g14042850	3.00E-47	unnamed protein product
741	2	197	695	1285	g12805201	3.00E-27	Similar to zinc finger protein 97
741	2	197	695	1285	g5453423	1.00E-21	epstein-barr virus-induced zinc finger protein
742	3	79	783	1019	g16553727	3.00E-08	unnamed protein product
742	3	79	783	1019	g16553745	8.00E-07	unnamed protein product
742	3	79	783	1019	g9929935	8.00E-07	hypothetical protein
745	1	639	1	1917	g15797278	0	unnamed protein product
745	1	639	1	1917	g15797260	0	unnamed protein product
745	1	639	1	1917	g15797254	0	unnamed protein product
747	3	887	513	3173	g433338	0	protein-tyrosine kinase
747	3	887	513	3173	g12659212	0	discoidin-1 domain receptor-2
747	3	887	513	3173	g435162	0	tyro 10 receptor kinase
748	2	337	17	1027	g2665641	0	immunoglobulin-like transcript 5
748	2	337	17	1027	g2351805	0	monocyte inhibitory receptor precursor
748	2	337	17	1027	g2662428	0	immunoglobulin-like transcript 5 protein
752	2	612	311	2146	g182193	0	estrogen receptor
752	2	612	311	2146	g31234	0	estrogen receptor
752	2	612	311	2146	g5702091	0	green fluorescent protein-estrogen receptor alpha fusion
753	2	209	80	706	g35311	1.00E-116	MHC class I promoter binding protein
753	2	209	80	706	g1804456	1.00E-115	Similar to retinoid X receptor beta
753	2	209	80	706	g4249766	1.00E-112	retinoid X receptor beta
754	2	680	2	2041	g3153241	0	class I cytokine receptor
754	2	680	2	2041	g11022747	0	CRL1 protein
754	2	680	2	2041	g11036792	0	type-I T cell cytokine receptor
757	1	371	1	1113	g13517983	0	G-protein coupled receptor 91

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
757	1	371	1	1113	g12711491	1.00E-134	G-protein coupled receptor GPR91
757	1	371	1	1113	g1660636	2.00E-48	P2Y1 nucleotide receptor
758	2	222	131	796	g12214287	7.00E-83	cd402H5.1 (novel 7 transmembrane receptor of the rhodopsin family)
758	2	222	131	796	g15797318	3.00E-82	unnamed protein product
758	2	222	131	796	g440626	6.00E-19	opsin
759	3	253	156	914	g1381181	1.00E-143	ubiquitin-conjugating enzyme E2-32k
759	3	253	156	914	g15029782	1.00E-140	Unknown (protein for MGC:19259)
759	3	253	156	914	g13436071	1.00E-140	Unknown (protein for MGC:10481)
760	3	149	777	1223	g2343109	2.00E-65	MIR-7
760	3	149	777	1223	g11876371	2.00E-65	unnamed protein product
760	3	149	777	1223	g2267170	2.00E-65	leucocyte immunoglobulin-like receptor-1
761	3	77	1221	1451	g9280253	2.00E-15	unnamed protein product
761	3	77	1221	1451	g930041	2.00E-12	36/8-8 fusion protein with epitope for anti-IgG antibody
761	3	77	1221	1451	g1653745	1.00E-11	unnamed protein product
762	3	154	3	464	g4097253	5.00E-70	calcitonin gene-related peptide receptor component protein
762	3	154	3	464	g12653975	5.00E-70	calcitonin gene-related peptide-receptor component protein
762	3	154	3	464	g3290205	5.00E-70	CGRP-receptor component protein
763	2	286	182	1039	g2702319	1.00E-164	aryl hydrocarbon receptor nuclear translocator; Arnt
763	2	286	182	1039	g179004	1.00E-164	Arnt
764	1	190	70	639	g12232595	1.00E-164	aryl hydrocarbon receptor nuclear translocator; ARNT
764	1	190	70	639	g59571	5.00E-05	RS1
764	1	190	70	639	g59558	5.00E-05	RS1
764	1	190	70	639	g291504	5.00E-05	Immediate-early protein Vmw175
767	3	150	3	452	g1419016	2.00E-56	odorant receptor
767	3	150	3	452	g18480958	1.00E-55	olfactory receptor MOR267-13
767	3	150	3	452	g18480188	2.00E-54	olfactory receptor MOR267-8
768	1	235	1	705	g12578457	1.00E-117	unnamed protein product
768	1	235	1	705	g5442038	1.00E-117	stromal cell-derived receptor-1 alpha
768	1	235	1	705	g1806276	1.00E-107	glycoprotein 55
769	1	283	1	849	g4309953	1.00E-107	T cell receptor gamma chain; similar to PID:g339160
769	1	283	1	849	g4309950	2.00E-95	T cell receptor gamma chain; match to S08328 (PID:g106470)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
769	1	283	1	849	g296680	9.00E-56	T-cell receptor gamma-chain
770	2	365	80	1174	g11226987	1.00E-165	unnamed protein product
770	2	365	80	1174	g817957	1.00E-147	glycine receptor subunit alpha 4
770	2	365	80	1174	g18448711	1.00E-137	glycine receptor alpha 4 subunit
771	3	577	156	1886	g2228562	0	activin receptor like kinase 1
771	3	577	156	1886	g425148	0	TGF-beta superfamily receptor type I
771	3	577	156	1886	g402197	0	ALK-1
772	2	203	56	664	g4102980	2.00E-06	virulent strain associated lipoprotein
772	2	203	56	664	g2690100	1.00E-05	B. burgdorferi predicted coding region BB116
772	2	203	56	664	g9886896	3.00E-05	Orf73
773	2	108	95	418	g688373	2.00E-14	neurofibromatosis type 2
773	2	108	95	418	g463121	3.00E-14	NF2
773	2	108	95	418	g14388331	1.00E-12	hypothetical protein
775	1	75	304	528	g10438620	2.00E-08	unnamed protein product
775	1	75	304	528	g16041132	6.00E-08	hypothetical protein
775	1	75	304	528	g3253117	1.00E-07	TA2R_HUMAN, BETA ISOFORM; TXA2-R; PROSTANOID TP RECEPTOR
777	1	105	397	711	g7262613	2.00E-16	candidate taste receptor T2R7
777	1	105	397	711	g7262619	7.00E-15	candidate taste receptor T2R10
777	1	105	397	711	g7262615	2.00E-13	candidate taste receptor T2R8
778	3	194	408	989	g35535	5.00E-94	putative receptor (AA 1-192)
778	3	194	408	989	g13528954	5.00E-94	putative receptor protein
778	3	194	408	989	g12803945	5.00E-94	putative receptor protein
780	2	136	32	439	g247112	1.00E-62	glutamate receptor subunit 4c; GluR-4c
780	2	136	32	439	g940272	1.00E-59	glutamate receptor subunit 2B
780	2	136	32	439	g2300329	3.00E-59	unnamed protein product
781	3	781	408	2750	g458657	0	glucocorticoid receptor alpha-2
781	3	781	408	2750	g2218074	0	glucocorticoid receptor alpha
781	3	781	408	2750	g183033	0	glucocorticoid receptor alpha (94 kD)
784	3	143	3	431	g3861488	5.00E-73	vesicle soluble NSF attachment protein receptor VTI2
784	3	143	3	431	g13111941	5.00E-73	vesicle-associated soluble NSF attachment protein receptor (v-SNARE; homolog of S. cerevisiae VTI1)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
784	3	143	3	431	g2687400	5.00E-73	vesicle soluble NSF attachment protein receptor
785	3	460	3	1382	g5006811	3.00E-22	serpentine receptor
785	3	460	3	1382	g4456467	9.00E-22	TM7XN1 protein
785	3	460	3	1382	g4836765	5.00E-21	G-protein-coupled receptor
786	2	211	1574	2206	g18480746	1.00E-102	olfactory receptor MOR261-10
786	2	211	1574	2206	g18480744	1.00E-100	olfactory receptor MOR261-9
786	2	211	1574	2206	g18480184	1.00E-97	olfactory receptor MOR261-5
789	2	99	74	370	g10433120	2.00E-17	unnamed protein product
789	2	99	74	370	g6650802	4.00E-09	PRO1848
789	2	99	74	370	g18255512	2.00E-08	Unknown (protein for MGC:24986)
790	2	224	2	673	g987667	2.00E-07	alpha 1 type IX collagen chain
790	2	224	2	673	g12847742	2.00E-07	data source:MGD, source key:MGI:88465 evidence:ISS-procollagen, type IX, alpha 1-putative
790	2	224	2	673	g192676	2.00E-07	alpha-1 type IX collagen
791	1	155	1	465	g18028273	8.00E-84	hypothetical protein S88157
791	1	155	1	465	g8250239	5.00E-81	protein phosphatase 4 regulatory subunit 2
791	1	155	1	465	g9837385	5.00E-06	refinitis pigmentosa GTPase regulator-like protein
792	2	191	719	1291	g986879	4.00E-96	cyclin-dependent kinase
792	2	191	719	1291	g984724	2.00E-95	cyclin-dependent kinase
792	2	191	719	1291	g495287	6.00E-95	alternate gene name=WAF1
793	3	1049	39	3185	g6630609	0	cyclin-E binding protein 1
793	3	1049	39	3185	g10047261	0	KIAA1593 protein
793	3	1049	39	3185	g517115	1.00E-178	KIAA0032
796	1	297	1186	2076	g7801278	1.00E-08	putative translation initiation factor IF-2(fragment)
796	1	297	1186	2076	g3599478	1.00E-07	Myosin-IA
796	1	297	1186	2076	g16974791	3.00E-07	dragline silk protein spidroin 2
798	1	476	292	1719	g397935	0	alpha 2-chimerin
798	1	476	292	1719	g15030254	0	Similar to chimerin (chimerin) 1
798	1	476	292	1719	g899452	0	beta2-chimerin
799	3	252	774	1529	g14043783	1.00E-115	Unknown (protein for MGC:14256)
799	3	252	774	1529	g10436857	1.00E-115	unnamed protein product



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
799	3	252	774	1529	g15215451	1.00E-112	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
800	1	166	364	861	g14041850	2.00E-85	unnamed protein product
800	1	166	364	861	g12855057	2.00E-85	data source:SPTR, source key:P51646, evidence:ISS-homolog to ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 5--putative
800	1	166	364	861	g1150556	2.00E-72	ARF-like protein 5
801	2	333	2	1000	g16878290	0	Unknown (protein for IMAGE:4869353)
801	2	333	2	1000	g12830335	0	bA55008.2 (novel protein kinase)
801	2	333	2	1000	g16511401	1.00E-128	unnamed protein product
802	1	499	1	1497	g4426595	0	multifunctional calcium/calmodulin-dependent protein kinase II delta2
802	1	499	1	1497	g1661132	0	calcium/calmodulin-dependent protein kinase II delta 2-subunit
802	1	499	1	1497	g3241849	0	calcium/calmodulin-dependent protein kinase II-delta dash
803	3	155	3	467	g407075	2.00E-09	MAP kinase activated protein kinase-2
803	3	155	3	467	g1089896	2.00E-09	MAP kinase-activated protein kinase 2
803	3	155	3	467	g559435	2.00E-09	MapKap kinase 2
804	1	270	406	1215	g8331757	1.00E-147	Ca2+/Calmodulin-dependent protein kinase I
804	1	270	406	1215	g3135197	1.00E-139	Ca2+/calmodulin-dependent protein kinase I beta 2
804	1	270	406	1215	g6841608	1.00E-139	pregnancy upregulated nonubiquitous Ca2+/calmodulin-dependent kinase Pnck
805	2	409	491	1717	g2736151	0	myotonic dystrophy kinase-related Cdc42-binding kinase
805	2	409	491	1717	g14133241	1.00E-135	KIAA1124 protein
805	2	409	491	1717	g5006445	1.00E-135	CDC42-binding protein kinase beta
806	3	175	684	1208	g530162	1.00E-100	tyrosine phosphatase
806	3	175	684	1208	g2961199	1.00E-100	tyrosine phosphatase
806	3	175	684	1208	g1814024	1.00E-100	protein tyrosine phosphatase
807	3	432	3	1298	g14794515	0	interleukin-4 induced gene-1 protein
807	3	432	3	1298	g14794519	0	interleukin-4 induced gene-1 protein
807	3	432	3	1298	g1924980	1.00E-171	Fig-1 protein
808	1	435	67	1371	g10435919	0	unnamed protein product
808	1	435	67	1371	g3327128	7.00E-83	KIAA00657 protein
808	1	435	67	1371	g15026974	5.00E-51	obscutin

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
809	3	430	258	1547	g1463127	0	JNK3 alpha1 protein kinase
809	3	430	258	1547	g468151	0	MAP kinase
809	3	430	258	1547	g1463125	0	JNK3 alpha2 protein kinase
810	1	265	1708	2502	g632964	1.00E-130	clt1; putative
810	1	265	1708	2502	g1335932	1.00E-130	hypothetical protein
810	1	265	1708	2502	g9437515	1.00E-128	CLK4
811	2	235	1130	1834	g4886477	1.00E-130	hypothetical protein
811	2	235	1130	1834	g2648021	1.00E-130	cICF0811.4.1 (RAB2, member RAS oncogene family-like, isoform 1)
811	2	235	1130	1834	g15799218	1.00E-115	cICF0811.4.2 (RAB2, member RAS oncogene family-like, isoform 2)
812	2	231	497	1189	g7263960	1.00E-130	ba395L14.11.1 (RAB, member of RAS oncogene family-like 2A (isoform 1))
812	2	231	497	1189	g15928838	1.00E-130	RAB, member of RAS oncogene family-like 2B
812	2	231	497	1189	g7263961	1.00E-129	ba395L14.11.2 (RAB, member of RAS oncogene family-like 2A (isoform 2))
813	2	688	545	2608	g2735857	0	cAMP-specific phosphodiesterase PDE4D5
813	2	688	545	2608	g10184352	0	fusion between Aequorea victoria and human
813	2	688	545	2608	g347130	0	phosphodiesterase
814	3	351	3	1055	g13435506	8.00E-56	Similar to RIKEN cDNA 2610510-H03 gene
814	3	351	3	1055	g4884188	5.00E-32	hypothetical protein
814	3	351	3	1055	g7301399	6.00E-25	CG5913 gene product
815	1	457	328	1698	g15211844	0	putative myotubularin related protein 8
815	1	457	328	1698	g15211846	0	putative myotubularin related protein 8
815	1	457	328	1698	g7020538	0	unnamed protein product
819	2	202	5	610	g18088786	3.00E-91	Similar to RIKEN cDNA 1500012D09 gene
819	2	202	5	610	g12837642	4.00E-90	data source:SPTR, source key:P53994, evidence:ISS-putative-similar to RAS
819	2	202	5	610	g1943772	8.00E-87	RELATED PROTEIN RAB-2
820	3	230	69	758	g14041850	1.00E-101	Hypothetical protein F53F10.4
820	3	230	69	758	g12855057	1.00E-101	unnamed protein product
820	3	230	69	758	g12855057	1.00E-101	data source:SPTR, source key:P51646, evidence:ISS-homolog to ADP- RIBOSYLATION FACTOR-LIKE PROTEIN 5-putative
820	3	230	69	758	g1150556	2.00E-84	ARF-like protein 5
821	2	71	977	1189	g16553745	2.00E-14	unnamed protein product
821	2	71	977	1189	g930041	3.00E-10	36/8-8 fusion protein with epitope for anti-lectin antibody

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
821	2	71	977	1189	g15208249	5.00E-10	hypothetical protein
822	1	166	118	615	g16511330	3.00E-69	unnamed protein product
822	1	166	118	615	g18479336	7.00E-57	olfactory receptor MOR270-1
822	1	166	118	615	g18480770	2.00E-56	olfactory receptor MOR271-1
823	3	486	291	1748	g12830367	0	serine/threonine kinase 33
823	3	486	291	1748	g14148952	1.00E-157	serine/threonine kinase 33
823	3	486	291	1748	g1498250	2.00E-56	myosin light chain kinase
825	1	115	283	627	g15795911	2.00E-39	unnamed protein product
825	1	115	283	627	g10764163	1.00E-36	GCN2beta
825	1	115	283	627	g6066585	1.00E-36	GCN2 eif2alpha kinase
826	2	117	2	352	g625159	5.00E-22	GTP-binding protein gamma subunit
826	2	117	2	352	g6164867	5.00E-22	G-protein gamma 8 subunit
826	2	117	2	352	g6164869	5.00E-22	G-protein gamma 8 subunit
827	1	391	1	1173	g9837357	1.00E-122	GTP-binding protein RAB11B
827	1	391	1	1173	g763130	1.00E-121	YPT3
827	1	391	1	1173	g433064	1.00E-121	Rab11b
828	1	454	1	1362	g12407081	0	protein kinase/ribonuclease IRE1 beta
828	1	454	1	1362	g3766209	0	IRE1
828	1	454	1	1362	g3300094	1.00E-153	protein kinase/endoribonuclease
830	2	121	110	472	g3088551	6.00E-56	calcium/calmodulin-dependent protein kinase II delta
830	2	121	110	472	g1661132	6.00E-56	calcium/calmodulin-dependent protein kinase II delta 2 subunit
830	2	121	110	472	g4426895	6.00E-56	multifunctional calcium/calmodulin-dependent protein kinase II delta2
831	1	324	19	990	g530090	0	MAP kinase activated protein kinase 2
831	1	324	19	990	g407075	1.00E-175	MAP kinase activated protein kinase-2
831	1	324	19	990	g1089896	1.00E-174	MAP kinase-activated protein kinase 2
832	2	175	530	1054	g189510	2.00E-84	p70 ribosomal S6 kinase alpha-II
832	2	175	530	1054	g189508	2.00E-84	p70 ribosomal S6 kinase alpha-II
832	2	175	530	1054	g12848541	7.00E-84	data source:SPTR, source key:P23443, evidence:ISS-homolog to RIBOSOMAL PROTEIN S6 KINASE (EC 2.7.1.-) (S6K) (P70-S6K)-putative
833	3	103	39	347	g299471	3.00E-13	X-linked retinopathy protein
833	3	103	39	347	g15680002	1.00E-11	Unknown (protein for MGC:22647)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability	Score	Annotation
833	3	103	39	347	g18043611	8.00E-10		Similar to hypothetical protein FLJ21463
834	3	250	216	965	g8331757	1.00E-133		Ca2+/calmodulin-dependent protein kinase I
834	3	250	216	965	g3135197	1.00E-125		Ca2+/calmodulin-dependent protein kinase I beta 2
834	3	250	216	965	g6841608	1.00E-125		pregnancy upregulated nonubiquitous Ca2+/calmodulin-dependent kinase Pnck
836	1	255	1270	2034	g13241761	1.00E-134		transmembrane protein induced by tumor necrosis factor alpha
836	1	255	1270	2034	g18490438	2.00E-97		Unknown (protein for IMAGE4038363)
836	1	255	1270	2034	g6691812	5.00E-59		/prediction=(method:"genscan", version:"1.0", score:"109.13"); /match=(method:"blastn", version:"1.4.9"); /prediction=(method:"blastn", version:"1.4.9"); /match=(method:"blastn", version:"1.4.9"); Drosophila melanogaster cDNA clone GH06126.5prime GH06126.5prime similar to X81644; D. melanogaster P element Casper-1 gene, mRNA sequence; species:"Drosophila melanogaster (fruit fly)", ranges:(query:31242..31383, target:EMBL:AI106876:516..375, score:"710.00"), (query:30496..30618, target:EMBL:AI106876:637..515, score:"615.00"), method:"blastn", version:"1.4.9"); /match=(method:"blastn", version:"1.4.9"); melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD44075.5prime, mRNA sequence", species:"Drosophila melanogaster (fruit fly)", ranges:(query:31242..31382, target:EMBL:AI512291:227..87, score:"705.00"), (query:30496..30618, target:EMBL:AI512291:348..226, score:"615.00"), (query:26999..27132, target:EMBL:AI512291:480..347, score:"652.00"), (query:26539..26696, target:EMBL:AI512291:628..471, score:"718.00"), method:"blastn", version:"1.4.9"); Cam gene product calmodulin II calmodulin (148 AA) Similar to ELK motif kinase serine/threonine protein kinase Ser/Thr protein kinase PAR-1balpha p21-activated protein kinase I serine/threonine kinase
837	2	82	350	595	g7303488	8.00E-22		
837	2	82	350	595	g818020	2.00E-21		
837	2	82	350	595	g7688	2.00E-21		
839	1	412	640	1875	g14250622	1.00E-174		
839	1	412	640	1875	g1749794	1.00E-173		
839	1	412	640	1875	g15042611	1.00E-166		
840	2	246	212	949	g12360654	1.00E-128		
840	2	246	212	949	g1016005	1.00E-128		

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability	Score	Annotation
840	2	246	212	949	g1245844	1.00E-128		gamma-PAK
841	2	160	704	1183	g35784	3.00E-38		protein-tyrosine phosphatase
841	2	160	704	1183	g338082	3.00E-38		phosphotyrosyl-protein phosphatase
841	2	160	704	1183	g292407	3.00E-38		protein-tyrosine phosphatase
843	2	190	2	571	g665588	1.00E-80		calmodulin
843	2	190	2	571	g5901755	1.00E-80		calmodulin; CaMl
843	2	190	2	571	g57835	1.00E-80		calmodulin
844	2	143	2330	2758	g6690248	6.00E-16		PRO0657
844	2	143	2330	2758	g16550881	4.00E-12		unnamed protein product
844	2	143	2330	2758	g288145	8.00E-11		put. ORF
845	3	1136	393	3800	g2570359	0		receptor-associated tyrosine kinase
845	3	1136	393	3800	g17384438	0		bA39K24.1 (Janus kinase 2 (a protein tyrosine kinase))
846	2a	150	2	451	g12830335	8.00E-84		Jak2 kinase
846	2a	150	2	451	g16878290	8.00E-84		bA550O8.2 (novel protein kinase)
846	2a	150	2	451	g16511401	7.00E-55		Unknown (protein for IMAGE:4869353)
848	2	288	698	1561	g31744	1.00E-152		unnamed protein product
848	2	288	698	1561	g15779126	1.00E-152		G protein alpha-subunit (AA 1-355)
848	2	288	698	1561	g15082440	1.00E-152		Similar to guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2
849	1	105	46	360	g14149100	1.00E-40		Similar to guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2
849	1	105	46	360	g13492052	1.00E-40		activity polypeptide 2
849	1	105	46	360	g16306928	1.00E-40		PTEN induced putative kinase 1
851	2	95	2	286	g1679668	2.00E-41		protein kinase BRPK
851	2	95	2	286	g3646067	2.00E-41		Unknown (protein for IMAGE:3891886)
851	2	95	2	286	g1805500	8.00E-41		mitogen-activated kinase kinase 5
853	3	45	411	545	g6690248	4.00E-08		MEK5 (MAP/ERK kinase kinase 5 (ASK1, MAPKK5, Mitogen Activated Protein kinase kinase kinase 5))
853	3	45	411	545	g5042226	3.00E-07		ASK1
853	3	45	411	545	g288145	7.00E-06		PRO0657
853	3	45	411	545	g288145	7.00E-06		E1 fusion protein
853	3	45	411	545	g288145	7.00E-06		put. ORF

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
854	3	281	3	845	g2589221	1.00E-130	cerebellar leucine rich acidic nuclear protein
854	3	281	3	845	g1763273	1.00E-130	acidic nuclear phosphoprotein pp32
854	3	281	3	845	g1408224	1.00E-130	patent heat-stable protein phosphatase 2A inhibitor IIPP2A
859	3	199	30	626	g15213265	3.00E-97	RAS guanyl releasing protein 4 variant 1
859	3	199	30	626	g15213263	2.00E-96	RAS guanyl releasing protein 4
859	3	199	30	626	g15213267	4.00E-95	RAS guanyl releasing protein 4 variant 2
861	3	573	1365	3083	g577293	0	female sterile homeotic (fsh) homolog RING3
861	3	573	1365	3083	g182769	0	putative
861	3	573	1365	3083	g2980663	0	FSH
862	1	562	490	2175	g15186754	0	RalGDS-related effector protein of M-Ras
862	1	562	490	2175	g8650435	0	RalGDS-like protein 3
862	1	562	490	2175	g12836390	1.00E-126	RALGDS-LIKE PROTEIN 3--data source:SPTR, source key:G9JID4, evidence:ISS--putative
863	2	230	137	826	g1702926	1.00E-123	RIN (RIC-related gene expressed in neurons)
863	2	230	137	826	g2286099	1.00E-123	RIBA
863	2	230	137	826	g17390126	1.00E-122	Ric (Drosophila)-like, expressed in neurons
865	2	571	209	1921	g190222	0	protein phosphatase 2A 72 kDa regulatory subunit
865	2	571	209	1921	g190220	0	protein phosphatase 2A 130 kDa regulatory subunit
865	2	571	209	1921	g9367828	0	protein phosphatase 2A 72 kDa regulatory subunit
866	3	255	78	842	g18098166	1.00E-147	unnamed protein product
866	3	255	78	842	g13311007	1.00E-143	protein kinase NYD-SP15
866	3	255	78	842	g13905210	1.00E-133	Similar to protein kinase NYD-SP15
867	3	156	1230	1697	g3420023	5.00E-06	gag-pol precursor polyprotein gp180
867	3	156	1230	1697	g323891	5.00E-06	P160gag-fms polyprotein
867	3	156	1230	1697	g4759948	9.00E-06	CAPSID PROTEIN PRECURSOR
868	1	727	427	2607	g10434667	9.00E-85	unnamed protein product
868	1	727	427	2607	g7959159	9.00E-85	KIAA1450 protein
868	1	727	427	2607	g12805005	6.00E-27	Similar to PDZ domain-containing guanine nucleotide exchange factor 1
869	3	188	24	587	g2317723	1.00E-102	Polycomb 2 homolog
869	3	188	24	587	g2781392	7.00E-83	transcriptional repressor Mpc2
869	3	188	24	587	g3649787	3.00E-28	chromobox protein (CHCB3)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
870	2	297	167	1057	g780128	1.00E-165	also called HHL
870	2	297	167	1057	g7020488	1.00E-165	unnamed protein product
870	2	297	167	1057	g8118620	1.00E-165	hairy
871	3	217	291	941	g5737759	3.00E-83	polyamine modulated factor-1
871	3	217	291	941	g13158047	3.00E-83	unnamed protein product
871	3	217	291	941	g5737757	3.00E-83	polyamine modulated factor-1
872	2	309	65	991	g6690017	2.00E-12	NIR
872	2	309	65	991	g9798133	1.00E-09	Hypothetical protein C18H7.3
872	2	309	65	991	g1334643	2.00E-08	APEG precursor protein
873	1	308	898	1821	g12583650	1.00E-167	leucine-zipper protein
873	1	308	898	1821	g10732829	1.00E-167	transcription factor ATfx
873	1	308	898	1821	g13444178	1.00E-167	unnamed protein product
875	2	122	257	622	g6650810	8.00E-17	PRO1902
875	2	122	257	622	g16553789	4.00E-16	unnamed protein product
875	2	122	257	622	g3002527	5.00E-16	neuronal thread protein AD7c-NTP
876	1	527	244	1824	g9714266	0	DRBP76 alpha
876	1	527	244	1824	g5762315	0	translational control protein 80
877	2	346	800	1837	g2922290	0	nuclear factor associated with dsRNA NFAR-2
877	2	346	800	1837	g15524590	0	enhancer binding factor 2C
877	2	346	800	1837	g298698	0	unnamed protein product
879	1	148	154	597	g16550231	1.00E-178	myocyte enhancer-binding factor 2; MEF2
879	1	148	154	597	g3970712	2.00E-18	unnamed protein product
879	1	148	154	597	g12804323	2.00E-18	zinc finger protein 10
880	3	93	132	410	g15929491	7.00E-18	Unknown (protein for MGC:4054)
880	3	93	132	410	g12655143	1.00E-48	Unknown (protein for MGC:10149)
880	3	93	132	410	g12804963	1.00E-48	Similar to ubiquinol-cytochrome c reductase hinge protein
881	2	209	2	628	g4165087	1.00E-122	Similar to ubiquinol-cytochrome c reductase hinge protein
881	2	209	2	628	g6683496	1.00E-118	Williams-Beuren syndrome deletion transcript 9
881	2	209	2	628	g4153860	1.00E-113	bromodomain adjacent to zinc finger domain 18
882	2	195	62	646	g12314057	1.00E-105	similar to U47321 (PID:g1245146)
							cd1167H4.1.1 (novel protein, isoform 1)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
882	2	195	62	646	g14272832	1.00E-105	unnamd protein product
882	2	195	62	646	g17389366	1.00E-104	Unknown (protein for MGC:21371)
885	3	154	408	869	g7341372	3.00E-76	retinoblastoma-binding protein 1-related protein
885	3	154	408	869	g13629869	3.00E-76	retinoblastoma-binding protein 1-like 1
885	3	154	408	869	g435776	1.00E-62	retinoblastoma binding protein 1; RBP1
888	1	406	67	1284	g2459797	0	epithelial-specific ets protein
888	1	406	67	1284	g2384740	0	Ets transcription factor
888	1	406	67	1284	g2338756	0	Ets-related transcription factor
889	3	182	1920	2465	g15145797	2.00E-05	basic proline-rich protein
890	1	243	1	729	g4455609	1.00E-143	d1742C19.5 (chromobox homolog 7)
890	1	243	1	729	g18204009	6.00E-38	Unknown (protein for MGC:29271)
890	1	243	1	729	g2317723	7.00E-27	Polycomb 2 homolog
891	2	2735	1751	9955	g5106572	0	transcriptional activator SRCAP
891	2	2735	1751	9955	g2224559	0	KIAA0309
891	2	2735	1751	9955	g8953897	1.00E-174	helicase DOMINO A
892	3	161	213	695	g2460124	2.00E-60	putative transcription factor CA150
892	3	161	213	695	g6329166	3.00E-59	transcription factor CA150b
892	3	161	213	695	g7298925	8.00E-29	CG15187 gene product
893	2	126	2	379	g6683492	8.00E-27	bromodomain PHD finger transcription factor
893	2	126	2	379	g18204482	2.00E-26	Unknown (protein for IMAGE:5345342)
893	2	126	2	379	g18265798	2.00E-15	nucleosome remodeling factor large subunit NURF301
894	1	236	1153	1860	g13938329	4.00E-87	H2.0 (Drosophila)-like homeo box 1
894	1	236	1153	1860	g7643911	4.00E-87	homeobox protein
894	1	236	1153	1860	g51331	1.00E-61	putative start codon
895	2	193	128	706	g490013	8.00E-63	ORF; HEIR-1; put. neuroblastoma-associated regulator
895	2	193	128	706	g395338	8.00E-63	helix-loop-helix protein
895	2	193	128	706	g6782311	6.00E-53	ID3 protein
896	3	91	3	275	g211607	6.00E-06	alpha-2 type I collagen
896	3	91	3	275	g63249	6.00E-06	collagen
896	3	91	3	275	g15145797	2.00E-05	basic proline-rich protein
897	3	192	471	1046	g882393	7.00E-68	TBP-associated factor TAF131



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
897	3	192	471	1046	g841308	7.00E-68	TAFII32 precursor
897	3	192	471	1046	g940151	7.00E-68	TAFII31
898	3	182	1920	2465	g15145797	2.00E-05	basic proline-rich protein
899	1	1052	691	3846	g4165087	0	Williams-Beuren syndrome deletion transcript 9
899	1	1052	691	3846	g6683496	0	bromodomain adjacent to zinc finger domain 1B
899	1	1052	691	3846	g4049922	0	transcription factor WSTF
900	1	1445	175	4509	g14211816	0	HBV pX associated protein 8 large isoform
900	1	1445	175	4509	g10803733	0	HBV pX associated protein-8; XAP-8
900	1	1445	175	4509	g7022417	0	unnamed protein product
902	3	95	3	287	g6690167	2.00E-07	PRO0117
903	2	745	248	2482	g5163089	0	P38IP
903	2	745	248	2482	g6523258	0	putative transcription factor
903	2	745	248	2482	g7381239	0	p38 interacting protein
904	1	122	679	1044	g14189960	2.00E-26	PRO0764
904	1	122	679	1044	g7020625	3.00E-26	unnamed protein product
905	3	390	3	1172	g10121865	1.00E-25	topoisomerase II alpha-4
905	3	390	3	1172	g13938351	1.00E-160	Similar to zinc finger protein 268
905	3	390	3	1172	g10047297	1.00E-156	KIAA1611 protein
905	3	390	3	1172	g10440398	1.00E-156	FLJ00032 protein
906	3	865	3	2597	g498152	0	ha0946 protein is Kruppel-related.
906	3	865	3	2597	g1181880	0	ba1021019.1 (zinc finger protein 33a (KOX 31))
907	3	170	33	542	g7023216	0	ZNF118
907	3	170	33	542	g7023703	3.00E-65	unnamed protein product
907	3	170	33	542	g14348588	2.00E-30	unnamed protein product
908	2	129	182	568	g2810991	6.00E-24	KRAB zinc finger protein
908	2	129	182	568	g13938639	3.00E-10	KRAB-zinc finger protein KZF-1
908	2	129	182	568	g3289985	7.00E-10	Unknown (protein for MGC:6654)
909	3	396	3	1190	g10047297	7.00E-08	KIAA0412
909	3	396	3	1190	g10440398	0	KIAA1611 protein
909	3	396	3	1190	g15929737	0	FLJ00032 protein
909	3	396	3	1190	g15929737	0	Similar to zinc finger protein 347

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
910	2	93	164	442	g347906	1.00E-33	zinc finger protein
910	2	93	164	442	g14348591	1.00E-26	KRAB zinc finger protein
910	2	93	164	442	g4235144	4.00E-26	BC39498_1
911	2	241	2	724	g10436807	3.00E-94	unnamed protein product
911	2	241	2	724	g13623354	5.00E-93	Similar to zinc finger protein 136 (clone pHZ-20)
911	2	241	2	724	g487785	2.00E-90	zinc finger protein ZNF136
912	3	221	3	665	g5441615	6.00E-84	zinc finger protein
912	3	221	3	665	g16549180	1.00E-83	unnamed protein product
912	3	221	3	665	g16550223	2.00E-82	unnamed protein product
913	2	166	23	520	g2970038	1.00E-66	HKL1
913	2	166	23	520	g4164083	2.00E-66	zinc finger protein E2NF
913	2	166	23	520	g15929737	3.00E-66	Similar to zinc finger protein 347
914	1	663	757	2745	g16553661	0	unnamed protein product
914	1	663	757	2745	g4164083	0	zinc finger protein E2NF
914	1	663	757	2745	g2970038	0	HKL1
915	3	237	3	713	g16552067	1.00E-105	unnamed protein product
915	3	237	3	713	g1336158	1.00E-95	pancreas only zinc finger protein
915	3	237	3	713	g633990	5.00E-95	zinc finger protein
917	3	186	3	560	g9502403	4.00E-07	Hypothetical zinc finger-like protein
918	1	107	379	699	g2739353	3.00E-47	ZNF91L
918	1	107	379	699	g184440	6.00E-40	Kruppel-related DNA-binding protein
918	1	107	379	699	g186774	6.00E-40	zinc finger protein
919	2	613	1472	3310	g6088100	0	zinc finger protein (ZFD25)
919	2	613	1472	3310	g16306806	0	zinc finger protein 43 (HIF6)
919	2	613	1472	3310	g38032	0	ZNF43
920	2	270	2	811	g6693371	1.00E-114	ZNF225
920	2	270	2	811	g6118387	1.00E-114	zinc finger protein ZNF225
920	2	270	2	811	g9502402	1.00E-114	ZNF225
922	2	317	2	952	g2085786	0	similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185)
922	2	317	2	952	g4454855	1.00E-166	zinc finger transcription factor Kaiso
922	2	317	2	952	g18252393	1.00E-115	BTB/POZ zinc finger transcription factor Xkai30

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
923	1	175	553	1077	g644871	6.00E-94	DNA/RNA-binding protein
923	1	175	553	1077	g551535	1.00E-92	transcription factor IIIA
923	1	175	553	1077	g1616942	4.00E-87	Xenopus transcription factor IIIA homologue
924	3	96	177	464	g5640017	4.00E-26	zinc finger protein ZFP113
924	3	96	177	464	g16552172	6.00E-26	unnamed protein product
924	3	96	177	464	g7020166	7.00E-26	unnamed protein product
925	2	114	413	754	g12853416	4.00E-24	KRAB box containing protein--data source:Pfam, source key:PF01352, evidence:ISS-putative
925	2	114	413	754	g13529497	8.00E-23	Unknown (protein for MGC:6652)
925	2	114	413	754	g4514561	1.00E-21	KRAB-containing zinc-finger protein KRAZ2
927	2	638	266	2179	g12804011	0	KIAA0798 gene product
927	2	638	266	2179	g3882317	0	KIAA0798 protein
927	2	638	266	2179	g18643896	0	zinc finger protein
928	2	162	107	592	g1488275	2.00E-44	zinc finger protein basonuclein
928	2	162	107	592	g179337	2.00E-44	basonuclein
928	2	162	107	592	g2408219	2.00E-44	basonuclein
929	2	365	41	1135	g1480005	1.00E-166	Zc4 protein
929	2	365	41	1135	g1208429	1.00E-120	Zc protein
929	2	365	41	1135	g6979926	1.00E-119	zic protein
930	3	375	54	1178	g488551	1.00E-118	zinc finger protein ZNF132
930	3	375	54	1178	g13543419	1.00E-118	Similar to zinc finger protein 304
930	3	375	54	1178	g1199604	1.00E-117	zinc finger protein C2H2-25
931	1	157	1	471	g12852573	2.00E-17	Zinc finger domain containing protein--data source:InterPro, source key:IPR000822, evidence:ISS-putative
931	1	157	1	471	g14250235	2.00E-17	RIKEN cDNA 4633401C23 gene
931	1	157	1	471	g340446	2.00E-17	zinc finger protein 7 (ZFP7)
932	3	257	3	773	g9502404	1.00E-110	Hypothetical zinc finger-like protein
932	3	257	3	773	g6002478	1.00E-110	BWSCR2 associated zinc-finger protein BAZ1
932	3	257	3	773	g5640019	1.00E-107	zinc finger protein ZFP235
933	3	359	3	1079	g10434142	1.00E-140	unnamed protein product
933	3	359	3	1079	g5817149	1.00E-140	hypothetical protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
933	3	359	3	1079	g498152	1.00E-139	ha0946 protein is Kruppel-related.
934	3	83	3	251	g5262560	5.00E-16	hypothetical protein
934	3	83	3	251	g13623607	6.00E-16	zinc finger protein 136 (clone pHZ-20)
934	3	83	3	251	g487785	6.00E-16	zinc finger protein ZNF136
935	3	239	3	719	g14042550	8.00E-44	unnamed protein product
935	3	239	3	719	g13937909	8.00E-44	Similar to KIAA0961 protein
935	3	239	3	719	g4589566	3.00E-40	KIAA0961 protein
936	1	407	1	1221	g2689444	1.00E-141	ZNF134
936	1	407	1	1221	g10440218	1.00E-130	unnamed protein product
937	1	482	1	1446	g16532223	1.00E-128	unnamed protein product
937	1	482	1	1446	g2689442	0	r28830_1
937	1	482	1	1446	g1572600	0	Zfk1
939	3	751	36	2288	g12652759	1.00E-176	hypothetical protein FLJ20557
939	3	751	36	2288	g18644082	0	Cezanne 2 protein
939	3	751	36	2288	g18644084	0	Cezanne 2 protein
939	3	751	36	2288	g9367763	0	zinc finger protein Cezanne
940	2	89	614	880	g15559591	5.00E-09	Unknown (protein for IMAGE:4564684)
940	2	89	614	880	g13359183	6.00E-09	KIAA1655 protein
940	2	89	614	880	g11493409	2.00E-08	PRO0898
941	3	628	162	2045	g12848204	0	data source:SPTR, source key:P52739, evidence:ISS-homolog to ZINC
941	3	628	162	2045	g493572	0	FINGER PROTEIN 131 (FRAGMENT)-putative
941	3	628	162	2045	g726284	5.00E-40	zinc finger protein ZNF131
942	2	582	173	1918	g1017722	0	polyomavirus late initiator promoter binding protein
942	2	582	173	1918	g7959207	0	repressor transcriptional factor
942	2	582	173	1918	g4559318	0	KIAA1473 protein
943	2	414	266	1507	g14602838	1.00E-140	BC273239_1
943	2	414	266	1507	g10442700	1.00E-140	zinc-finger protein ZBRK1
943	2	414	266	1507	g10435411	1.00E-140	zinc-finger protein ZBRK1
945	1	143	193	621	g14042882	2.00E-07	unnamed protein product
945	1	143	193	621	g10435738	4.00E-07	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
945	1	143	193	621	g5453423	2.00E-06	epstein-barr virus-induced zinc finger protein
946	3	143	147	575	g13937909	2.00E-28	Similar to KIAA0961 protein
946	3	143	147	575	g14042550	2.00E-28	unnamed protein product
946	3	143	147	575	g18044177	5.00E-28	Similar to hypothetical protein FUJ14779
947	3	564	33	1724	g8099348	0	zinc finger protein
947	3	564	33	1724	g15929737	1.00E-159	Similar to zinc finger protein 347
947	3	564	33	1724	g10436789	1.00E-155	unnamed protein product
948	2	564	305	1996	g2384653	0	Kueppel family zinc finger protein
948	2	564	305	1996	g4559318	1.00E-160	BC273239_1
948	2	564	305	1996	g38032	1.00E-156	ZNF43
949	1	680	88	2127	g16551429	0	unnamed protein product
949	1	680	88	2127	g13543419	0	Similar to zinc finger protein 304
949	1	680	88	2127	g5441615	0	zinc finger protein
950	2	520	98	1657	g18490277	0	Similar to zinc finger protein 223
950	2	520	98	1657	g6118383	0	zinc finger protein ZNF223
950	2	520	98	1657	g10835284	0	Zinc finger protein ZNF223
951	1	175	1	525	g16552123	1.00E-59	unnamed protein product
951	1	175	1	525	g6467206	3.00E-57	gonadotropin inducible transcription repressor-4
951	1	175	1	525	g12835831	5.00E-56	data source:SPR, source key:SQULZ5, evidence:ISS-homolog to GONADOTROPIN INDUCIBLE TRANSCRIPTION REPRESSOR-4-putative
952	3	91	657	929	g16550881	3.00E-36	unnamed protein product
952	3	91	657	929	g16551398	3.00E-36	unnamed protein product
952	3	91	657	929	g7959207	1.00E-35	KIAA1473 protein
953	1	868	1	2604	g498152	0	ha0946 protein is Kruppel-related.
953	1	868	1	2604	g11181880	0	ba1021Q19.1 (zinc finger protein 33a (KOX 31))
953	1	868	1	2604	g938238	0	ZNF118
954	3	396	3	1190	g10047297	0	KIAA1611 protein
954	3	396	3	1190	g10440398	0	FLJ00032 protein
954	3	396	3	1190	g15929737	0	Similar to zinc finger protein 347
955	1	97	322	612	g10435738	1.00E-15	unnamed protein product
955	1	97	322	612	g14042682	5.00E-11	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
955	1	97	322	612	g2317769	1.00E-09	probable zinc finger protein H101
956	1	362	16	1101	g14042190	0	unnamed protein product
956	1	362	16	1101	g9651765	0	zinc finger protein 289
956	1	362	16	1101	g13529563	0	RIKEN cDNA 2310032E02 gene
957	2	287	2	862	g6693371	1.00E-118	ZNF225
957	2	287	2	862	g6118387	1.00E-118	zinc finger protein ZNF225
957	2	287	2	862	g9502402	1.00E-118	ZNF225
958	2	134	173	574	g220637	5.00E-52	zinc finger protein
958	2	134	173	574	g5730196	2.00E-51	Kruppel-type zinc finger
958	2	134	173	574	g14456631	1.00E-50	cd54820.4 (novel KRAB box containing C2H2 type zinc finger protein)
959	3	139	3	419	g487785	2.00E-50	zinc finger protein ZNF136
959	3	139	3	419	g13623607	2.00E-50	zinc finger protein 136 (clone pHZ-20)
959	3	139	3	419	g13623354	5.00E-49	Similar to zinc finger protein 136 (clone pHZ-20)
960	2	146	62	499	g27393353	1.00E-55	ZNF91L
960	2	146	62	499	g7959207	8.00E-50	KIAA1473 protein
960	2	146	62	499	g3342002	1.00E-49	hematopoietic cell derived zinc finger protein
961	3	150	222	671	g7023216	1.00E-38	unnamed protein product
961	3	150	222	671	g10436789	6.00E-17	unnamed protein product
961	3	150	222	671	g7023703	7.00E-17	unnamed protein product
962	2	114	2	343	g3342002	7.00E-37	hematopoietic cell derived zinc finger protein
962	2	114	2	343	g7959207	2.00E-35	KIAA1473 protein
962	2	114	2	343	g186774	3.00E-35	zinc finger protein
963	3	114	81	422	g13938351	1.00E-23	Similar to zinc finger protein 268
963	3	114	81	422	g488557	4.00E-18	zinc finger protein ZNF137
963	3	114	81	422	g10436789	2.00E-15	unnamed protein product
964	1	149	1	447	g9502404	6.00E-28	Hypothetical zinc finger-like protein
964	1	149	1	447	g5640019	3.00E-17	zinc finger protein ZFP235
964	1	149	1	447	g13529452	2.00E-16	Similar to zinc finger protein 111
965	1	214	16	657	g15081398	1.00E-75	Kruppel-like zinc finger protein
965	1	214	16	657	g14456629	7.00E-66	cd54820.2 (novel KRAB box containing C2H2 type zinc finger protein)
965	1	214	16	657	g3702137	2.00E-48	cd733D15.1 (Zinc-finger protein)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
966	3	474	3	1424	g3511122	0	zinc finger protein
966	3	474	3	1424	g14043454	1.00E-139	Similar to zinc finger protein
966	3	474	3	1424	g10436218	1.00E-124	unnamed protein product
968	3	208	33	656	g498736	6.00E-84	zinc finger protein
968	3	208	33	656	g16551398	3.00E-82	unnamed protein product
968	3	208	33	656	g16304806	7.00E-82	zinc finger protein 43 (HF6)
969	2	752	1472	3727	g6088100	0	zinc finger protein (ZFD25)
969	2	752	1472	3727	g2739353	0	ZNF91L
969	2	752	1472	3727	g186774	0	zinc finger protein
970	2	106	170	487	g32071	1.00E-26	HF.10 finger protein (AA 1-491)
970	2	106	170	487	g1162933	1.00E-26	zinc finger protein
970	2	106	170	487	g15488944	1.00E-26	Similar to zinc finger protein 35 (clone HF.10)
971	3	158	159	632	g12483902	2.00E-36	zinc finger protein HF-10
971	3	158	159	632	g9963806	5.00E-22	zinc finger protein ZNF287
971	3	158	159	632	g6002480	9.00E-19	BWSCR2 associated zinc-finger protein BAZ2
972	2	373	2	1120	g2618752	1.00E-125	zinc finger protein
972	2	373	2	1120	g8571417	4.00E-45	zinc finger protein
972	2	373	2	1120	g6984172	4.00E-45	zinc finger protein ZNF226
973	1	270	100	909	g14042190	1.00E-137	unnamed protein product
973	1	270	100	909	g13529563	1.00E-123	RIKEN cDNA 2310032E02 gene
973	1	270	100	909	g9651765	1.00E-123	zinc finger protein 289
974	3	158	303	776	g15081398	3.00E-34	kruppel-like zinc finger protein
974	3	158	303	776	g14456629	2.00E-26	cl54820.2 (novel KRAB box containing C2H2 type zinc finger protein)
974	3	158	303	776	g6467204	5.00E-25	gonadotropin inducible transcription repressor-3
975	3	375	54	1178	g488851	1.00E-118	zinc finger protein ZNF132
975	3	375	54	1178	g13543419	1.00E-118	Similar to zinc finger protein 304
975	3	375	54	1178	g1199604	1.00E-117	zinc finger protein C2H2-25
976	1	321	190	1152	g12652727	1.00E-31	Unknown (protein for IMAGE:3352566)
976	1	321	190	1152	g1049301	5.00E-26	KRAB zinc finger protein; Method: conceptual translation supplied by
976	1	321	190	1152	g15080547	2.00E-25	Unknown (protein for MGC:21259)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
977	1	211	448	1080	g4309888	8.00E-54	similar to zinc finger proteins; similar to protein S47071 (PID:g631503); match to EST AA339462 (NID:g1991774)
977	1	211	448	1080	g9502403	5.00E-06	Hypothetical zinc finger-like protein
977	1	211	448	1080	g6467204	2.00E-05	gonadotropin inducible transcription repressor-3
978	2	445	140	1474	g14042293	0	unnamed protein product
978	2	445	140	1474	g12052983	0	hypothetical protein
978	2	445	140	1474	g5262560	1.00E-149	hypothetical protein
979	2	470	2	1411	g4159888	0	zinc finger protein from gene of uncertain exon structure; similar to G99676 (PID:g3025333)
979	2	470	2	1411	g488555	1.00E-128	zinc finger protein ZNF135
979	2	470	2	1411	g8453103	1.00E-125	zinc finger protein
980	1	479	1	1437	g186774	0	zinc finger protein
980	1	479	1	1437	g16306806	0	zinc finger protein 43 (HTF6)
980	1	479	1	1437	g38032	0	ZNF43
981	1	572	1	1716	g13543419	0	Similar to zinc finger protein 304
981	1	572	1	1716	g12652759	4.00E-94	hypothetical protein FLJ20557
981	1	572	1	1716	g7020745	4.00E-94	unnamed protein product
982	2	395	158	1342	g4235144	7.00E-95	BC39498_1
982	2	395	158	1342	g4235142	1.00E-94	BC39498_2
982	2	395	158	1342	g14042822	1.00E-94	unnamed protein product
983	3	132	3	398	g14043841	8.00E-42	Unknown (protein for MGC:14429)
983	3	132	3	398	g12052983	3.00E-41	hypothetical protein
983	3	132	3	398	g14042293	3.00E-41	unnamed protein product
984	2	340	377	1396	g5757625	4.00E-76	C2H2 zinc finger protein
984	2	340	377	1396	g3294544	4.00E-76	C2H2-type zinc finger protein
984	2	340	377	1396	g3294542	4.00E-76	C2H2-type zinc finger protein
985	2	202	2	607	g4235142	1.00E-36	BC39498_2
985	2	202	2	607	g14042822	1.00E-36	unnamed protein product
985	2	202	2	607	g4235144	1.00E-36	BC39498_1
986	2	369	2	1108	g13623607	1.00E-141	zinc finger protein 136 (clone pHZ-20)
986	2	369	2	1108	g487785	1.00E-141	zinc finger protein ZNF136



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
986	2	369	2	1108	g10436807	1.00E-135	unnamed protein product
987	1	185	1	555	g14042293	2.00E-71	unnamed protein product
987	1	185	1	555	g12052983	5.00E-69	hypothetical protein
987	1	185	1	555	g5262560	9.00E-70	hypothetical protein
988	3	137	132	542	g13543419	3.00E-13	Similar to zinc finger protein 304
988	3	137	132	542	g14249844	6.00E-13	Similar to hypothetical protein FLJ23233
988	3	137	132	542	g7020745	2.00E-12	unnamed protein product
989	1	487	1	1461	g1020145	0	DNA binding protein
989	1	487	1	1461	g18643896	0	zinc finger protein
989	1	487	1	1461	g14579579	0	ZNF2688
990	2	295	2	886	g13752754	1.00E-145	zinc finger 1111
990	2	295	2	886	g10440398	1.00E-118	FLJ00032 protein
990	2	295	2	886	g10047297	1.00E-118	KIAA1611 protein
991	3	100	309	608	g6760445	1.00E-14	Smad- and Olf-interacting zinc finger protein
991	3	100	309	608	g207696	4.00E-12	zinc finger protein
991	3	100	309	608	g18204060	2.00E-07	Unknown (protein for MGC:29358)
992	1	111	211	543	g7023703	2.00E-29	unnamed protein product
992	1	111	211	543	g7023216	2.00E-23	unnamed protein product
992	1	111	211	543	g7239109	4.00E-19	HSPC069
993	3	111	18	350	g16878329	1.00E-15	Unknown (protein for MGC:29628)
993	3	111	18	350	g12804415	1.00E-15	Similar to hypothetical protein FLJ10891
993	3	111	18	350	g7023216	1.00E-15	unnamed protein product
994	3	153	3	461	g5020362	2.00E-17	zinc finger protein dp
994	3	153	3	461	g17389328	2.00E-17	C2H2 (Kruppel-type) zinc finger protein
994	3	153	3	461	g5453423	2.00E-17	epstein-barr virus-induced zinc finger protein
995	1	214	1	642	g488555	5.00E-77	zinc finger protein ZNF135
995	1	214	1	642	g220637	7.00E-72	zinc finger protein
995	1	214	1	642	g16549180	1.00E-71	unnamed protein product
996	1	325	241	1215	g2085786	0	similar to zinc finger 5 protein from Gallus gallus, U51640 (PID:g1399185)
996	1	325	241	1215	g4454855	1.00E-164	zinc finger transcription factor Kalso
996	1	325	241	1215	g18252393	1.00E-114	B1B/POZ zinc finger transcription factor Xkalso

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
998	2	612	266	2101	g12804011	0	KIAA0798 gene product
998	2	612	266	2101	g3882317	0	KIAA0798 protein
998	2	612	266	2101	g14042330	0	unnamed protein product
999	3	375	54	1178	g488551	1.00E-118	zinc finger protein ZNF132
999	3	375	54	1178	g13543419	1.00E-118	Similar to zinc finger protein 304
999	3	375	54	1178	g1199604	1.00E-117	zinc finger protein C2H2-25
1000	1	81	580	822	g14250004	5.00E-08	Similar to cAMP responsive element binding protein-like 1
1000	1	81	580	822	g7021902	5.00E-08	unnamed protein product
1000	1	81	580	822	g7023820	2.00E-07	unnamed protein product
1001	1	663	757	2745	g16553661	0	unnamed protein product
1001	1	663	757	2745	g4164083	0	zinc finger protein EZNF
1001	1	663	757	2745	g2970038	0	HLK1
1002	3	280	84	923	g15081398	1.00E-110	Kruppel-like zinc finger protein
1002	3	280	84	923	g14456629	1.00E-90	cl54820.2 (novel KRAB box containing C2H2 type zinc finger protein)
1002	3	280	84	923	g3378094	1.00E-72	KRAB domain zinc finger protein
1003	1	211	1687	2319	g4559318	3.00E-88	BC273239.1
1003	1	211	1687	2319	g12052732	5.00E-87	hypothetical protein
1003	1	211	1687	2319	g16551398	3.00E-86	unnamed protein product
1004	1	518	193	1746	g16306806	0	zinc finger protein 43 (HTr6)
1004	1	518	193	1746	g38032	0	ZNF43
1004	1	518	193	1746	g186774	0	zinc finger protein
1005	2	147	2	442	g14042293	2.00E-79	unnamed protein product
1005	2	147	2	442	g12052983	1.00E-59	hypothetical protein
1005	2	147	2	442	g16552123	2.00E-54	unnamed protein product
1006	2	390	2	1171	g13938351	1.00E-161	Similar to zinc finger protein 268
1006	2	390	2	1171	g11917507	1.00E-157	HPF1 protein
1006	2	390	2	1171	g13752754	1.00E-156	zinc finger 1111
1007	2	196	2	589	g18490277	1.00E-120	Similar to zinc finger protein 223
1007	2	196	2	589	g10835284	1.00E-120	Zinc finger protein ZNF223
1007	2	196	2	589	g6118383	1.00E-104	zinc finger protein ZNF223
1008	2	163	83	571	g2739353	9.00E-82	ZNF91L

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1008	2	163	83	571	g186774	9.00E-69	zinc finger protein
1008	2	163	83	571	g7959207	7.00E-65	KIAA1473 protein
1009	1	214	1	642	g1017722	2.00E-91	repressor transcriptional factor
1009	1	214	1	642	g16041769	2.00E-91	Unknown (protein for MGC:23189)
1009	1	214	1	642	g2723316	3.00E-91	Zinc-finger protein
1011	2	163	143	631	g1480005	9.00E-48	Zic4 protein
1011	2	163	143	631	g4028592	1.00E-33	ZIC2 protein
1011	2	163	143	631	g1345413	1.00E-33	Zic2 protein
1012	3	257	3	773	g9602404	1.00E-110	Hypothetical zinc finger-like protein
1012	3	257	3	773	g6002478	1.00E-110	BWSCR2 associated zinc-finger protein BAZ1
1012	3	257	3	773	g5640019	1.00E-107	zinc finger protein ZFP235
1013	2	242	80	805	g14042550	8.00E-44	unnamed protein product
1013	2	242	80	805	g13937909	8.00E-44	Similar to KIAA0961 protein
1013	2	242	80	805	g4589566	3.00E-40	KIAA0961 protein
1014	3	314	819	1760	g14042253	0	unnamed protein product
1014	3	314	819	1760	g14042715	1.00E-177	unnamed protein product
1014	3	314	819	1760	g7023417	1.00E-176	unnamed protein product
1015	2	233	2	700	g14042590	1.00E-144	unnamed protein product
1015	2	233	2	700	g15928783	1.00E-143	hypothetical protein MGC13071
1015	2	233	2	700	g5262557	2.00E-84	hypothetical protein
1016	3	219	3	659	g14042850	1.00E-47	unnamed protein product
1016	3	219	3	659	g12805201	1.00E-32	Similar to zinc finger protein 97
1016	3	219	3	659	g12843503	3.00E-16	data source: SPTB, source key: G9H7R5, evidence: ISS-homolog to CDNA FLJ14345 FS, CLONE THYRO1001189, WEAKLY SIMILAR TO ZINC-FINGER PROTEIN 91-putative
1017	1	666	1	1998	g7280338	0	UIM domain ZNF185 peptide
1017	1	666	1	1998	g2370126	0	UIM-domain protein
1017	1	666	1	1998	g7619724	1.00E-77	Zinc finger protein 185
1019	1	393	25	1203	g1226235	1.00E-141	Ac39/physophillin
1019	1	393	25	1203	g3955100	1.00E-141	vacuolar adenosine triphosphatase subunit D
1019	1	393	25	1203	g736727	1.00E-141	32 kd accessory protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1020	3	104	51	362	g12859507	1.00E-48	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit g-data source:MGD, source key:MG1:1351597, evidence:ISS-putative
1020	3	104	51	362	g12859498	1.00E-48	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit g-data source:MGD, source key:MG1:1351597, evidence:ISS-putative
1020	3	104	51	362	g12859469	1.00E-48	ATP synthase, H <sup>+</sup> transporting, mitochondrial F0 complex, subunit g-data source:MGD, source key:MG1:1351597, evidence:ISS-putative
1021	3	319	3	959	g4455609	1.00E-147	cu742C19.5 (Chromobax homolog 7)
1021	3	319	3	959	g18204009	4.00E-42	Unknown (protein for MGC:29271)
1021	3	319	3	959	g2317723	2.00E-30	Polycomb 2 homolog
1022	1	337	406	1416	g9622335	0	two-pore domain potassium channel TREK-1
1022	1	337	406	1416	g5712621	0	TREK-1 potassium channel
1022	1	337	406	1416	g4584799	0	TREK-1 K <sup>+</sup> channel subunit
1023	1	598	1	1794	g3789785	0	yolk sac permease-like molecule 3
1023	1	598	1	1794	g15420631	0	sodium dependent vitamin C transporter 1
1023	1	598	1	1794	g11125153	0	sodium-dependent vitamin C transporter
1024	1	528	286	1869	g1665759	0	Similar to Schistosoma mansoni amino acid permease (255068).
1024	1	528	286	1869	g4581435	0	SLC7A7
1024	1	528	286	1869	g3982910	0	Y-L amino acid transporter-1
1025	2	82	593	838	g1177607	4.00E-16	pval
1025	2	82	593	838	g7019976	2.00E-11	unnamed protein product
1025	2	82	593	838	g14388331	6.00E-10	hypothetical protein
1027	1	151	1	453	g8927560	4.00E-63	glucose transporter 3
1027	1	151	1	453	g306821	4.00E-63	glucose transporter-like protein
1027	1	151	1	453	g529030	1.00E-58	neuron glucose transporter 3
1028	1	651	1	1953	g12852467	0	data source:SPTR, source key:O88576, evidence:ISS-putative-similar to SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER XTRP2
1028	1	651	1	1953	g3347922	0	orphan transporter isoform A12
1028	1	651	1	1953	g531469	0	renal osmotic stress-induced Na-Cl organic solute cotransporter
1029	2	77	20	250	g7020440	5.00E-08	unnamed protein product
1029	2	77	20	250	g6690252	1.00E-07	PRO0663
1029	2	77	20	250	g3002527	2.00E-07	neuronal thread protein AD7c-NTP

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1030	1	1107	1	3321	g184039	0	sodium channel alpha subunit
1030	1	1107	1	3321	g15072487	0	voltage-gated sodium channel type V alpha subunit jejunal variant
1030	1	1107	1	3321	g6782382	0	voltage-gated sodium channel
1031	2	186	254	811	g4165326	2.00E-81	plasma membrane calcium ATPase isoform 1
1031	2	186	254	811	g203047	1.00E-79	ATPase
1031	2	186	254	811	g553195	1.00E-57	calcium ATPase C
1034	2	197	1253	1843	g17512130	4.00E-21	Unknown (protein for MGC:20634)
1034	2	197	1253	1843	g12711199	2.00E-20	unnamed protein product
1034	2	197	1253	1843	g7018306	2.00E-20	glucose transporter
1035	1	282	55	900	g567250	1.00E-153	human aquaporin-2 water channel
1035	1	282	55	900	g474059	1.00E-153	water channel aquaporin-2
1035	1	282	55	900	g5052748	1.00E-153	aquaporin 2
1038	1	211	1	633	g4455609	1.00E-117	dJ742C19.5 (chromobox homolog 7)
1038	1	211	1	633	g18204009	7.00E-31	Unknown (protein for MGC:29271)
1039	2	117	2	352	g2587023	5.00E-27	HERV-E integrase
1039	2	117	2	352	g1049231	5.00E-27	Method: conceptual translation supplied by author, putative hybrid protein similar to HERV-H protease and HERV-E integrase
1039	2	117	2	352	g2587026	5.00E-27	HERV-E integrase
1040	1	190	1	570	g12313899	9.00E-93	dJ1003J2.3.2 (potassium voltage-gated channel, Shaw-related subfamily, member 4)
1040	1	190	1	570	g57649	1.00E-88	voltage-gated potassium channel
1040	1	190	1	570	g338077	4.00E-52	potassium channel protein
1042	3	386	3	1160	g18088929	0	Similar to channel-interacting PDZ domain protein
1042	3	386	3	1160	g3108057	0	channel interacting PDZ domain protein
1042	3	386	3	1160	g11933155	1.00E-119	PDZ domain protein 3' variant 4
1044	2	92	215	490	g441200	8.00E-39	calpain
1044	2	92	215	490	g495222	8.00E-39	calpain
1044	2	92	215	490	g16303243	3.00E-36	stomach specific calpain nCL-2
1046	1	307	1	921	g5923786	4.00E-21	zinc metalloprotease ADAMTS6
1046	1	307	1	921	g14134925	1.00E-17	unnamed protein product
1046	1	307	1	921	g11935122	2.00E-17	papilin

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1047	2	122	113	478	g2443873	7.00E-64	CAN5_Human
1047	2	122	113	478	g1905903	7.00E-64	calcium-dependent protease, small (regulatory) subunit (calpain)
1047	2	122	113	478	g18314496	7.00E-64	(calcium-activated neutral proteinase) (CANP)
1048	3	531	426	2018	g306886	0	calpain, small subunit 1
1048	3	531	426	2018	g15422560	0	hepsin (serine protease) precursor
1048	3	531	426	2018	g32064	0	Nucleotide sequence encoding human hepsin
1049	2	156	71	538	g15012124	2.00E-41	hepsin
1049	2	156	71	538	g5921601	4.00E-40	Similar to distal intestinal serine protease
1049	2	156	71	538	g4336619	6.00E-27	distal intestinal serine protease
1050	3	537	42	1652	g1199598	0	most cell trypsin beta 1
1050	3	537	42	1652	g13366579	0	cyclophilin-like protein CYP-60
1050	3	537	42	1652	g12844270	0	Similar to peptidylprolyl isomerase (cyclophilin)-like 2
1051	2	77	293	523	g1389766	6.00E-14	data source:SPTR, source key:Q13356, evidence:ISS-homolog to
1051	2	77	293	523	g6855613	4.00E-13	CYCLOPHILIN-LIKE PROTEIN CYP-60-putative
1051	2	77	293	523	g9929935	3.00E-10	unknown
1052	1	1037	43	3153	g5809678	0	PRO0974
1052	1	1037	43	3153	g2293556	0	hypothetical protein
1052	1	1037	43	3153	g857368	0	sperm membrane protein BS-63
1053	1	478	1	1434	g15620895	0	Ran binding protein 2
1053	1	478	1	1434	g971459	0	nucleoporin
1053	1	478	1	1434	g304259	0	KIAA1918 protein
1055	1	254	133	894	g16306743	1.00E-141	UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase
1055	1	254	133	894	g1117968	1.00E-141	UDP-GalNAc:polypeptide, N-acetylgalactosaminyltransferase
1055	1	254	133	894	g1770526	1.00E-141	CARS-Cyp
1056	1	222	1	666	g441200	1.00E-111	SRECP protein
1056	1	222	1	666	g495222	1.00E-111	calpain
1056	1	222	1	666	g16303243	1.00E-109	calpain
1057	2	306	128	1045	g10303335	1.00E-127	stomach specific calpain nCL-2
1057	2	306	128	1045	g10303330	1.00E-127	calpain 12

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1057	2	306	128	1045	g10303329	1.00E-127	calpain 12
1058	2	327	398	1378	g441200	1.00E-156	calpain
1058	2	327	398	1378	g495222	1.00E-156	calpain
1058	2	327	398	1378	g16303243	1.00E-148	stomach specific calpain nCL-2
1061	2	293	173	1051	g13183078	1.00E-166	a disintegrin-like and metalloprotease domain with thrombospondin type I motifs-like 3
1061	2	293	173	1051	g15593890	1.00E-165	unnamed protein product
1061	2	293	173	1051	g15593888	1.00E-161	unnamed protein product
1062	2	261	2	784	g18098062	7.00E-61	unnamed protein product
1062	2	261	2	784	g18098059	7.00E-61	unnamed protein product
1062	2	261	2	784	g11493589	4.00E-60	zinc metalloendopeptidase
1063	3	114	324	665	g1619837	5.00E-18	collagen-like protein
1063	3	114	324	665	g2275260	4.00E-15	tracfin
1063	3	114	324	665	g331008	1.00E-12	gene products
1064	3	198	48	641	g13182747	1.00E-107	microsomal signal peptidase subunit
1064	3	198	48	641	g16307229	1.00E-107	Unknown (protein for MG:9299)
1064	3	198	48	641	g164084	1.00E-106	signal peptidase 21 kDa subunit
1065	2	261	758	1540	g521218	1.00E-144	trypsinogen
1065	2	261	758	1540	g1552517	1.00E-144	trypsinogen E
1065	2	261	758	1540	g2275595	1.00E-144	anionic trypsinogen
1066	1	348	1	1044	g557646	0	meprin a
1066	1	348	1	1044	g957204	1.00E-153	meprin beta-subunit
1066	1	348	1	1044	g387871	1.00E-152	meprin beta-subunit
1067	2	69	200	406	g202857	2.00E-05	alpha-1-macroglobulin
1067	2	69	200	406	g205384	2.00E-05	alpha-1-macroglobulin
1067	2	69	200	406	g199086	4.00E-05	alpha-2-macroglobulin
1068	3	346	39	1076	g15593888	0	unnamed protein product
1068	3	346	39	1076	g15593890	0	unnamed protein product
1068	3	346	39	1076	g13183078	1.00E-160	a disintegrin-like and metalloprotease domain with thrombospondin type I motifs-like 3
1069	3	310	381	1310	g6525045	2.00E-71	thyroxine-binding globulin

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1069	3	310	381	1310	g6525043	5.00E-71	thyroxine-binding globulin
1069	3	310	381	1310	g405514	1.00E-69	thyroxine-binding globulin
1070	1	62	322	507	g10434899	2.00E-11	unnamed protein product
1070	1	62	322	507	g2224695	3.00E-11	KIAA0377
1070	1	62	322	507	g11493483	6.00E-11	PRO2550
1071	3	400	3	1202	g13183078	0	a disintegrin-like and metalloprotease domain with thrombospondin type I motifs-like 3
1071	3	400	3	1202	g15593890	0	unnamed protein product
1071	3	400	3	1202	g15593888	0	unnamed protein product
1072	3	100	3	302	g12804335	2.00E-33	Unknown (protein for IMAGE:2823490)
1072	3	100	3	302	g6651171	1.00E-28	cyclophilin 18
1072	3	100	3	302	g30309	1.00E-28	cyclophilin (AA 1-165)
1074	3	436	60	1367	g1235672	0	metalloprotease/disintegrin/cysteine-rich protein precursor
1074	3	436	60	1367	g1235676	0	metalloprotease/disintegrin/cysteine rich protein precursor
1074	3	436	60	1367	g6630618	1.00E-179	KIAA0021 protein
1075	3	410	12	1241	g903934	0	cysteine protease
1075	3	410	12	1241	g886050	0	Ich-2
1075	3	410	12	1241	g4096346	0	Mih1/TX isoform alpha
1076	3	222	516	1181	g17390251	9.00E-79	ubiquitin specific protease 3
1076	3	222	516	1181	g16877850	9.00E-79	Similar to ubiquitin specific protease 3
1076	3	222	516	1181	g4689128	9.00E-79	SIH003
1078	2	62	329	514	g288145	4.00E-07	put. ORF
1078	2	62	329	514	g6690248	1.00E-06	PRO0657
1078	2	62	329	514	g9955914	7.00E-05	platelet glycoprotein VI-3
1080	3	685	3	2057	g3776076	0	poly(A)-specific ribonuclease
1080	3	685	3	2057	g9997509	0	unnamed protein product
1080	3	685	3	2057	g18256918	0	poly(A)-specific ribonuclease (deadenylation nuclease)
1081	2	169	119	625	g1263081	2.00E-77	maternal transposase
1081	2	169	119	625	g3005702	1.00E-76	unknown
1081	2	169	119	625	g2231380	1.00E-75	orf; encodes putative chimeric protein with SET domain in N-terminus with similarity to several other human, Drosophila, nematode and yeast



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1082	2	170	2	511	g14141216	2.00E-83	SRP46 splicing factor
1082	2	170	2	511	g13544107	2.00E-83	Similar to splicing factor, arginine/serine-rich 2 (SC-35)
1082	2	170	2	511	g14141201	2.00E-83	SRP46 splicing factor
1083	2	101	893	1195	g619863	1.00E-16	DNA helicase
1084	3	117	228	578	g37543	9.00E-29	C protein (AA 1-159)
1084	3	117	228	578	g1562574	9.00E-29	U1 snRNP-specific protein C
1084	3	117	228	578	g14198360	9.00E-29	U1 small nuclear ribonucleoprotein 1C
1087	2	231	323	1015	g31395	3.00E-87	fibritarin
1087	2	231	323	1015	g18044582	3.00E-87	Unknown (protein for IMAGE:4538098)
1087	2	231	323	1015	g17939435	3.00E-87	fibritarin
1088	2	147	431	871	g605	2.00E-58	polynucleotide adenylyltransferase
1088	2	147	431	871	g1377872	2.00E-58	poly(A) polymerase V
1089	2	108	464	787	g1377870	2.00E-58	poly(A) polymerase VI
1091	3	390	48	1217	g12698135	4.00E-32	hypothetical protein
1091	3	390	48	1217	g182177	2.00E-82	excision repair protein
1091	3	390	48	1217	g182174	2.00E-82	excision repair protein
1092	2	305	110	1024	g3005587	2.00E-95	Ser/Arg-related nuclear matrix protein
1092	2	305	110	1024	g3153821	6.00E-91	plenty-of-prolines-101; POP101; SH3-philo-protein
1092	2	305	110	1024	g530876	7.00E-24	amino acid feature: Rod protein domain, aa 266 .. 468; amino acid feature: globular protein domain, aa 32 .. 265
1093	2	108	2	325	g2231380	4.00E-33	orf; encodes putative chimeric protein with SET domain in N-terminus with similarity to several other human, Drosophila, nematode and yeast
1093	2	108	2	325	g3005702	4.00E-33	unknown
1093	2	108	2	325	g1263081	2.00E-32	mariner transposase
1098	1	680	1	2040	g6488786	1.00E-167	mouse fat 1 cadherin
1098	1	680	1	2040	g1107887	1.00E-165	homologue of Drosophila Fat protein
1098	1	680	1	2040	g4426629	1.00E-165	protocadherin
1099	3	516	3	1550	g7023112	1.00E-163	unnamed protein product
1099	3	516	3	1550	g6807875	1.00E-163	hypothetical protein
1099	3	516	3	1550	g16550856	1.00E-157	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1100	3	1042	420	3545	g14388339	0	hypothetical protein
1100	3	1042	420	3545	g9845485	0	protocadherin-9
1100	3	1042	420	3545	g13874450	0	hypothetical protein
1101	3	198	951	1544	g4699892	7.00E-77	integrin alpha 7 chain
1101	3	198	951	1544	g3930583	7.00E-77	integrin alpha-7
1101	3	198	951	1544	g2897116	7.00E-77	integrin alpha-7
1105	3	142	3	428	g33742	4.00E-61	immunoglobulin lambda light chain
1105	3	142	3	428	g32813	2.00E-56	immunoglobulin light chain precursor
1105	3	142	3	428	g33724	2.00E-56	immunoglobulin lambda light chain
1106	2	93	2	280	g567121	2.00E-42	immunoglobulin heavy chain
1106	2	93	2	280	g464043	2.00E-35	immunoglobulin mu chain
1106	2	93	2	280	g567127	2.00E-33	immunoglobulin heavy chain
1107	3	153	3	461	g3170879	5.00E-56	immunoglobulin heavy chain variable region
1107	3	153	3	461	g185337	1.00E-55	Ig heavy chain
1107	3	153	3	461	g185335	2.00E-55	Ig heavy chain
1108	1	141	1	423	g185985	9.00E-67	immunoglobulin kappa light chain VC region
1108	1	141	1	423	g185043	2.00E-64	immunoglobulin light chain variable region
1108	1	141	1	423	g3954893	8.00E-64	immunoglobulin kappa light chain
1109	1	112	1	336	g16974102	2.00E-52	anti-peptide/MHC complex HLA-A1/MAGE-A1 monoclonal antibody heavy chain
1109	1	112	1	336	g10183778	2.00E-48	unnamed protein product
1109	1	112	1	336	g11275324	9.00E-47	anti HBs antibody heavy-chain Fab fragment
1111	1	171	1	513	g3954893	2.00E-74	immunoglobulin kappa light chain
1111	1	171	1	513	g2765423	2.00E-71	immunoglobulin kappa light chain
1111	1	171	1	513	g17645750	3.00E-71	unnamed protein product
1114	3	280	576	1415	g11121545	1.00E-158	dJ324O17.1.1 (A novel protein, isoform 1)
1114	3	280	576	1415	g11121544	1.00E-130	dJ324O17.1.2 (A novel protein similar to Drosophila CG11840, isoform2)
1114	3	280	576	1415	g13185197	1.00E-130	unnamed protein product
1115	3	285	363	1217	g17045936	1.00E-154	unnamed protein product
1115	3	285	363	1217	g17045933	1.00E-154	unnamed protein product
1115	3	285	363	1217	g557288	2.00E-35	protein tyrosine phosphatase 1E

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1117	1	238	4	717	g16741061	1.00E-120	Similar to immunoglobulin kappa constant
1117	1	238	4	717	g17644683	1.00E-119	unnamed protein product
1117	1	238	4	717	g17645754	1.00E-119	unnamed protein product
1119	1	59	1	177	g2344986	5.00E-19	IgM heavy chain VH1 region precursor
1119	1	59	1	177	g5834046	5.00E-19	immunoglobulin heavy chain variable region
1119	1	59	1	177	g16075463	1.00E-18	immunoglobulin heavy chain variable region
1120	1	65	1	195	g9357869	7.00E-09	immunoglobulin heavy chain variant
1120	1	65	1	195	g3819788	7.00E-09	immunoglobulin heavy chain, constant region, alpha-2 subunit
1120	1	65	1	155	g184761	7.00E-09	immunoglobulin alpha-2 heavy chain
1121	1	73	1	219	g4512302	4.00E-25	immunoglobulin heavy chain variable region
1121	1	73	1	219	g33627	4.00E-25	immunoglobulin heavy chain
1121	1	73	1	219	g3170891	4.00E-25	immunoglobulin heavy chain variable region
1123	1	110	151	480	g33742	2.00E-25	immunoglobulin lambda light chain
1123	1	110	151	480	g33724	2.00E-24	immunoglobulin lambda light chain
1123	1	110	151	480	g1864141	7.00E-23	Ig lambda chain V-region
1124	2	330	482	1471	g2980663	1.00E-129	FSH
1124	2	330	482	1471	g15706263	1.00E-129	putative
1124	2	330	482	1471	g15706263	1.00E-129	OZ7.1.1 (tromodomain-containing protein 2 (RING3, KIAA9001), isoform 1)
1125	2	231	2	694	g18042965	1.00E-89	Unknown (protein for IMAGE:3451144)
1125	2	231	2	694	g12847527	7.00E-39	data source:MGD, source key:MGI:1931352, evidence:ISS-prostate
1125	2	231	2	694	g3462515	5.00E-37	cancer overexpressed gene 1-putative
1127	1	88	19	282	g1043752	4.00E-05	PB39
1129	3	240	3	722	g583510	1.00E-126	unnamed protein product
1129	3	240	3	722	g17644679	1.00E-122	3D6 antibody light chain
1129	3	240	3	722	g17645750	1.00E-122	unnamed protein product
1130	1	97	1	291	g5833974	9.00E-38	unnamed protein product
1130	1	97	1	291	g3170819	2.00E-37	immunoglobulin heavy chain variable region precursor
1130	1	97	1	291	g560840	2.00E-37	immunoglobulin heavy chain variable region
1131	3	626	147	2024	g14042044	0	anti-Sm antibody VH chain (VH1/DK1 or DM1/JH4b)
1131	3	626	147	2024	g15779199	0	unnamed protein product
1131	3	626	147	2024	g15779199	0	NG22 protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1131	3	626	147	2024	g4529890	0	NG22
1132	2	85	2	256	g12655666	2.00E-19	immunoglobulin kappa chain variable region
1132	2	85	2	256	g12655503	2.00E-19	immunoglobulin kappa chain variable region
1132	2	85	2	256	g619601	6.00E-19	immunoglobulin kappa light chain V region
1133	1	63	1	189	g567128	1.00E-24	immunoglobulin heavy chain
1133	1	63	1	189	g567121	1.00E-24	immunoglobulin heavy chain
1133	1	63	1	189	g567127	6.00E-23	immunoglobulin heavy chain
1134	2	252	2	757	g583510	1.00E-109	3D6 antibody light chain
1134	2	252	2	757	g17644679	1.00E-109	unnamed protein product
1134	2	252	2	757	g17645750	1.00E-109	unnamed protein product
1135	2	247	8	748	g413215	1.00E-101	Y22 light chain
1135	2	247	8	748	g492350	1.00E-101	Y22 light chain antitibin antibody
1136	2	247	8	748	g4768677	1.00E-101	kappa 1 immunoglobulin light chain
1136	1	129	1	387	g34427	5.00E-53	immunoglobulin gamma light chain variable region
1136	1	129	1	387	g33715	5.00E-53	lg light chain V11 region
1137	2	228	446	1129	g30184	1.00E-102	11beta-hydroxylase precursor
1137	2	228	446	1129	g1263088	1.00E-101	steroid 11-beta-hydroxylase
1138	2	625	446	2320	g9964003	0	11beta hydroxylase
1138	2	625	446	2320	g11414998	0	NADPH-cytochrome P450 reductase
1138	2	625	446	2320	g247307	0	NADPH-cytochrome P-450 reductase
1140	1	103	1	309	g12858580	5.00E-37	cytochrome c oxidase, subunit Va--data source:MCD, source key:MGI:88474, evidence:ISS-putative
1140	1	103	1	309	g50527	5.00E-37	cytochrome c oxidase subunit Va preprotein
1140	1	103	1	309	g55971	1.00E-36	cytochrome c oxidase subunit Va preprotein
1141	3	226	21	698	g12836111	2.00E-96	data source:MCD, source key:MGI:102849, evidence:ISS-kallikrein B, plasma 1-putative
1141	3	226	21	698	g13161409	2.00E-96	family 4 cytochrome P450
1141	3	226	21	698	g7331756	1.00E-36	Hypothetical protein Y17G98.3
1142	1	103	178	486	g9280553	5.00E-42	thioredoxin 2

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1142	1	103	178	486	g1809135	5.00E-42	thioredoxin
1142	1	103	178	486	g15489245	5.00E-42	Unknown (protein for MGC:5312)
1143	1	93	190	468	g4092857	5.00E-39	cytochrome c oxidase subunit IV precursor
1143	1	93	190	468	g2738492	5.00E-39	cytochrome c oxidase subunit IV precursor
1143	1	93	190	468	g1913896	5.00E-39	cytochrome c oxidase subunit IV
1144	3	155	30	494	g15680169	6.00E-84	cytochrome b5 outer mitochondrial membrane precursor
1144	3	155	30	494	g13325120	1.00E-81	Unknown (protein for MGC:10477)
1144	3	155	30	494	g2662291	3.00E-81	cytochrome b5
1145	2	185	3512	4066	g1263287	3.00E-05	fibrin-3
1148	1	124	193	564	g178841	4.00E-52	apolipoprotein D precursor
1148	1	124	193	564	g13938509	4.00E-52	apolipoprotein D
1148	1	124	193	564	g178847	4.00E-52	apolipoprotein D precursor
1151	1	315	259	1203	g14017771	0	fibrillin3
1151	1	315	259	1203	g762831	1.00E-144	fibrillin-2
1151	1	315	259	1203	g4959652	1.00E-144	fibrillin-2
1152	3	175	3	527	g5102836	1.00E-17	bk150C2.5 (PUTATIVE novel protein similar to APOBEC1 (Apolipoprotein B mRNA editing protein) and Phorbollin)
1152	3	175	3	527	g4097433	2.00E-16	phorbollin-1-related protein
1152	3	175	3	527	g5102831	2.00E-16	bk150C2.2 (Phorbollin 3)
1153	1	760	103	2382	g5306260	1.00E-62	hypothetical protein
1153	1	760	103	2382	g11994733	3.00E-57	contains similarity to cell wall-plasma membrane linker protein-gene_id:MKA23.5
1153	1	760	103	2382	g5305335	3.00E-45	proline-rich mucin homolog
1154	3	285	3	857	g29462	1.00E-155	extracellular matrix protein BM-40 (AA 1 - 303)
1154	3	285	3	857	g15524596	1.00E-155	unnamec protein product
1154	3	285	3	857	g14124970	1.00E-155	secreted protein, acidic, cysteine-rich (osteonectin)
1155	2	308	191	1114	g348912	1.00E-135	glycoprotein
1155	2	308	191	1114	g14919433	1.00E-135	Similar to chitinase 3-like 1 (cartilage glycoprotein-39)
1155	2	308	191	1114	g2121310	1.00E-135	GP-39 cartilage protein
1156	3	386	2094	3251	g2388555	0	alpha2(I) collagen
1156	3	386	2094	3251	g1418930	0	prepro-alpha2(I) collagen

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1156	3	386	2094	3251	g2735715	0	pro-alpha 2(I) collagen
1157	3	155	570	1034	g49492	1.00E-86	adenylate cyclase-stimulatory G-protein (AA 1-394)
1157	3	155	570	1034	g4262551	1.00E-86	G-protein XLaiphas
1157	3	155	570	1034	g4206785	1.00E-86	guanine nucleotide-binding protein
1159	1	378	139	1272	g508729	0	thymopoietin gamma
1159	1	378	139	1272	g3283900	0	thymopoietin gamma
1159	1	378	139	1272	g1335847	1.00E-177	thymopoietin gamma
1160	1	961	1768	4650	g14017771	0	fibrillin3
1160	1	961	1768	4650	g437972	0	fibrillin-2
1160	1	961	1768	4650	g762831	0	fibrillin 2
1161	3	331	3	995	g505053	1.00E-105	lysosomal acid lipase
1161	3	331	3	995	g460143	1.00E-105	lysosomal acid lipase/cholesteryl ester hydrolase
1161	3	331	3	995	g434306	1.00E-105	sterol esterase
1162	2	97	1235	1525	g14789779	2.00E-05	RIKEN cDNA 270055X07 gene
1162	2	97	1235	1525	g12844772	2.00E-05	data source:SPTR, source key:G9Y6H0, evidence:ISS-homolog to BRAIN
1162	2	97	1235	1525	g12849178	2.00E-05	data source:SPTR, source key:G9Y6H0, evidence:ISS-homolog to BRAIN
1163	2	265	23	817	g5917666	8.00E-08	SPECIFIC PROTEIN-putative
1163	2	265	23	817	g7270175	1.00E-07	extensin-like protein
1163	2	265	23	817	g3063699	1.00E-07	putative protein kinase
1164	2	445	791	2125	g14017771	0	putative protein
1164	2	445	791	2125	g437972	1.00E-142	fibrillin3
1164	2	445	791	2125	g762831	1.00E-142	fibrillin-2
1165	3	212	945	1580	g530878	3.00E-07	amino acid feature: N-glycosylation sites, aa 41 .. 43, 46 .. 48, 51 .. 53, 72 .. 74, 107 .. 109, 128 .. 130, 132 .. 134, 158 .. 160, 163 .. 165; amino acid feature: Rod protein domain, aa 169 .. 340; amino acid feature: globular protein domain, aa 32 .. 168
1165	3	212	945	1580	g17940758	4.00E-07	cask-interacting protein 1
1165	3	212	945	1580	g7242967	4.00E-07	KIAA1306 protein
1166	2	366	3683	4780	g4755085	0	pro alpha 1(I) collagen

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1166	2	366	3683	4780	g1418928	0	prepro-alpha 1(I) collagen
1166	2	366	3683	4780	g14596603	0	unnamed protein product
1167	3	602	39	1844	g307082	0	keratin type II
1167	3	602	39	1844	g9739763	0	keratin 5
1167	3	602	39	1844	g13904996	0	Unknown (protein for MGC:8116)
1169	2	98	29	322	g7689897	4.00E-34	myosin light chain-2
1169	2	98	29	322	g2460247	4.00E-34	cardiac ventricular myosin light chain 2
1169	2	98	29	322	g16198355	4.00E-34	myosin, light polypeptide 2, regulatory, cardiac, slow
1170	2	101	2	304	g56703	1.00E-39	myosin RLC-B
1170	2	101	2	304	g473731	1.00E-39	myosin regulatory light chain
1170	2	101	2	304	g2605594	1.00E-39	myosin regulatory light chain
1171	3	2141	75	6497	g338441	0	beta-spectrin
1171	3	2141	75	6497	g338440	0	spectrin Rouen (beta-220-218) mutant coding sequence
1171	3	2141	75	6497	g440900	0	beta-spectrin
1172	3	187	3	563	g509201	7.00E-91	cofilin
1172	3	187	3	563	g12851520	2.00E-90	cofilin 1, non-muscle--data source:MGD, source key:MG1:101757, evidence:ISS-putative
1172	3	187	3	563	g220384	2.00E-90	cofilin
1173	1	1259	3808	7584	g3550977	0	beta-spectrin III
1173	1	1259	3808	7584	g3452553	0	brain beta 3 spectrin
1173	1	1259	3808	7584	g3550975	0	beta-spectrin III
1174	1	173	1	519	g1419370	5.00E-74	actin depolymerizing factor
1174	1	173	1	519	g10441256	7.00E-46	actin-depolymerizing factor 1
1174	1	173	1	519	g14906219	7.00E-46	actin-depolymerizing factor 1
1176	1	59	1	177	g14250822	3.00E-22	kinesin 2 (60-70kD)
1176	1	59	1	177	g3347846	8.00E-21	kinesin light chain 1
1176	1	59	1	177	g1208772	4.00E-20	kinesin light chain
1177	1	188	52	615	g13278858	1.00E-104	dyncactin 4
1177	1	188	52	615	g14042028	1.00E-104	unnamed protein product
1177	1	188	52	615	g6176550	1.00E-104	dyncactin subunit p25
1178	2	876	566	3193	g7959303	0	KIAA1518 protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1178	2	876	566	3193	g10435224	0	unnamed protein product
1178	2	876	566	3193	g16307401	0	Unknown (protein for MGC:12143)
1180	3	542	216	1841	g2072425	0	non-lens beta gamma-crystallin like protein
1180	3	542	216	1841	g14626963	0	cd448k1.1.2 (absent in melanoma 1, isoform 2)
1180	3	542	216	1841	g14626964	1.00E-176	cd448k1.1.1 (absent in melanoma 1, isoform 1)
1181	2	690	2	2071	g178052	0	alpha-actinin
1181	2	690	2	2071	g16041771	0	actinin, alpha 1
1181	2	690	2	2071	g13097756	0	actinin, alpha 1
1182	1	228	112	795	g13506797	1.00E-117	myosin-VIb
1182	1	228	112	795	g9944235	3.00E-91	myosin VIIA
1182	1	228	112	795	g9944237	3.00E-91	myosin VIIA
1183	1	322	1	966	g1526432	0	neutral calponin
1183	1	322	1	966	g17391137	1.00E-171	calponin 2
1183	1	322	1	966	g14318693	1.00E-171	calponin 2
1184	2	287	1076	1936	g9739163	1.00E-148	keratin 5
1184	2	287	1076	1936	g307082	1.00E-148	keratin type II
1184	2	287	1076	1936	g386850	1.00E-147	keratin K5
1185	1	59	1	177	g14250822	3.00E-22	knesin 2 (60-70kD)
1185	1	59	1	177	g3347846	8.00E-21	knesin light chain 1
1185	1	59	1	177	g1208772	4.00E-20	knesin light chain
1186	2	1606	2	4819	g338441	0	beta-spectrin
1186	2	1606	2	4819	g338440	0	spectrin Rouen (beta-220-218) mutant coding sequence
1186	2	1606	2	4819	g338330	0	muscle beta spectrin
1187	1	586	1084	2841	g7188794	0	myosin X
1187	1	586	1084	2841	g7108753	0	myosin X
1187	1	586	1084	2841	g9910111	0	myosin X
1188	2	626	2	1879	g13477151	0	Unknown (protein for MGC:12692)
1188	2	626	2	1879	g2804273	0	alpha actinin 4
1188	2	626	2	1879	g3157976	0	alpha actinin
1189	1	646	1	1938	g15212240	0	knesin superfamily protein 1B
1189	1	646	1	1938	g407339	0	Krl1b



TABLE 7

SEQ ID NO.	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1189	1	646	1	1938	g7959155	0	KIAA1448 protein
1190	1	208	442	1065	g10436084	1.00E-102	unnamed protein product
1192	1	159	1126	1602	g790202	2.00E-34	skeletal alpha actin
1192	1	189	1126	1602	g64527	2.00E-34	sarcomeric actin
1192	1	159	1126	1602	g63029	2.00E-34	alpha-actin
1193	1	205	112	726	g13506797	1.00E-105	myosin-VIb
1193	1	205	112	726	g9944235	4.00E-80	myosin VIIA
1193	1	205	112	726	g9944237	4.00E-80	myosin VIIA
1194	1	1240	1645	5364	g1147783	0	myosin-Xb
1194	1	1240	1645	5364	g6002741	0	unconventional myosin 9bc
1194	1	1240	1645	5364	g639999	0	myosin heavy chain
1195	1	99	295	591	g487906	3.00E-26	VMCH
1195	1	99	295	591	g4567054	1.00E-24	fertilization envelope outer layer protein
1195	1	99	295	591	g7332240	9.00E-13	contains similarity to Cyprinus carpio fertilization envelope outer layer protein (G8:AF123591) and Gallus gallus vitelline membrane outer layer protein 1 VMOH (G8:D26093)
1196	1	269	106	912	g1212917	1.00E-140	axonal transporter of synaptic vesicles
1196	1	269	106	912	g976235	1.00E-139	kinesin family protein KIF1a
1196	1	269	106	912	g11229634	1.00E-120	unnamed protein product
1197	1	205	604	1218	g9650954	7.00E-84	beta-1,6-N-acetylglucosaminyltransferase B
1197	1	205	604	1218	g12860327	1.00E-64	data source:SPTR, source key:p97402, evidence:ISS-putative-similar to N-ACETYLACTOSAMINIDE BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.150) (N-ACETYLGLUCOSAMINYLTRANSFERASE) (I-BRANCHING ENZYME) (GNT) (LARGE ANTIGEN-FORMING BETA-1,6-N-ACETYLGLUCOSAMINYLTRANSFERASE)
1197	1	205	604	1218	g9650956	4.00E-61	beta-1,6-N-acetylglucosaminyltransferase A
1198	2	321	2	964	g2293871	1.00E-155	RECEPTOR GR33 DE RAT
1198	2	321	2	964	g1526556	1.00E-155	syntaxin 1B
1198	2	321	2	964	g15072437	1.00E-155	syntaxin 1B2
1201	3	251	3	755	g13810306	1.00E-140	transmembrane protein 7

TABLE 7

SEQ ID NO.	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1201	3	251	3	755	g18250724	2.00E-66	transmembrane protein 7
1201	3	251	3	755	g15341942	2.00E-41	28kD interferon responsive protein
1202	1	339	343	1359	g7777776	2.00E-27	apical endosomal glycoprotein
1202	1	339	343	1359	g7110575	2.00E-21	receptor protein tyrosine kinase ALK splice variant A
1202	1	339	343	1359	g7302901	2.00E-21	Alk gene product
1204	1	158	1	474	g396170	4.00E-59	CMRF-35 antigen
1204	1	158	1	474	g14495324	4.00E-59	CMRF35A
1204	1	158	1	474	g18490143	4.00E-59	CMRF35 leukocyte immunoglobulin-like receptor
1205	3	405	1521	2735	g17028334	0	clathrin-associated protein AP47
1205	3	405	1521	2735	g13491974	0	clathrin-associated protein AP47
1205	3	405	1521	2735	g7406853	0	clathrin-associated adaptor medium chain mu 1A
1206	3	97	651	941	g10434441	3.00E-22	unnamed protein product
1206	3	97	651	941	g7020440	2.00E-21	unnamed protein product
1206	3	97	651	941	g1872200	2.00E-19	alternatively spliced product using exon 13A
1207	1	220	184	843	g7708438	1.00E-110	dj885A10.1 (similar to cerebellin precursor)
1207	1	220	184	843	g5702371	2.00E-72	precerebellin-1
1207	1	220	184	843	g180251	4.00E-72	precerebellin
1208	1	182	1	546	g15012026	5.00E-91	Similar to hypothetical protein FL20580
1208	1	182	1	546	g7020783	5.00E-91	unnamed protein product
1208	1	182	1	546	g17512533	5.00E-87	RIKEN cDNA 0610037L13 gene
1209	3	231	183	875	g17939582	1.00E-130	Unknown (protein for MSC:13042)
1209	3	231	183	875	g14042242	1.00E-129	unnamed protein product
1209	3	231	183	875	g12851507	1.00E-115	data source:SPTR, source key:G9Y3Q3, evidence:ISS-homolog to P248
1210	2	272	1262	2077	g179371	1.00E-140	PROTEIN PRECURSOR (INTEGRAL TYPE I PROTEIN)-putative
1210	2	272	1262	2077	g12309968	1.00E-140	bcl-2 protein
1210	2	272	1262	2077	g288448	1.00E-140	Human BCL-2
1211	1	135	235	639	g12803531	8.00E-70	bcl2-Ig fusion gene
1211	1	135	235	639	g473947	3.00E-69	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
1211	1	135	235	639	g262377	2.00E-68	similar to Canis oligosaccharyltransferase 48 kDa subunit (M98392).
1211	1	135	235	639	g262377	2.00E-68	oligosaccharyltransferase
1212	1	240	67	786	g18490143	9.00E-31	CMRF35 leukocyte immunoglobulin-like receptor

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1212	1	240	67	786	g14495324	9.00E-31	CMRF35A
1212	1	240	67	786	g396170	9.00E-31	CMRF-35 antigen
1213	2	734	2	2203	g439296	0	gap
1213	2	734	2	2203	g7301872	1.00E-35	CG7896 gene product
1213	2	734	2	2203	g16184821	1.00E-35	LD30178p
1214	3	115	69	413	g190234	1.00E-32	acidic ribosomal phosphoprotein (P1)
1214	3	115	69	413	g17932966	1.00E-32	ribosomal protein P1
1214	3	115	69	413	g14043204	1.00E-32	ribosomal protein, large, P1
1215	3	203	3	611	g206736	1.00E-104	ribosomal protein L7
1215	3	203	3	611	g200785	1.00E-101	ribosomal protein L7
1215	3	203	3	611	g12856147	1.00E-101	data source:MGD, source key:MG198073, evidence:ISS-putative-ribosomal protein L7
1217	2	177	2	532	g338447	2.00E-74	RPS16
1217	2	177	2	532	g17932976	2.00E-74	ribosomal protein S16
1217	2	177	2	532	g14044116	2.00E-74	ribosomal protein S16
1218	2	167	2	502	g57698	2.00E-95	ribosomal protein L3
1218	2	167	2	502	g16307136	2.00E-95	ribosomal protein L3
1218	2	167	2	502	g7159730	3.00E-95	ribosomal protein L3
1219	3	117	210	560	g550015	6.00E-40	ribosomal protein L21
1219	3	117	210	560	g17932946	6.00E-40	ribosomal protein L21
1219	3	117	210	560	g13960128	6.00E-40	Unknown (protein for MGC:4136)
1220	1	130	58	447	g292443	9.00E-63	ribosomal protein S20
1220	1	130	58	447	g17932978	9.00E-63	ribosomal protein S20
1220	1	130	58	447	g15030141	9.00E-63	Similar to ribosomal protein S20
1221	2	118	83	436	g414349	8.00E-49	ribosomal protein
1221	2	118	83	436	g15294057	8.00E-49	40S ribosomal protein S23
1221	2	118	83	436	g12851192	8.00E-49	data source:MGD, source key:MG1913725, evidence:ISS-putative-ribosomal protein S23
1222	3	153	207	665	g57111	1.00E-22	ribosomal protein L22
1222	3	153	207	665	g34199	1.00E-22	putative ribosomal protein (AA 1-184)
1222	3	153	207	665	g202990	1.00E-22	amino acid starvation-induced protein

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability	Score	Annotation
1223	1	78	256	489	g15293931	5.00E-10		ribosomal protein L31
1223	1	78	256	489	g361130	2.00E-09		ribosomal protein L31 (AA 1-125)
1223	1	78	256	489	g17932954	2.00E-09		ribosomal protein L31
1224	2	190	356	925	g36647	2.00E-90		ribosomal protein L7a
1224	2	190	356	925	g35512	2.00E-90		PLA-X polypeptide
1224	2	190	356	925	g34203	2.00E-90		L7a protein
1225	3	163	12	500	g643074	6.00E-76		putative 40S ribosomal protein s12
1225	3	163	12	500	g6716785	2.00E-75		40S ribosomal protein S23
1225	3	163	12	500	g7413571	9.00E-75		putative protein
1226	2	229	2	688	g15680000	1.00E-127		Similar to ribosomal protein L10
1226	2	229	2	688	g190814	1.00E-121		Wilm's tumor-related protein
1226	2	229	2	688	g189266	1.00E-121		may code for Wilm's tumor-related protein
1227	1	196	16	603	g4165247	1.00E-107		CU69E11.3 (Yeast YPR037W and worm C02C2.6 predicted proteins LIKE)
1227	1	196	16	603	g4678751	1.00E-107		hypothetical protein
1227	1	196	16	603	g12805269	1.00E-102		Similar to ribosomal protein L34 pseudogene 1
1228	3	129	219	605	g361132	8.00E-30		rpl32 (aa 1-135)
1228	3	129	219	605	g200781	8.00E-30		ribosomal protein L32-3A
1228	3	129	219	605	g17932956	8.00E-30		ribosomal protein L32
1230	1	115	337	681	g190234	1.00E-32		acidic ribosomal phosphoprotein (P1)
1230	1	115	337	681	g17932956	1.00E-32		ribosomal protein P1
1230	1	115	337	681	g14043204	1.00E-32		ribosomal protein, large, P1
1231	2	155	674	1138	g550015	1.00E-39		ribosomal protein L21
1231	2	155	674	1138	g17932946	1.00E-39		ribosomal protein L21
1231	2	155	674	1138	g13960128	1.00E-39		Unknown (protein for MGC:4136)
1232	1	152	1	456	g13489168	6.00E-77		60S ribosomal protein L17
1232	1	152	1	456	g13430182	4.00E-76		ribosomal protein L17
1232	1	152	1	456	g7547099	2.00E-75		ribosomal protein L17, putative
1233	1	68	1	204	g550025	1.00E-28		ribosomal protein S10
1233	1	68	1	204	g18043938	1.00E-28		RIKEN cDNA 2210402A09 gene
1233	1	68	1	204	g13477115	1.00E-28		ribosomal protein S10
1234	2	57	125	295	g361130	2.00E-19		ribosomal protein L31 (AA 1-125)

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1234	2	57	125	295	g17932954	2.00E-19	ribosomal protein L31
1234	2	57	125	295	g16878295	2.00E-19	ribosomal protein L31
1235	1	99	529	825	g854179	1.00E-11	ribosomal protein S3a
1235	1	99	529	825	g5441551	1.00E-11	ribosomal protein
1235	1	99	529	825	g495140	1.00E-11	rat ribosomal protein S3a
1237	2	150	95	544	g15214837	5.00E-75	Unknown (protein for MGC:13410)
1237	2	150	95	544	g11640588	5.00E-75	MSIP040
1237	2	150	95	544	g7022681	1.00E-74	unnamed protein product
1238	1	115	334	678	g190234	1.00E-32	acidic ribosomal phosphoprotein (P1)
1238	1	115	334	678	g17932966	1.00E-32	ribosomal protein P1
1238	1	115	334	678	g14043204	1.00E-32	ribosomal protein, large, P1
1243	3	248	270	1013	g4165247	1.00E-136	cl69E11.3 (Yeast YPR037W and worm C02C2.6 predicted proteins LKE)
1243	3	248	270	1013	g4678751	1.00E-136	hypothetical protein
1243	3	248	270	1013	g12805269	1.00E-132	Similar to ribosomal protein L34 pseudogene 1
1244	2	87	1145	1405	g4379066	3.00E-24	cl240C2.2 (Core histone H2A/H2B/H3/H4)
1244	2	87	1145	1405	g6706208	3.00E-24	cl839M11.1 (histone H2B.2)
1244	2	87	1145	1405	g4379067	6.00E-18	cl240C2.1 (Core histone H2A/H2B/H3/H4)
1245	1	178	112	645	g3242649	2.00E-05	alpha 1 type I collagen
1245	1	178	112	645	g156432	7.00E-05	collagen (rol-6)
1245	1	178	112	645	g3879235	7.00E-05	contains similarity to P1am domain: PF01391 (Collagen triple helix repeat (20 copies)). Score=70.9, E-value=8.7e-18, N=2; PF01484 (Nematode cuticle collagen N-terminal domain). Score=62.7, E-value=2.6e-15, N=1--cDNA EST cm10c4 comes from this gene--cDNA EST EMBL:M88874 comes from this gene--cDNA EST yk255e2.3 comes from this gene--cDNA EST yk255e2.5 comes from this gene
1246	1	529	1	1587	g178281	1.00E-31	AHNK nucleoprotein
1246	1	529	1	1587	g50675	2.00E-30	desmoyokin
1246	1	529	1	1587	g897824	2.00E-29	AHNK gene product
1247	2	62	35	220	g4454682	6.00E-07	NADH-ubiquinone oxidoreductase subunit B9 homolog
1247	2	62	35	220	g18490215	6.00E-07	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3 (9kD, B9)
1247	2	62	35	220	g4164444	6.00E-07	NADH:ubiquinone oxidoreductase B9 subunit

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1248	1	444	64	1395	g189306	1.00E-144	nucleolin
1248	1	444	64	1395	g5929884	1.00E-123	nucleolin-related protein NRP
1248	1	444	64	1395	g205792	1.00E-108	nucleolin
1250	2	429	131	1417	g14286274	1.00E-157	Similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
1250	2	429	131	1417	g14250567	1.00E-157	Similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
1250	2	429	131	1417	g14043791	1.00E-157	Similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5
1251	2	237	68	778	g8099669	7.00E-24	golgin-like protein
1251	2	237	68	778	g8101071	1.00E-23	golgin-like protein
1251	2	237	68	778	g7644350	2.00E-15	golgi matrix protein GM130
1252	3	1000	3	3002	g7678804	0	mitochondrial isoleucine tRNA synthetase
1252	3	1000	3	3002	g7022287	0	unnamed protein product
1252	3	1000	3	3002	g16307358	0	Unknown (protein for MGC:17464)
1253	3	532	1278	2873	g2827207	0	general transcription factor 2-I
1253	3	532	1278	2873	g2827205	0	general transcription factor 2-I
1253	3	532	1278	2873	g2827203	0	general transcription factor 2-I
1254	2	141	2	424	g563810	6.00E-64	cysteine-rich protein
1254	2	141	2	424	g181071	3.00E-63	cysteine-rich protein
1254	2	141	2	424	g181064	3.00E-63	cysteine-rich protein
1255	3	330	174	1163	g10803415	1.00E-170	Golgi protein
1255	3	330	174	1163	g15082415	1.00E-170	Golgi phosphoprotein 3
1255	3	330	174	1163	g12853929	1.00E-168	data source:MGD, source key:MGI:1913879, evidence:ISS-golgi phosphoprotein 3--putative
1256	2	541	2	1624	g3127193	0	kidney-specific protein
1256	2	541	2	1624	g16553412	0	unnamed protein product
1256	2	541	2	1624	g5070357	0	xenobiotic/medium-chain fatty acid:CoA ligase form XL-III
1257	2	153	203	661	g18028950	2.00E-36	beta glucuronidase
1257	2	153	203	661	g15559560	2.00E-34	Similar to glucuronidase, beta
1257	2	153	203	661	g14346709	2.00E-34	unnamed protein product

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability	Score	Annotation
1258	3	107	180	500	g3116436	7.00E-50	7.00E-50	short chain L-3-hydroxyacyl-CoA dehydrogenase
1258	3	107	180	500	g3116434	7.00E-50	7.00E-50	short chain L-3-hydroxyacyl-CoA dehydrogenase
1258	3	107	180	500	g2558754	7.00E-50	7.00E-50	amyloid beta-peptide binding protein
1259	1	134	1	402	g7022046	5.00E-76	5.00E-76	unnamed protein product
1259	1	134	1	402	g8671586	5.00E-76	5.00E-76	ataxin 2-binding protein
1259	1	134	1	402	g8671588	1.00E-75	1.00E-75	ataxin 2-binding protein
1261	1	381	1444	2586	g8101071	2.00E-53	2.00E-53	golgin-like protein
1261	1	381	1444	2586	g8099669	2.00E-53	2.00E-53	golgin-like protein
1261	1	381	1444	2586	g7211438	2.00E-32	2.00E-32	golgin-67
1263	3	230	1206	1895	g5102812	1.00E-06	1.00E-06	putative serine/threonine protein kinase
1263	3	230	1206	1895	g2760483	2.00E-06	2.00E-06	SH3-domain interacting protein
1263	3	230	1206	1895	g2906006	2.00E-06	2.00E-06	WASP interacting protein
1264	2	181	2729	3271	g4938296	1.00E-48	1.00E-48	cd64K7.3.1 (heterogenous nuclear ribonucleoprotein RALY or autoantigen p542, isoform 1)
1264	2	181	2729	3271	g13016655	1.00E-48	1.00E-48	cd64K7.3.2 (heterogenous nuclear ribonucleoprotein RALY or autoantigen p542, isoform 2)
1264	2	181	2729	3271	g6164674	1.00E-48	1.00E-48	heterogeneous nuclear ribonucleoprotein, alternate transcript
1265	1	272	466	1281	g16506178	1.00E-147	1.00E-147	mitochondrial solute carrier-like protein
1265	1	272	466	1281	g7578783	1.00E-129	1.00E-129	HT015 protein
1265	1	272	466	1281	g13926047	1.00E-111	1.00E-111	putative mitochondrial solute carrier splice variant
1266	3	263	654	1442	g14424773	1.00E-142	1.00E-142	MMS19 (MET18 S. cerevisiae)-like
1266	3	263	654	1442	g14029386	1.00E-142	1.00E-142	MMS19
1266	3	263	654	1442	g13938337	1.00E-142	1.00E-142	Similar to MMS19 (MET18 S. cerevisiae)-like
1269	1	393	664	1842	g8099669	2.00E-54	2.00E-54	golgin-like protein
1269	1	393	664	1842	g8101071	2.00E-54	2.00E-54	golgin-like protein
1269	1	393	664	1842	g6808611	1.00E-32	1.00E-32	88-kDa Golgi protein
1273	1	751	280	2532	g577625	0	0	holocarboxylase synthetase
1273	1	751	280	2532	g15823777	0	0	holocarboxylase synthetase
1273	1	751	280	2532	g6712196	0	0	holocarboxylase synthetase (blot)-
1276	2	140	179	598	g6841462	1.00E-54	1.00E-54	HSPC120
1276	2	140	179	598	g4680298	1.00E-54	1.00E-54	nuclear protein NOP5/NOP58

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1276	2	140	179	598	g9652082	1.00E-54	nucleolar protein 5
1277	3	257	12	782	g13540302	5.00E-62	nucleolar protein C7C
1277	3	257	12	782	g13561516	8.00E-62	nucleolar protein C7
1277	3	257	12	782	g13540300	1.00E-61	nucleolar protein C7B
1279	1	63	58	246	g10438620	4.00E-18	unnamed protein product
1279	1	63	58	246	g7020625	5.00E-17	unnamed protein product
1279	1	63	58	246	g18255512	8.00E-17	Unknown (protein for MGC:24986)
1281	3	584	216	1967	g2062698	0	butyrophilin
1281	3	584	216	1967	g16198347	0	butyrophilin, subfamily 3, member A3
1281	3	584	216	1967	g3336972	0	cd4921.1 (butyrophilin, subfamily 3, member A3 (BIF3))
1282	1	106	19	336	g560791	8.00E-23	calgizatin
1282	1	106	19	336	g2605598	8.00E-23	calcium binding protein
1282	1	106	19	336	g15680066	8.00E-23	Similar to S100 calcium-binding protein A11 (calgizatin)
1284	1	749	79	2325	g15341763	0	Unknown (protein for MGC:17103)
1284	1	749	79	2325	g1549241	0	SWI/SNF complex 170 KDa subunit
1284	1	749	79	2325	g1816635	0	SRG3
1285	2	385	2	1156	g220064	0	polyprotein precursor
1285	2	385	2	1156	g337760	0	cerebroside sulfate activator protein
1285	2	385	2	1156	g337767	0	cerebroside sulfate activator protein
1286	2	284	2	853	g10434110	1.00E-150	unnamed protein product
1286	2	284	2	853	g14042427	1.00E-149	unnamed protein product
1286	2	284	2	853	g13559174	1.00E-119	cd423822.2 (novel protein similar to C.elegans protein CE08529)
1287	3	541	54	1676	g18088181	0	karyopherin alpha 6 (importin alpha 7)
1287	3	541	54	1676	g3091280	0	importin alpha 7 subunit
1287	3	541	54	1676	g2507661	0	importin alpha S2
1288	2	188	341	904	g12232324	1.00E-80	hUPF3B
1288	2	188	341	904	g12620408	1.00E-80	UPF3X
1288	2	188	341	904	g12620406	1.00E-11	UPF3
1289	1	902	319	3024	g186541	0	Interstitial retinol-binding protein 3
1289	1	902	319	3024	g307074	0	IRBP precursor
1289	1	902	319	3024	g386835	0	Interstitial retinol-binding protein precursor



TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1290	2	166	707	1204	g7529575	3.00E-54	dl336M4.5 (cardiovascular heat shock protein)
1290	2	166	707	1204	g6580426	3.00E-54	heat shock protein
1290	2	166	707	1204	g13623439	3.00E-54	heat shock 27KD protein family, member 7 (cardiovascular)
1291	3	248	69	812	g1163174	1.00E-129	similar to yeast Sec6p, Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author
1291	3	248	69	812	g12226540	3.00E-89	unnamed protein product
1291	3	248	69	812	g12226542	3.00E-89	unnamed protein product
1295	3	117	54	404	g13359183	5.00E-26	KIAA1655 protein
1295	3	117	54	404	g3002527	5.00E-26	neuronal thread protein AD7c-NIP
1295	3	117	54	404	g10439739	1.00E-24	unnamed protein product
1296	2	272	821	1636	g1176422	1.00E-88	rhophilin
1296	2	272	821	1636	g12836344	2.00E-36	data source:SPTR, source key:S61085, evidence:ISS-putative-similar to GTP-RHO BINDING PROTEIN 1 (RHOPHILIN)
1296	2	272	821	1636	g14279409	3.00E-31	rhophilin-like protein
1298	1	108	202	525	g9280152	1.00E-11	unnamed protein product
1298	1	108	202	525	g10437569	3.00E-10	unnamed protein product
1298	1	108	202	525	g18027740	3.00E-10	unknown
1299	3	223	3	671	g15215290	1.00E-105	Similar to RIKEN cDNA 281040511 gene
1299	3	223	3	671	g17933108	1.00E-105	C18orf2
1299	3	223	3	671	g12805505	1.00E-104	Similar to CHMP1.5 protein
1300	3	146	3	440	g204859	1.00E-79	major alpha-hemoglobin
1300	3	146	3	440	g3367720	1.00E-78	alpha-2-globin chain
1300	3	146	3	440	g1304381	1.00E-78	hemoglobin alpha chain
1301	2	143	2	430	g3327142	3.00E-26	KIAA0664 protein
1301	2	143	2	430	g10434718	2.00E-22	unnamed protein product
1301	2	143	2	430	g7302977	5.00E-20	CG8443 gene product
1302	2	210	2	631	g1673433	1.00E-26	translocan-associated protein delta subunit precursor
1302	2	210	2	631	g15929882	1.00E-26	signal sequence receptor, delta (translocan-associated protein delta)
1302	2	210	2	631	g13097213	1.00E-26	signal sequence receptor, delta (translocan-associated protein delta)
1303	3	222	1359	2024	g28435	1.00E-93	apoferritin H chain

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1303	3	222	1359	2024	g762940	8.00E-86	apoferritin H subunit
1303	3	222	1359	2024	g507252	8.00E-86	ferritin heavy chain
1307	2	210	44	673	g9719420	2.00E-99	SNARE Vti1a protein
1307	2	210	44	673	g3213227	1.00E-97	putative v-SNARE Vti1a
1307	2	210	44	673	g18043878	1.00E-97	vesicle transport through interaction with t-SNAREs 1 homolog
1309	1	105	511	825	g2393894	7.00E-15	gag
1309	1	105	511	825	g61758	1.00E-14	reading frame (gag?)
1309	1	105	511	825	g263645	4.00E-12	matrix protein; MA
1311	3	211	1941	2573	g1731809	1.30E-88	c-myc binding protein
1311	3	211	1941	2573	g7209590	1.00E-82	ElG-1
1311	3	211	1941	2573	g13097219	6.00E-81	prefoldin 5
1312	2	120	2	361	g914925	3.00E-58	DAD-1
1312	2	120	2	361	g3063921	3.00E-58	DAD-1
1312	2	120	2	361	g3063891	3.00E-58	DAD-1
1313	3	133	21	419	g13097603	2.00E-07	Unknown (protein for MGC:10764)
1313	3	133	21	419	g10436424	5.00E-06	unnamed protein product
1313	3	133	21	419	g16588389	1.00E-04	B lymphocyte activation-related protein BC-1514
1314	2	397	458	1648	g3550080	0	formin binding protein 21
1314	2	397	458	1648	g3550077	1.00E-162	formin binding protein 21
1314	2	397	458	1648	g1255023	4.00E-30	FBP 21
1315	2	298	530	1423	g14250095	1.00E-134	uncharacterized hematopoietic stem/progenitor cells protein MDS032
1315	2	298	530	1423	g14250095	1.00E-134	uncharacterized hematopoietic stem/progenitor cells protein MDS032
1315	2	298	530	1423	g1689011	1.00E-134	data source:SPTR, source key:G9NZ43, evidence:ISS-homolog to
1315	2	298	530	1423	g12849269	1.00E-115	UNCHARACTERIZED HEMATOPOIETIC STEM/PROGENITOR CELLS PROTEIN
1316	2	167	572	1072	g16877739	1.00E-80	MDS032-putative
1316	2	167	572	1072	g6652820	1.00E-80	cell division protein FtsJ
1316	2	167	572	1072	g12856472	8.00E-64	cell division protein FtsJ
1317	1	230	262	951	g18181974	5.00E-88	data source:SPTR, source key:G9UJ43, evidence:ISS-homolog to CELL
1317	1	230	262	951	g18157374	3.00E-85	DIVISION PROTEIN FtsJ-putative
							Jun dimerization protein 2
							Jun dimerization protein 2

TABLE 7

SEQ ID NO.	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1317	1	230	262	951	g18043174	3.00E-85	Jun dimerization protein 2
1319	2	287	146	1006	g14042913	1.00E-120	unnamed protein product
1319	2	287	146	1006	g12855460	1.00E-99	data source:SPTR, source key:QW2P9, evidence:ISS--putative-related to CG10440 PROTEIN
1319	2	287	146	1006	g18490453	1.00E-99	RIKEN cDNA 4933402K10 gene
1320	2	174	1529	2050	g12005511	3.00E-83	HT027
1320	2	174	1529	2050	g10436844	3.00E-78	unnamed protein product
1320	2	174	1529	2050	g11036973	2.00E-45	HSP22-like protein interacting protein 17
1322	3	136	126	533	g1806040	5.00E-39	adipophilin
1322	3	136	126	533	g13477307	5.00E-39	adipose differentiation-related protein
1322	3	136	126	533	g10185012	5.00E-39	unnamed protein product
1323	1	646	1	1938	g6539606	0	metastasis suppressor protein
1323	1	646	1	1938	g12803855	2.00E-99	Unknown (protein for IMAGE3616574)
1323	1	646	1	1938	g18445135	9.00E-88	Unknown (protein for MGC:26697)
1325	1	59	562	738	g10433120	4.00E-16	unnamed protein product
1325	1	59	562	738	g15214765	3.00E-15	Similar to hypothetical protein
1325	1	59	562	738	g11493463	2.00E-14	PRO2852
1326	1	46	193	330	g6690248	3.00E-09	PRO0657
1326	1	46	193	330	g16505680	6.00E-09	unnamed protein product
1326	1	46	193	330	g5042226	4.00E-08	E1 fusion protein
1327	2	575	41	1765	g310100	0	developmentally regulated protein
1327	2	575	41	1765	g6807690	2.00E-78	hypothetical protein
1327	2	575	41	1765	g6382026	2.00E-78	KIAA1253 protein
1328	2	353	131	1189	g4587965	1.00E-171	JAW1-related protein MRV1A long isoform
1328	2	353	131	1189	g4587967	1.00E-171	JAW1-related protein MRV1B short isoform
1328	2	353	131	1189	g7341099	1.00E-159	IP3 receptor associated cGMP kinase substrate B
1329	1	113	1	339	g4689203	7.00E-10	gila maturation factor gamma
1329	1	113	1	339	g3046869	7.00E-10	gila maturation factor gamma
1329	1	113	1	339	g3329382	7.00E-10	gila maturation factor beta
1331	2	173	359	877	g9106252	4.00E-11	1,4-beta-cellobiosidase
1331	2	173	359	877	g3916718	8.00E-10	serichn-1

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1331	2	173	359	877	g12850969	7.00E-09	DNA segment, KIST 6--data source:MGD, source key:MG1:108435, evidence:SS-putative
1332	1	366	67	1164	g4165083	0	growth factor independence-18
1332	1	366	67	1164	g3080757	1.00E-173	growth factor independence-18
1332	1	366	67	1164	g2331056	1.00E-133	zinc finger protein
1333	2	492	638	2113	g9852976	0	NUMB isoform 4
1333	2	492	638	2113	g4102705	0	NUMB protein
1333	2	492	638	2113	g4050088	0	ST1
1334	2	1653	56	5014	g189165	0	GAP-related protein
1334	2	1653	56	5014	g292354	0	neurofibromin
1334	2	1653	56	5014	g1841314	0	neurofibromin
1335	2	153	44	502	g6531681	3.00E-80	cell division cycle 42
1335	2	153	44	502	g6012993	3.00E-80	hypothetical protein
1335	2	153	44	502	g6012991	3.00E-80	hypothetical protein
1337	3	420	3	1262	g6683815	0	MLL septin-like fusion protein MSF-B
1337	3	420	3	1262	g5106557	0	MLL septin-like fusion protein
1337	3	420	3	1262	g4589626	0	KIAA0991 protein
1339	2	373	62	1180	g14042419	0	unnamed protein product
1339	2	373	62	1180	g4585374	4.00E-49	Wnt inhibitory factor-1
1339	2	373	62	1180	g211718	3.00E-47	cytotactin precursor
1340	1	169	1	507	g29509	1.00E-94	BTG1
1340	1	169	1	507	g293306	1.00E-94	B-cell translocation gene-1 protein
1340	1	169	1	507	g17390724	1.00E-94	B-cell translocation gene 1, anti-proliferative
1342	3	90	3	272	g12652861	8.00E-12	thymosin, beta, identified in neuroblastoma cells
1342	3	90	3	272	g11877205	8.00E-12	cd77O19.1 (NB thymosin beta)
1342	3	90	3	272	g1841340	8.00E-12	NB thymosin beta
1345	1	103	538	846	g13310191	4.00E-28	recombinant envelope protein
1345	1	103	538	846	g6760401	6.00E-26	syncytin precursor
1345	1	103	538	846	g4773880	6.00E-26	envelope protein precursor
1347	2	473	2	1420	g18157547	0	pecanex-like 3
1347	2	473	2	1420	g13171105	1.00E-142	pecanex

TABLE 7

SEQ ID NO:	Frame	Length	Start	Stop	GI Number	Probability Score	Annotation
1347	2	473	2	1420	g3892331	1.00E-142	KIAA0805 protein

TABLE 8

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) <i>J. Mol. Biol.</i> 215:403-410; Altschul, S.F. et al. (1997) <i>Nucleic Acids Res.</i> 25:3389-3402.	ESTs: Probability value= 1.0E-8 or less; Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises at least five functions: fasta, ifasta, fastx, tfastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) <i>Proc. Natl. Acad. Sci. USA</i> 85:2444-2448; Pearson, W.R. (1990) <i>Methods Enzymol.</i> 183:63-98; and Smith, T.F. and M.S. Waterman (1981) <i>Adv. Appl. Math.</i> 2:482-489.	ESTs: fasta E value=1.0E-6; Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less; Full Length sequences: fastx score=100 or greater
BLIMPS	A BLOCKS IMPROVED Searcher that matches a sequence against those in BLOCKS, PRINTS, DOMO, PRODOM, and PFAM databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff (1991) <i>Nucleic Acids Res.</i> 19:6565-6572; Henikoff, J.G. and S. Henikoff (1996) <i>Methods Enzymol.</i> 266:88-105; and Altmann, T.K. et al. (1997) <i>J. Chem. Inf. Comput. Sci.</i> 37:417-424.	Probability value= 1.0E-3 or less
HMMER	An algorithm for searching a query sequence against hidden Markov model (HMM)-based databases of protein family consensus sequences, such as PFAM.	Krogh, A. et al. (1994) <i>J. Mol. Biol.</i> 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) <i>Nucleic Acids Res.</i> 26:320-322; Durbin, R. et al. (1998) <i>Our World View, in a Nussliell, Cambridge Univ. Press</i> , pp. 1-350.	PFAM hits: Probability value= 1.0E-3 or less; Signal peptide hits: Score= 0 or greater
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribkov, M. et al. (1988) <i>CABIOS</i> 4:61-66; Gribkov, M. et al. (1989) <i>Methods Enzymol.</i> 183:146-159; Bairoch, A. et al. (1997) <i>Nucleic Acids Res.</i> 25:217-221.	Normalized quality score>GCG-specified "HIGH" value for that particular Prosite motif. Generally, score=1.4-2.1.

TABLE 8

Program	Description	Reference	Parameter Threshold
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) <i>Genome Res.</i> 8:175-185; Ewing, B. and P. Green (1998) <i>Genome Res.</i> 8:186-194.	
Phrap	A Phits Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M.S. Waterman (1981) <i>Adv. Appl. Math.</i> 2:482-489; Smith, T.F. and M.S. Waterman (1981) <i>J. Mol. Biol.</i> 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies.	Gordon, D. et al. (1998) <i>Genome Res.</i> 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) <i>Protein Engineering</i> 10:1-6; Claverie, J.M. and S. Audic (1997) <i>CABIOS</i> 12:431-439.	Score=3.5 or greater
TMAP	A program that uses weight matrices to delineate transmembrane segments on protein sequences and determine orientation.	Persson, B. and P. Argos (1994) <i>J. Mol. Biol.</i> 237:182-192; Persson, B. and P. Argos (1996) <i>Protein Sci.</i> 5:363-371.	
TMHMMER	A program that uses a hidden Markov model (HMM) to delineate transmembrane segments on protein sequences and determine orientation.	Sonnhammer, E.L. et al. (1998) <i>Proc. Sixth Intl. Conf. On Intelligent Systems for Mol. Biol., Glasgow et al., eds., The Am. Assoc. for Artificial Intelligence (AAAI) Press, Menlo Park, CA, and MIT Press, Cambridge, MA, pp. 175-182.</i>	
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch, A. et al. (1997) <i>Nucleic Acids Res.</i> 25:217-221; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

## CLAIMS

## What is claimed is:

1. An isolated polynucleotide selected from the group consisting of:
  - a) a polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670,
  - b) a polynucleotide comprising a naturally occurring polynucleotide sequence at least 90% identical to a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670,
  - c) a polynucleotide complementary to a polynucleotide of a),
  - d) a polynucleotide complementary to a polynucleotide of b), and
  - e) an RNA equivalent of a)-d).
2. An isolated polynucleotide of claim 1, comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:1-670.
3. An isolated polynucleotide comprising at least 60 contiguous nucleotides of a polynucleotide of claim 1.
4. A composition for the detection of expression of diagnostic and therapeutic polynucleotides comprising at least one of the polynucleotides of claim 1 and a detectable label.
5. A method for detecting a target polynucleotide in a sample, said target polynucleotide having a sequence of a polynucleotide of claim 1, the method comprising:
  - a) amplifying said target polynucleotide or fragment thereof using polymerase chain reaction amplification, and
  - b) detecting the presence or absence of said amplified target polynucleotide or fragment thereof, and, optionally, if present, the amount thereof.
6. A method for detecting a target polynucleotide in a sample, said target polynucleotide comprising a sequence of a polynucleotide of claim 1, the method comprising:
  - a) hybridizing the sample with a probe comprising at least 20 contiguous nucleotides comprising a sequence complementary to said target polynucleotide in the sample, and which probe specifically hybridizes to said target polynucleotide, under conditions whereby a hybridization complex is formed between said probe and said target polynucleotide or fragments thereof, and
  - b) detecting the presence or absence of said hybridization complex, and, optionally, if



present, the amount thereof.

7. A method of claim 5, wherein the probe comprises at least 30 contiguous nucleotides.
- 5 8. A method of claim 5, wherein the probe comprises at least 60 contiguous nucleotides.
9. A recombinant polynucleotide comprising a promoter sequence operably linked to a polynucleotide of claim 1.
- 10 10. A cell transformed with a recombinant polynucleotide of claim 9.
11. A transgenic organism comprising a recombinant polynucleotide of claim 9.
12. A method for producing a diagnostic and therapeutic polypeptide, the method  
15 comprising:
  - a) culturing a cell under conditions suitable for expression of the diagnostic and therapeutic polypeptide, wherein said cell is transformed with a recombinant polynucleotide of claim 9, and
  - b) recovering the diagnostic and therapeutic polypeptide so expressed.
- 20 13. A purified diagnostic and therapeutic polypeptide (DTHP) encoded by at least one of the polynucleotides of claim 2.
14. An isolated antibody which specifically binds to a diagnostic and therapeutic polypeptide of claim 13.
- 25 15. A method of identifying a test compound which specifically binds to the diagnostic and therapeutic polypeptide of claim 13, the method comprising the steps of:
  - a) providing a test compound;
  - b) combining the diagnostic and therapeutic polypeptide with the test compound for a  
30 sufficient time and under suitable conditions for binding; and
  - c) detecting binding of the diagnostic and therapeutic polypeptide to the test compound, thereby identifying the test compound which specifically binds the diagnostic and therapeutic polypeptide.
- 35 16. A microarray wherein at least one element of the microarray is a polynucleotide of claim 3.

17. A method for generating a transcript image of a sample which contains polynucleotides, the method comprising the steps of:

- a) labeling the polynucleotides of the sample,
- b) contacting the elements of the microarray of claim 16 with the labeled polynucleotides of the sample under conditions suitable for the formation of a hybridization complex, and
- c) quantifying the expression of the polynucleotides in the sample.

18. A method for screening a compound for effectiveness in altering expression of a target polynucleotide, wherein said target polynucleotide comprises a polynucleotide sequence of claim 1, the method comprising:

- a) exposing a sample comprising the target polynucleotide to a compound, under conditions suitable for the expression of the target polynucleotide,
- b) detecting altered expression of the target polynucleotide, and
- c) comparing the expression of the target polynucleotide in the presence of varying amounts of the compound and in the absence of the compound.

19. A method for assessing toxicity of a test compound, said method comprising:

- a) treating a biological sample containing nucleic acids with the test compound;
- b) hybridizing the nucleic acids of the treated biological sample with a probe comprising at least 20 contiguous nucleotides of a polynucleotide of claim 1 under conditions whereby a specific hybridization complex is formed between said probe and a target polynucleotide in the biological sample, said target polynucleotide comprising a polynucleotide sequence of a polynucleotide of claim 1 or fragment thereof;
- c) quantifying the amount of hybridization complex; and
- d) comparing the amount of hybridization complex in the treated biological sample with the amount of hybridization complex in an untreated biological sample, wherein a difference in the amount of hybridization complex in the treated biological sample is indicative of toxicity of the test compound.

20. An array comprising different nucleotide molecules affixed in distinct physical locations on a solid substrate, wherein at least one of said nucleotide molecules comprises a first oligonucleotide or polynucleotide sequence specifically hybridizable with at least 30 contiguous nucleotides of a target polynucleotide, said target polynucleotide having a sequence of claim 1.

21. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 30 contiguous nucleotides of said target polynucleotide.

22. An array of claim 20, wherein said first oligonucleotide or polynucleotide sequence is completely complementary to at least 60 contiguous nucleotides of said target polynucleotide

23. An array of claim 20, which is a microarray.

24. An array of claim 20, further comprising said target polynucleotide hybridized to said first oligonucleotide or polynucleotide.

25. An array of claim 20, wherein a linker joins at least one of said nucleotide molecules to said solid substrate.

26. An array of claim 20, wherein each distinct physical location on the substrate contains multiple nucleotide molecules having the same sequence, and each distinct physical location on the substrate contains nucleotide molecules having a sequence which differs from the sequence of nucleotide molecules at another physical location on the substrate.

27. An isolated polypeptide selected from the group consisting of:

a) a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347,

b) a polypeptide comprising a naturally occurring amino acid sequence at least 90% identical to an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347,

c) a biologically active fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347, and

d) an immunogenic fragment of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:671-1347.

28. An isolated polypeptide of claim 27, comprising a polypeptide sequence selected from the group consisting of SEQ ID NO:671-1347.